

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 12, 2004, 13:26:25 ; Search time 21.2583 Seconds

(without alignments)
3040.721 Million cell updates/sec

Title: US-09-900-766-1

Perfect score: 3522

Sequence: 1 EVQLQQSGPDLVKPCASVKI.....EATHKTSPIVKSFNENES 672

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 segs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 78:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1107	31.4	257	2 A38179	enterotoxin E prec
2	1036.5	29.4	225	2 S37484	Ig kappa chain - m
3	973	27.6	446	2 S40295	Ig gamma-2a chain
4	952	27.0	220	2 A31790	Ig kappa chain v r
5	951.5	27.0	469	2 S37483	Ig gamma-2a chain
6	948	26.9	257	2 A28664	enterotoxin A prec
7	931	26.4	548	2 S38864	Ig epsilon chain C
8	929	26.4	246	2 S38950	Ig gamma chain - m
9	926	26.3	214	2 S68212	Ig kappa chain (Ma
10	918	26.1	260	2 C89984	enterotoxin P (imp
11	914.5	26.0	219	2 S20028	Ig kappa chain - m
12	914	26.0	214	2 PC4202	monoclonal antibody
13	910.5	25.9	219	2 PC4203	Ig kappa chain (mo
14	903.5	25.7	219	2 S16112	Ig kappa chain v r
15	900.5	25.6	474	1 G2MS11	Ig gamma-2b chain
16	896.5	25.5	219	2 S38865	Ig kappa chain - m
17	892	25.3	218	2 JC5810	monoclonal antibody
18	890.5	25.3	221	2 S49220	Ig gamma-1 chain -
19	886.5	25.2	217	2 S42772	Ig kappa chain - m
20	880	25.0	218	2 S68241	Ig kappa chain v r
21	878.5	24.9	235	2 S25058	Ig kappa chain - m
22	876.5	24.9	225	2 JL00029	Ig kappa chain pre
23	875	24.8	234	2 S14237	Ig kappa chain pre
24	874	24.8	234	2 S01320	Ig kappa chain pre
25	873	24.8	475	2 S01321	Ig kappa chain pre
26	870	24.7	444	2 PC4436	monoclonal antibody
27	857	24.3	210	2 A56169	Ig kappa chain v r
28	853	24.2	240	2 S06084	Ig kappa chain pre
29	808	22.9	220	2 S68211	Ig heavy chain (Ma

30	737.5	20.9	213	2 S68213	Ig heavy chain (Ma
31	715	20.3	231	2 PC4155	Ig gamma-2b chain
32	702.5	19.9	215	2 JE0244	Ig kappa chain NIG
33	700.5	19.9	549	2 S04845	Ig heavy chain pre
34	695.5	19.7	215	2 JE0242	Ig kappa chain NIG
35	683.5	19.4	254	2 B31790	Ig heavy chain v r
36	679.5	19.3	215	2 JE0243	Ig kappa chain NIG
37	675	19.2	230	2 S33161	Ig kappa chain - s
38	673.5	19.1	470	2 S22080	Ig heavy chain pre
39	663.5	18.8	137	2 S29593	Ig kappa chain (WM
40	661.5	18.8	241	2 S69131	Ig heavy chain (DO
41	659.5	18.7	215	2 A23746	Ig kappa chain V-I
42	658	18.7	216	2 JE0241	Ig kappa chain Am3
43	619.5	17.6	472	2 S31459	Ig gamma-1 chain -
44	611	17.3	220	2 A49444	Ig gamma-1 heavy c
45	611	17.3	258	2 A33953	enterotoxin D prec
46	595.5	16.9	627	2 S14683	Ig mu chain precu
47	591	16.8	178	2 PT0219	Ig kappa chain V-C
48	570.5	16.2	229	2 A20969	Ig kappa chain pre
49	562	16.0	178	2 S29594	Ig gamma chain (WM
50	561	15.9	126	2 I54782	gene Pvt-1a/Ig-Ck
51	560.5	15.9	151	2 PL0011	Ig heavy chain pre
52	557	15.8	324	1 G1MS	Ig gamma-1 chain C
53	557	15.8	393	1 G1MSM	Ig kappa chain C r
54	556	15.8	106	1 K1MS	Ig heavy chain v r
55	556	15.8	268	2 A56446	Ig gamma-1 chain C
56	550	15.6	326	2 PS0017	Ig gamma-1 chain C
57	539	15.3	322	2 PS0019	Ig gamma-2a chain
58	536	15.2	288	2 S29690	Ig heavy chain VDU
59	530	15.0	170	2 A35944	Ig gamma-2a chain
60	529.5	15.0	249	2 S41374	single chain Fv an
61	527	15.0	150	2 PN0444	Ig heavy chain v r
62	516.5	14.7	585	2 A46507	Ig alpha chain - c
63	514	14.6	130	2 A49382	Ig heavy chain v r
64	513.5	14.6	238	2 A49633	Ig lambda-like cha
65	510.5	14.5	166	2 PL0012	Ig heavy chain pre
66	506	14.4	139	2 A27609	Ig heavy chain pre
67	503	14.3	128	2 I37267	Ig heavy chain v r
68	502	14.3	135	2 PS0057	Ig heavy chain pre
69	495.5	14.1	568	2 A34891	Ig heavy chain pre
70	495	14.1	138	2 C37267	Ig heavy chain v r
71	492	14.0	139	2 PS0024	Ig heavy chain pre
72	491.5	14.0	330	1 G2MSA	Ig gamma-2a chain
73	491.5	14.0	399	1 G2MSAM	Ig gamma-2a chain
74	489.5	13.9	125	2 S20639	Ig heavy chain v r
75	488	13.9	120	2 S41394	Ig heavy chain v r
76	485.5	13.8	125	2 PH0100	Ig heavy chain v r
77	483	13.7	287	4 PC4402	pelB leader/Ig hea
78	482	13.7	114	2 S26319	Ig heavy chain v r
79	481.5	13.7	117	1 MHMS4E	Ig heavy chain v r
80	481.5	13.7	140	2 T01407	Ig heavy chain (my
81	481	13.7	139	1 MHMS18	Ig heavy chain pre
82	480.5	13.6	117	1 MHMSJ5	Ig heavy chain v r
83	480	13.6	118	1 MHMS38	Ig heavy chain v r
84	480	13.6	126	2 S31930	Ig gamma chain pre
85	479.5	13.6	116	2 S55542	Ig heavy chain v r
86	479	13.6	112	2 S09957	Ig heavy chain V-D
87	479	13.6	122	2 PH0887	Ig heavy chain v r
88	479	13.6	405	1 G2MSBM	Ig gamma-2b chain
89	478.5	13.6	233	2 JC5322	p53 specific singl
90	478	13.6	117	2 PL0237	Ig heavy chain v r
91	478	13.6	131	2 S65537	Ig heavy chain v r
92	477	13.5	92	2 B45837	Ig gamma-1 chain C
93	477	13.5	117	2 B27563	Ig heavy chain v r
94	477	13.5	122	2 S37267	Ig heavy chain v r
95	477	13.5	137	2 H32513	Ig heavy chain pre
96	475	13.5	117	2 PL0235	Ig heavy chain v r
97	475	13.5	119	2 F30502	Ig heavy chain v r
98	474.5	13.5	119	2 PH0099	Ig heavy chain v r
99	474	13.5	141	2 JL0076	Ig heavy chain pre
100	473.5	13.4	119	2 B53285	Ig heavy chain v a

ALIGNMENTS

RESULT 1

A28179
enterotoxin E precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 15-Oct-1999
C:Accession: A28179
R:Couch, J.L.; Soltis, M.T.; Betley, M.J.
J. Bacteriol. 170, 2954-2960, 1988
A:Title: Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gene.
A:Reference number: A28179; PMID:88257005; PMID:3384800
A:Accession: A28179
A:Molecule type: DNA
A:Residues: 1-257 <COU>
A:Cross-references: GB:M21319; NID:g153001; PID:AAA26617.1; PID:g153002
C:Superfamily: enterotoxin B

Query Match 31.4%; Score 1107; DB 2; Length 257;
Best Local Similarity 89.7%; Pred. No. 1.4e-50;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSLQGTALGNLKQIYYNKSIAITSEKSDAQFLNTLLFKGFFTG 285
DB 25 SEKSEINEKDLRKSLQGNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 286 HPVNDLLVDLGGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMGVTLHDNNRLT 345
DB 85 HPVNDLLVDLGGKDATNKYKKVDLYGAYGYQCAGGTPNKTACMGVTLHDNNRLT 144
QY 346 EEKVPINLMIDGKQTTVPIDKVTSKKEVTQVELDQARHYLHGKFGLYNSDSFGGKQV 405
DB 145 EEKVPINLMIDGKQTTVPIDKVTSKKEVTQVELDQARHYLHGKFGLYNSDSFGGKQV 204
QY 406 RGLIVFHSSGGSVSYDLFPAQGYQDPTLLRIYRDNTTISLSLSLYIT 458
DB 205 RGLIVFHSSGGSVSYDLFPAQGYQDPTLLRIYRDNTTISLSLSLYIT 257

RESULT 2

S37484
Ig kappa chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
C:Accession: S37484
R:Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37484
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-225 <DUC>
A:Cross-references: EMBL:X70424; NID:g406254; PID:CAA49869.1; PID:g406255
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin

Query Match 29.4%; Score 1036.5; DB 2; Length 225;
Best Local Similarity 93.9%; Pred. No. 5.1e-47;
Matches 200; Conservative 4; Mismatches 8; Indels 1; Gaps 1;
QY 459 SIYMTQPTSLIYSAGDRVTITKASQSVNDVAVYQKFGQSPKLLISVTSRYAGVPD 518
DB 13 SIYMTQPTKELLISAGDRVTITKASQSVNDVAVYQKFGQSPKLLIYASRYTGVPD 72
QY 519 RFGSGYGTDTLTISVQAEADAAYFCQDYNPPTFGGKLEIKRADAAPTWSIFPP 578
DB 73 RFTGSGYGTDTFTISTVQAEADLAVYFCQDYSS-YTFGGGKLEIKRADAAPTWSIFPP 131
QY 579 SSELQTSGGASVCFLLNFYKPDINVKWKTGDSERQNGVLSNWTDDSKDSTYSMSLT 638
DB 132 SSELQTSGGASVCFLLNFYKPDINVKWKTGDSERQNGVLSNWTDDSKDSTYSMSLT 191

QY 639 LTKDEYERHNSYTCETHTKTSTSPIVKSENRNE 671
DB 192 LTKDEYERHNSYTCETHTKTSTSPIVKSENRNE 224

RESULT 3

S40295
Ig gamma-2a chain (mAb735) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
C:Accession: S40295
R:Klibert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Frosch, M.; Weisgerber, C.; Bit
submitted to the EMBL Data Library, January 1993
A:Description: Primary structure of the murine monoclonal IgG2a antibody mAb735 against
A:Reference number: S40295
A:Accession: S40295
A:Molecule type: protein
A:Residues: 1-446 <KLE>
C:Genetics:
A:Map position: 12
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: disulfide bond; glycoprotein; immunoglobulin; pyroglutamic acid
F:1-446/Product: Ig gamma-2a chain #status experimental <MAT>
F:1-17/Domain: V-D-J region <VDJ>
F:118-446/Domain: C region <CHR>
F:118-214/Domain: C1 region <CH1>
F:215-230/Region: hinge
F:231-340/Domain: C2 region <CH2>
F:341-446/Domain: C3 region <CH3>
F:360-427/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:22-96/144-195,261-321,367-425/Disulfide bonds: #status predicted
F:132/Disulfide bonds: interchain (to light chain) #status predicted
F:224,227,229/Disulfide bonds: interchain #status predicted
F:297/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 27.6%; Score 973; DB 2; Length 446;
Best Local Similarity 34.9%; Pred. No. 2.3e-43;
Matches 241; Conservative 57; Mismatches 123; Indels 270; Gaps 14;
QY 1 EVQLQQSGPDLVPGASVKISCKASGYFTGYNHWVKQSPGKLEWIGRINPNNGVTLY 60
DB 1 QIQQQSGPELVPGASVKISCKASGYFTDYIHWVKQSPGEGLEWIGYPSGNTKY 60
QY 61 NQPKQKATLVDSKSTAYMELSLTSEDSAVYICARSTMITNYVDYQGQTSVTSS 120
DB 61 NEKFKGKATLVDTSSSTAYMQLSSLTSEDSAVYFCARG---GKFAMDYWGQGTSTVSS 117
QY 121 AKTTPPSVYPLAPGSAQTNSMTLGLVKGYPEPVTVTWNSGSLSSGVHTPFAVLQSD 180
DB 118 AKTAPSVYPLAPVCGDTTGTSSVTLGLVKGYPEPVTLTWNSGSLSSGVHTPFAVLQSD 177
QY 181 LYTSSSVTPSPSTWPTSETVTCNVAPASSTKVDKIVPRDSGGSPSEKSEINEKDLRKK 240
DB 178 LYTSSSVTPSTWPTSETVTCNVAPASSTKVDKIVPRDSGGSPSEKSEINEKDLRKK 225
QY 241 SELQGTALGNLKQIYYNKSIAITSEKSDAQFLNTLLFKGFFGHPWYNDLLVDLGSTA 300
DB 226 -----PCKCPAPN-----LLGGPSVF----- 241
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTACMGVTLHDNNRLTEKKVPINLWIDGKQ 360
DB 226 -----PCKCPAPN-----LLGGPSVF----- 241
QY 361 TTVIDKVTSSKEVTVQVELDQARHYLHGKFGLYNSDSFGKQVORGLIYVHSEGSTVS 420
DB 242 -----IPFPKIKDVLMI----- 260
QY 421 YDLFPAQGYQDPTLLRIYRDNTTISLSLSLYITTSVMTQTPTSLLSVSGDRVTIT 480
DB 261 CVVVDVSEDDPD-----VQLSMFVNNEVLTAQTQT----- 291
QY 481 CKASQSVNDVAVYQKFGQSPKLLISVTSRYAGVPDRFSGSGYGTDFLTITSSVQAE 540

Db 292 -----HREDNSTLRV----- 303
QY 541 AAVYFCQDYNPPPTFGGKLEIKRAD-----AAPTVPSPSSQOLT 584
Db 304 SALPIQHDDMSGKEF-----KCKVANKDLPAPIERTISKPKXGSRAPQVYVLPPEBEEMT 359
QY 585 SGGASVGCFLNFPKDNVKKWIDGSRQN-----GVLSNWTQDQSKDSTYSSTLTL 639
Db 360 KQVTLTCMVDTFMPEDIIYVWNTNGKTELYNKTEFVLDS-----DGSYFYMYSLRV 412
QY 640 TKDEYERHNSYTCEATHK-TSTSPIVKSFNR 669
Db 413 EKKWVERNYSYSCSVVHEGLNHHHTKFSR 443

RESULT 4

A1790
Ig kappa chain V region (17/9) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 21-Jan-2000
C:Accession: A31790
R:Schulze-Gahmen, U.; Rini, J.M.; Arevalo, J.; Stura, E.A.; Kenten, J.H.; Wilson, I.A.
J. Biol. Chem. 263, 17100-17105, 1998
A:Title: Preliminary crystallographic data, primary sequence, and binding data for an antibody that recognizes the C region of immunoglobulin V region; immunoglobulin homology
A:Reference number: A92686; MUID:89034213; PMID:3182835
A:Accession: A31790
A:Molecule type: mRNA
A:Residues: 1-220 <SCH>
A:Cross-references: GB:M03626; GB:J04061; NID:G533234; PIDN:AAA39162.1; PID:G533235
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-96/Domain: immunoglobulin homology <IMM>

Query Match 27.0%; Score 952; DB 2; Length 220;
Best Local Similarity 82.6%; Pred. No. 1.2e-42;
Matches 180; Conservative 19; Mismatches 13; Indels 6; Gaps 1;
QY 460 IVMTQPTSLVSAAGRVITCKASQVSND-----VAVYQKPGQPKLLISYTSRY 513
Db 2 IVMTQPSLITVAGEKVTMSCTSSQSLFNSQKQKNTWTQKPGQPKVLIYWASTRE 61
QY 514 AGVPRFSGSGVGTDTLTISVQAEADAANVFCQDYNPPPTFGGKLEIKRADAAPT 573
Db 62 SGVPRFTGSGSGTDTLTISVQAEADLAIVYQNDYNSNPLTFGGGKLEIKRADAAPT 121
QY 574 SIFPPSSQLTSGGASVVCFLNFPKDNVKKWIDGSRQNGVLSNWTQDQSKDSTYSM 633
Db 122 SIFPPSSQLTSGGASVVCFLNFPKDNVKKWIDGSRQNGVLSNWTQDQSKDSTYSM 181
QY 634 SSTLTLTDEYERHNSYTCEATHKTSSTPIVKSFNRE 671
Db 182 SSTLTLTDEYERHNSYTCEATHKTSSTPIVKSFNRE 219

RESULT 5

S37483
Ig gamma-2a chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C:Accession: S37483
R:Ducancel, F.F.D.
submitted to the EMBL Data Library, February 1993
A:Reference number: S37483
A:Accession: S37483
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-469 <DUC>
A:Cross-references: EMBL:X70423; NID:9406252; PIDN:CAA49868.1; PID:9406253
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:276-345/Domain: immunoglobulin homology <IMM>

Query Match 27.0%; Score 951.5; DB 2; Length 469;
Best Local Similarity 34.2%; Pred. No. 3.2e-42;
Matches 236; Conservative 62; Mismatches 126; Indels 267; Gaps 13;
QY 1 EVLOQSGPDLVKPGASVKISCKASGYSTGYMHVWVKOSPKGLEWIGRIINNNGVTL 60
Db 20 QILOQSGPELVKPGASVKISCKASGYSTGYMHVWVKOSPKGLEWIGRIINNNGVTL 79
QY 61 NQKFKDKATLTVDKSTTTAYMELRSITSDSAVYVCARSTMTLTINYMDYKGGTSTVSS 120
Db 80 NENFKKATLTVDKSTTTAYMELRSITSDSAVYVCARSTMTLTINYMDYKGGTSTVSS 139
QY 121 AKTTPSVVPLAPGSAATNSMVTGLCLVKGYFPEPVTVWNSGSLSSGHHFPAVLQSD 180
Db 140 AKTTPSVVPLAPGSAATNSMVTGLCLVKGYFPEPVTVWNSGSLSSGHHFPAVLQSD 199
QY 181 LYTLLSSVTVPSSTWPESTVTCNVAHPASSTKVDKKIIPRDSDGSRSEKSEENKDLRKK 240
Db 200 LYTLLSSVTVPSSTWPESTVTCNVAHPASSTKVDKKIIPRDSDGSRSEKSEENKDLRKK 247
QY 241 SELQGTALGNLKQIYYNYSKAITSEKSAQDLTNTLLEKFPFTGHPWYNDLLVLDLSTA 300
Db 248 ----- 247
QY 301 ATSEYEGSSVDLYGAVYQCAGTGNKTCAMVGVTLHDNNRLTEKKVPIINLWDGKQ 360
Db 248 -----PKCPAPN-----LLGSPSVF----- 263
QY 361 TTVPIDKVKTSKEVTVQELDLQARHLYHGKFLYNSDSFGGKVGORGLIVFHSSEGSTVS 420
Db 264 -----LPPKIKDVLMI-----SLSPVIT 282
QY 421 YDLFDAQQGYPTLLRIYRDNNTTISSTLSISLYLTTSTIVMTQPTTSLVSAAGRVIT 480
Db 283 CVVVDVSEDDPD-----VQISWFVANNVEVHTAQQT----- 313
QY 481 CKASQVSNDVAVYQKPGQPKLLISYTSRYAGVPRFSGSGYGTDTLTISVQAEAD 540
Db 314 -----HREDNSTLRV----- 325
QY 541 AAVYFCQDYNPPPTFGGKLEIKRAD-----AAPTVPSPSSQOLT 584
Db 326 SALPIQHDDMSGKEF-----KCKVANKDLPAPIERTISKPKXGSRAPQVYVLPPEBEEMT 381
QY 585 SGGASVVCFLNFPKDNVKKWIDGSRQN-----GVLSNWTQDQSKDSTYSMSSTLTL 639
Db 382 KQVTLTCMVDTFMPEDIIYVWNTNGKTELYNKTEFVLDS-----DGSYFYMYSLRV 434
QY 640 TKDEYERHNSYTCEATHK-TSTSPIVKSFNR 669
Db 435 EKKWVERNYSYSCSVVHEGLNHHHTKFSR 465

RESULT 6

A28664
enterotoxin A precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 15-Oct-1999
C:Accession: A28664; A29566
R:Betley, M.J.; Mekalanos, J.J.
J. Bacteriol. 170, 34-41, 1988
A:Title: Nucleotide sequence of the type A staphylococcal enterotoxin gene.
A:Reference number: A28664; MUID:88086892; PMID:3335483
A:Accession: A28664
A:Molecule type: DNA
A:Residues: 1-257 <BET>
A:Cross-references: GB:M18970; NID:G153120; PIDN:AAA26681.1; PID:G153121
A:Experimental source: strain FRI337
R:Huang, I.Y.; Hughes, J.L.; Bergdoll, M.S.; Schantz, E.J.
J. Biol. Chem. 262, 7006-7013, 1987
A:Title: Complete amino acid sequence of staphylococcal enterotoxin A.
A:Reference number: A29566; MUID:87222293; PMID:3584106
A:Accession: A29566

A:Molecule type: protein
A:Residues: 25-241, 'S', 243-257 <HUA>
C:Genetics:
A:Gene: enta
A:Map position: 6
C:Superfamily: enterotoxin B

Query Match 26.9%; Score 948; DB 2; Length 257;
Best Local Similarity 76.4%; Pred. No. 2.3e-42;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEERNEKDLRKSELOQTALGNLKOIYYNKAITSSEKSADQFLNTLLFKGFFTG 285
DB 25 SEKSEERNEKDLRKSELOQTALGNLKOIYYNEKAKENKSHDQFLQTLFLKGFDD 84
QY 286 HPWYNDLLVGLSTAATSEYEGSSVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLT 345
DB 85 HSWYNDLLVDFDSKIDVYKKGKVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWDGKQTPIDKVTKEVTVQELDLQARHYLHGKFLYNSDSGCKVQ 405
DB 145 EEKVPINLWDGKQTPLETYKTKXNVTVQELDLQARHYLQEKYNYNSDVFQKQV 204
QY 406 RGLIVHSSSGSVSYDLFDAQOQYPTLLRIYRDNTTISSTSLISLYLYTT 458
DB 205 RGLIVHSTSTPSVNYDLFDAQOQYNTLLRIYRDNTKNTINSENMHIDILYTS 257

RESULT 7
S38864
Ig epsilon chain C region - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 24-May-2001
C:Accession: S38864
R:Kipp, B.; Becker, W.; Schlaak, M.
Submitted to the EMBL Data Library, November 1993
A:Description: Combination of a defined specificity and desired isotype by cloning of an
A:Reference number: S38864
A:Accession: S38864
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-548 <KIP>
A:Cross-references: EMBL:Z27397; NID:G416537; PIDN:CAA81788.1; PID:G940782
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:353-421/Domain: immunoglobulin homology <IMM>

Query Match 26.4%; Score 931; DB 2; Length 548;
Best Local Similarity 35.0%; Pred. No. 4.5e-41;
Matches 241; Conservative 83; Mismatches 186; Indels 178; Gaps 19;

QY 1 EVQLQSGDPLVKGASVKISKASGYSTGYVMHWVKQSPGKLEWIGRINPNNGVTLY 60
DB 1 QVLLSEGGDLVKGSGSLKSCAASGLTSSYGMVVRQIPDKLEWVATISSGGTYTY 60
QY 61 NQKFKKATLTVDKSTTAYMERLSLTSEDSAVYICARSTMITNYVDYWGQGTSTVSS 120
DB 61 PDVSKGRFTISRDNKNTLYLQWSSLSKSDTANYCARQGVSTMRFPAYWGQGLTVTSA 120
QY 121 AKTTPPSVYPLAPGSAQAQTNMTLGLVKGYPEPVTYVWNSGSLSSGVHTFPVQLQSD 180
DB 121 GKTPPSVYPLAPGSAQAQTNMTLGLVKGYPEPVTYVWNSGSLSSGVHTFPVQLQSD 180
QY 181 LYTLLSSSVTPSWTSPSETVTCNVAHPASSTKVDDKIVPRDSG-----GPSKSEI--- 232
DB 181 LYTLLSSSVTPSWTSPSETVTCNVAHPASSTKVDDKIVPRDSGCKPCIVPEVSSVFIFPP 240
QY 233 NEDLRLKSELO-----GVALGNLQIYYNKAITSSEKSADQFLNTLLFKGFFTG 286
DB 241 KPDKVLRSTIQLYCYFIYGHILNDVSVWMLDREITD-----LAQTVLIK----- 287
QY 287 PWYNDLLVGLSTAATSEYEGSSVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLTE 346
DB 288 -----EKGKLASTCKLNITEQQWMSBESTFCK-----VTSGQVDYLAH 326

QY 347 EKVPIINLWDGKQTV-----PIDKVTSKKEVTVQELDLQARHYLHGKFLYNSD 398
DB 327 TRRCF-----DHEPRGVITVLLIPSPDLQYQNGAPKLTCLVWDLSEKYNV----- 372
QY 399 SFGKVGQGLIVPHSSSEGSTVSVDLFDQAQOYPTLLRIYRDNTTISSTSLISLYLYTT 458
DB 373 -----VTNQEKKTIVS-----ASQWYTK-----HNNATTSITS----- 403
QY 459 SIWMTQTPSLVSAQDRVTITCKASQSVSNDAVYQKQSPKLLISYTSRYAGVDP 518
DB 404 -----LPVAKD-----WIE----- 413
QY 519 RFSSGSGTDFTLTISVQAEADAAYFCQDYSN-----PPTFGGKTKLEIKADAAPTYSIF 576
DB 414 -----GYG-----YQICVDHPDPFKPIVRSITKTPGQR--SAPEYVVF 449
QY 577 PPSSEQLTSGGASVVCFLNFPKIDNWKIKIDGSEKQNGVLSWTDQDSKDS--YSMS 634
DB 450 PPPEEE--SEDKRTLTCLIQNFPPEDISQWLGDKLISNSQHSHTTTLKXNGSNRGFFIF 508
QY 635 STLTLTKDEYERHNSYTCETHTKTSTSP 662
DB 509 SRLSEVAKTLTKQKQTCQVHEALQKP 536

RESULT 8
S38950
Ig gamma chain - mouse
C:Species: Mus musculus (house mouse)
C:Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C:Accession: S38950
R:Klebert, S.; Kratzin, H.D.; Zimmermann, B.; Vaesen, M.; Weisgerber, C.; Bit
Biol.Chem. Hoppe-Seyler 374, 993-1000, 1993
A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha(G
A:Reference number: S38950; MUID:94128242; PMID:8297501
A:Accession: S38950
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-246 <KLE>
A:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:137-201/Domain: immunoglobulin homology <IMM>

Query Match 25.4%; Score 929; DB 2; Length 246;
Best Local Similarity 78.5%; Pred. No. 2.1e-41;
Matches 179; Conservative 18; Mismatches 25; Indels 6; Gaps 2;

QY 1 EVQLQSGDPLVKGASVKISKASGYSTGYVMHWVKQSPGKLEWIGRINPNNGVTLY 60
DB 1 QIQLQSGDPLVKGASVKISKASGYSTGYVMHWVKQSPGKLEWIGRINPNNGVTLY 60
QY 61 NQKFKKATLTVDKSTTAYMERLSLTSEDSAVYICARSTMITNYVDYWGQGTSTVSS 120
DB 61 NEKFKGKATLTVDKSTTAYMERLSLTSEDSAVYICARSTMITNYVDYWGQGTSTVSS 117
QY 121 AKTTPPSVYPLAPGSAQAQTNMTLGLVKGYPEPVTYVWNSGSLSSGVHTFPVQLQSD 180
DB 118 AKTTPPSVYPLAPGSAQAQTNMTLGLVKGYPEPVTYVWNSGSLSSGVHTFPVQLQSD 177
QY 181 LYTLLSSSVTPSWTSPSETVTCNVAHPASSTKVDDKIVPRDSGCKPCIVPEVSSVFIFPP 228
DB 178 LYTLLSSSVTPSWTSPSETVTCNVAHPASSTKVDDKIVPRDSGCKPCIVPEVSSVFIFPP 222

RESULT 9
S68212
Ig kappa chain (Mab03-1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 11-Jan-2000
C:Accession: S68212
R:Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995

A;Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
 A;Reference number: S68211; MUID:95085223; PMID:7498516
 A;Accession: S68212
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: mRNA
 A;Residues: 1-214 <TAK>
 A;Cross-references: EMBL:D29668
 C;Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 26.3%; Score 926; DB 2; Length 214;
 Best Local Similarity 83.1%; Pred. No. 2.5e-41; Indels 6; Gaps 1;
 Matches 177; Conservative 16; Mismatches 14

QY 460 IVMTQPTSLVSGADRVITICKASQSVND-----VAVYQKPGQSPKLLISYTSRY 513
 DB 2 IVMTQSPSLVSGVQKVTMSCKSSQLLNKRNQVLAWYQKPGQSPKLLVYFASTRE 61
 QY 514 AGVDRFSGSGYGTDFLTITISVQAEDAAVYFCQDYNSTPTFGGKLEIKRADAAPT 573
 DB 62 SGVDRFSGSGYGTDFLTITISVQAEDAAVYFCQDYNSTPTFGGKLEIKRADAAPT 121
 QY 574 SIFPPSSQLTSGGASVVCFLNNFYPKIDNVKWKIDGSEKQNGVLSWTDQSKDSTYSM 633
 DB 122 SIFPPSSQLTSGGASVVCFLNNFYPKIDNVKWKIDGSEKQNGVLSWTDQSKDSTYSM 181
 QY 634 SSTLTLTDEYERHNSYTCETHKTSPIVKS 666
 DB 182 SSTLTLTDEYERHNSYTCETHKTSPIVKS 214

RESULT 10
 C89984
 enterotoxin P [imported] - Staphylococcus aureus (strain N315)
 C;Species: Staphylococcus aureus
 C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C;Accession: C89984
 R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
 ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
 C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A;Reference number: A89758; MUID:21311952; PMID:11418146
 A;Accession: C89984
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-260 <KUR>
 A;Cross-references: GB:BA000018; PID:G13701743; PIDN:BA843036.1; GSPDB:GN00149
 A;Experimental source: strain N315
 C;Genetics:
 A;Gene: sep
 C;Superfamily: enterotoxin B

Query Match 26.1%; Score 918; DB 2; Length 260;
 Best Local Similarity 73.0%; Pred. No. 8.3e-41;
 Matches 170; Conservative 21; Mismatches 42; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSEQLQALGNLKOIYYNSKATTSSEKSDAQFLNTLLPKGFTG 285
 DB 28 SEKSEINEKDLRKSEQLQALGNLKOIYYNSKATTSSEKSDAQFLNTLLPKGFTG 87
 QY 286 HPVNDLLVDLSTAAATSEYEGSSVDLYGAYGYQCAGTPTNKTACMYGGVTLHDNNRLT 345
 DB 88 HPVNDLLVDLSTAAATSEYEGSSVDLYGAYGYQCAGTPTNKTACMYGGVTLHDNNRLT 147
 QY 346 BEKKVPINLWDGKQTTPIDKVTSEKVTVEQLDLQARHLYHGKGLNSDSFGKQV 405
 DB 148 BEKKVPINLWDGKQTTPIDKVTSEKVTVEQLDLQARHLYHGKGLNSDSFGKQV 207
 QY 406 RGLIVFHSSEGSTVSDYDFDAQGQVPTDLLRIYRNTTISSTLSISLYTT 458
 DB 208 RGLIVFHSSEGSTVSDYDFDAQGQVPTDLLRIYRNTTISSTLSISLYTT 260

RESULT 11

S52028
 IG kappa chain - mouse
 C;Species: Mus musculus (house mouse)
 C;Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jan-2000
 C;Accession: S52028
 R;Van Engelen, F.; Schouten, A.; Molthoff, J.W.; Roosien, J.; Dirkse, W.G.; Schots, A.; F
 submitted to the EMBL Data Library, August 1994
 A;Description: Coordinate expression of antibody subunit genes yields high levels of func
 A;Reference number: S52028
 A;Accession: S52028
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-219 <VAN>
 A;Cross-references: EMBL:L35138; NID:G522336; PIDN:AAA67525.1; PID:G522337
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;16-95/Domain: immunoglobulin homology <IM>

Query Match 26.0%; Score 914.5; DB 2; Length 219;
 Best Local Similarity 81.6%; Pred. No. 1e-40;
 Matches 177; Conservative 15; Mismatches 20; Indels 5; Gaps 2;

QY 460 IVMTQPTSLVSGADRVITICKASQSV--SND---VAVYQKPGQSPKLLISYTSRYA 514
 DB 2 IVMTQSPSLVSGADRVITICKASQSV--SND---VAVYQKPGQSPKLLISYTSRYA 61
 QY 515 GVPDRFSGSGYGTDFLTITISVQAEDAAVYFCQDYNSTPTFGGKLEIKRADAAPT 574
 DB 62 GVPDRFSGSGYGTDFLTITISVQAEDAAVYFCQDYNSTPTFGGKLEIKRADAAPT 121
 QY 575 IFFPSSEQLTSGASVVCFLNNFYPKIDNVKWKIDGSEKQNGVLSWTDQSKDSTYSMS 634
 DB 122 IFFPSSEQLTSGASVVCFLNNFYPKIDNVKWKIDGSEKQNGVLSWTDQSKDSTYSMS 181
 QY 635 STLTLTDEYERHNSYTCETHKTSPIVKSFNRE 671
 DB 182 STLTLTDEYERHNSYTCETHKTSPIVKSFNRE 218

RESULT 12

PC4202
 monoclonal antibody Maba34 gammal heavy chain - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 21-Jan-2000
 C;Accession: PC4202
 R;Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
 Gene 173, 257-259, 1996
 A;Title: Cloning and characterization of cDNAs coding for heavy and light chains of a mor
 A;Reference number: PC4202; MUID:97082978; PMID:8964510
 A;Accession: PC4202
 A;Molecule type: mRNA
 A;Residues: 1-214 <KWA>
 A;Cross-references: GB:U29146; NID:G159423; PIDN:AAC52820.1; PID:G159424
 C;Comment: This protein is specific for human plasma apolipoprotein A-I of high-density
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 F;1-112/Domain: V region status predicted <VR>
 F;113-214/Domain: C region status predicted <CR>
 F;132-196/Domain: immunoglobulin homology <IM>

Query Match 26.0%; Score 914; DB 2; Length 214;
 Best Local Similarity 80.1%; Pred. No. 1e-40;
 Matches 177; Conservative 14; Mismatches 22; Indels 8; Gaps 1;

QY 1 EVLOQSGPLVKGASVKISCKASGYSTGYVMHWKQSPGKLEWIGRINPNNGVTLY 60
 DB 1 EVLOQSGPLVKGASVKISCKASGYSTGYVMHWKQSPGKLEWIGRINPNNGVTLY 60
 QY 61 NQFKDKATLTVDKSTTAYMELSLTSDSAVYVCARSTMITNYMYMDYWGQGTSTVSS 120
 DB 61 NQFKDKATLTVDKSTTAYMELSLTSDSAVYVCARSTMITNYMYMDYWGQGTSTVSS 112
 QY 121 AKTTPSVPLAPGSAQAQNSWTLGCLVKGFPEPVTVTWNSGSLSSGSHVTFPAVLQSD 180

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Db 113 AKTTPSVVYELAPGSAATNSMTLGLGVGYEPPEVTVTWNSGLSSGVHTFPVAVLQSD 172
QY 181 LYTLLSSVTVPSSTWPSSETVTCNVAHPASSTKVDKXIVPRD 221
Db 173 LYTLLSSVTVPSSTWPSSETVTCNVAHPASSTKVDKXIVPRD 213

RESULT 13
PC4203
Ig kappa chain (monoclonal antibody Maba334) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1996 #sequence_revision 31-Dec-1996 #text_change 11-Jan-2000
C:Accession: PC4203
R:Kwak, J.W.; Lee, D.I.; Choi, B.K.; Cho, W.K.; Lee, S.H.; Park, Y.B.; Han, M.H.
Gene 173, 257-259, 1996
A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a m
A:Reference number: PC4202; MUID:97082978; PMID:8964510
A:Accession: PC4203
A:Molecule type: mRNA
A:Residues: 1-219 <KWA>
A:Cross-references: GB:U29147; NID:G1594225; PID:NAC52821.1; PID:G1594226
C:Comment: This protein is specific for human plasma apolipoprotein A-I of high-density
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:1-112/Domain: V region #status predicted <VRG>
F:113-219/Domain: C region #status predicted <CRG>

Query Match 25.9%; Score 910.5; DB 2; Length 219;
Best Local Similarity 80.6%; Pred. No. 1.6e-40;
Matches 175; Conservative 16; Mismatches 21; Indels 5; Gaps 1;

QY 460 IVMTQPTSLVVSAGDRVITCKASQSV-----SNDVAVQKPGQSPKLLISYSSRYA 514
Db 2 VLVMTQPLSPVSLGDAQSISCRSSQSVHTNGNTVLEWYLOKPGQSPKLLIYKVSNRFS 61

QY 515 GVDPFRSGSGYGTDFLTITSSVQAEADAAVFCQDYNPPTFGGGLKLEIKRAADAAPTVS 574
Db 62 GVDPFRSGSGYGTDFLTIKSRVEAEDLVGYVFCQSHVPTFGGGLKLEIKRAADAAPTVS 121

QY 575 IFPPSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTQDQSKDSTYSMS 634
Db 122 IFPPSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTQDQSKDSTYSMS 181

QY 635 STLTLTKDEYERNHNSYTCETHTKTSTSPVKSFNNE 671
Db 182 STLTLTKDEYERNHNSYTCETHTKTSTSPVKSFNNE 218

RESULT 14
S16112
Ig kappa chain V region (G2a) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S16112
R:Vaesen, M.; Frosch, M.; Weisgerber, C.; Eckart, K.; Kratzin, H.; Bitter-Suermann, D.;
Biol. Chem. Hoppe-Seyler 372, 451-453, 1991
A:Title: Primary structure of the murine monoclonal IgG2a antibody mAb735 against alpha
A:Reference number: S16112; MUID:92000313; PMID:1910583
A:Accession: S16112
A:Molecule type: protein
A:Status: preliminary
A:Residues: 1-219 <BIT>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:16-95/Domain: immunoglobulin homology <INW>

Query Match 25.7%; Score 903.5; DB 2; Length 219;
Best Local Similarity 81.6%; Pred. No. 3.8e-40;
Matches 177; Conservative 14; Mismatches 21; Indels 5; Gaps 2;

QY 460 IVMTQPTSLVVSAGDRVITCKASQSV---SND---VAVWQKPGQSPKLLISYSSRYA 514
Db 2 VLVMTQPLSPVSLGDAQSISCRSSQSLVHNSGNTVLYWYLOKPGQSPKLLIYKVSNRFS 61
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QY 515 GVDPFRSGSGYGTDFLTITSSVQAEADAAVFCQDYNPPTFGGGLKLEIKRAADAAPTVS 574
Db 62 GVDPFRSGSGYGTDFLTIKSRVEAEDLVGYVFCQSHVPTFGGGLKLEIKRAADAAPTVS 121

QY 575 IFPPSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTQDQSKDSTYSMS 634
Db 122 IFPPSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTQDQSKDSTYSMS 181

QY 635 STLTLTKDEYERNHNSYTCETHTKTSTSPVKSFNNE 671
Db 182 STLTLTKDEYERNHNSYTCETHTKTSTSPVKSFNNE 218

RESULT 15
G2MS11
Ig gamma-2b chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 31-Mar-1980 #sequence_revision 01-Dec-2000 #text_change 01-Dec-2000
C:Accession: S25057; A02157; A26235; A26232; A26233; A53598
R:Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
Submitted to the EMBL Data Library, July 1992
A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific m
A:Reference number: S25057
A:Accession: S25057
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-474 <FIS>
A:Cross-references: EMBL:X67210; NID:G54826; PID:CAA47649.1; PID:G54827
R:Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; Obata, M.; Honjo, T.
Nature 283, 786-789, 1980
A:Title: Complete nucleotide sequence of immunoglobulin gamma2b chain gene cloned from m
A:Reference number: A02157; MUID:80120716; PMID:6766534
A:Contents: a allele
A:Accession: A02157
A:Molecule type: DNA
A:Residues: 138-161, 'L', 163-189, 'FP', 193-474 <YAM>
A:Cross-references: GB:J00461
A:Note: the sequence was determined from the germline gene
R:Tucker, P.W.; Marcu, K.B.; Slightom, J.L.; Blattner, F.R.
Science 206, 1299-1303, 1979
A:Title: Structure of the constant and 3' untranslated regions of the murine gamma2b heav
A:Reference number: A26235; MUID:80081501; PMID:117548
A:Contents: MPC 11
A:Accession: A26235
A:Molecule type: mRNA
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUI>
A:Note: Lys-474 is probably removed posttranslationally
R:Tucker, P.W.; Marcu, K.B.; Newell, N.; Richards, J.; Blattner, F.R.
Science 206, 1303-1306, 1979
A:Title: Sequence of the cloned gene for the constant region of murine gamma2b immunoglob
A:Reference number: A26232; MUID:80081502; PMID:117549
A:Accession: A26232
A:Molecule type: DNA
A:Residues: 138-172, 'P', 174-189, 'FP', 193-376, 'T', 378-474 <TUD>
R:Ollo, R.; Rougeon, F.
Nature 296, 761-763, 1982
A:Title: Mouse immunoglobulin allotypes: post-duplication divergence of gamma2a and gamma
A:Reference number: A26233; MUID:82173203; PMID:6803173
A:Contents: b allele
A:Accession: A26233
A:Molecule type: DNA
A:Residues: 138-161, 'L', 163-189, 'FP', 193-300, 'R', 302-331, 'A', 333-437, 'DI', 440-474 <OLL>
R:Kim, H.; Yamaguchi, Y.; Masuda, K.; Matsunaga, C.; Yamamoto, K.; Irimura, T.; Takahashi
J. Biol. Chem. 269, 12345-12350, 1994
A:Title: O-glycosylation in hinge region of mouse immunoglobulin G2b.
A:Reference number: A53598; MUID:94216359; PMID:7512967
A:Accession: A53598
A:Status: preliminary
A:Molecule type: protein
A:Residues: 234-251 <KIM>
C:Comment: The a allele sequence is shown.
```

C;Genetics: 138/1; 236/1; 258/1; 368/1
A;Introns: An immunoglobulin heterotetramer subunit consists of two identical light (kap) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into a C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglobulin F;157-222/Domain: immunoglobulin homology <IM1>
F;236-257/Region: hinge
F;281-350/Domain: immunoglobulin homology <IM2>
F;387-454/Domain: immunoglobulin homology <IM3>
F;152/Disulfide bonds: interchain (to light chain) #status predicted
F;164-220,288-348,394-452/Disulfide bonds: #status predicted
F;247,250,253,256/Disulfide bonds: interchain (to heavy chain) #status predicted
F;324/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 25.6%; Score 900.5; DB 1; Length 474;
Best Local Similarity 35.4%; Pred. No. 1.4e-39;
Matches 238; Conservative 55; Mismatches 130; Indels 249; Gaps 17;

QY 1 EVQLQSGDPIKVPASVKISKASGYSTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
DB 20 EVQLQSGDFELVNPASVKMSCKASGYTFITYMHVWVKQSPGKLEWIGRINPNKDGTKE 79
QY 61 NQKFKDKATLTVDRKSTTAYNELSLTSEDSAVVYCARSTMTNRYVD---YWGQGTSTV 117
DB 80 NEKFKGKATLTSKSSNTAYNELSLTSEDSAVVYCAR---DYDYDFWFAVWQGTLT 134
QY 118 VSAKTTTPSPVPLAPGSAAGTNSMTLGLVKGYPFPEPVTVTWNSGLSGGVHTF-PAV 176
DB 135 VSAKTTTPSPVPLAPGCGDTGSSVTSGCLVKGYPFPEPVTVTWNSGLSSVHTLQAL 194
QY 177 LOSDLTSLSSVTWPSSTWPSSTVTCNVAPASSTKDKKIVPRDSDGSPSEKSEINE-- 234
DB 195 LOSGLYTWSSVTWPSSTWPSSTVTCNVAPASSTKDKKIVPRDSDGSPSEKSEINE-- 248
QY 235 --KDLRK--KSELQGTALGNLQVYVNSKAITSSKSAQDLNTLLFKGFFTGHPWYN 290
DB 249 PKCEKCKCPANLEG---GPSVFIFPPNKKV--- 277
QY 291 DLLVDLGSATASTSEYSSVDLYGAYGYQACAGTTPNKTACMYGGVTLHDNRLTEKKV 350
DB 278 -LMTSL---TP----- 284
QY 351 PINLWIDGKQTVPIDKVTKSKKEVTVQELDLQARHYLHGKFLYNSDSFGCKVQORGLIV 410
DB 285 -----KVTCVVVD-----VSEDDPQVQISWFFVN-----VE 310
QY 411 FHSSEGSTVSYDLFDAQOQYPTLLRIYRDNNTTSSLSLSLYLTSIWMTCPTSL 470
DB 311 VHTAQTHREDY-----NSTIRVVS----- 331
QY 471 VSAGRVITCKASQSVNDVAVYQKPGQPKLLISYTSRYAGVDPDRFGSGGYGTFT 530
DB 332 -----T 332
QY 531 LTIGSVQAEADAAYFCODYNSPPTFGGKTKLEIKRADAAPTYSIFPPSSEQLTSGGASV 590
DB 333 LPIQHODWMSKEFKCKVNNKDLSPERTISKLGVRAPQVILPPEAQEQRKDVSL 392
QY 591 VCFNNFYPKDVNWKIDGSEKQK-----GVLSWTDQDSDKSTYSMSSTLTITKDEYE 645
DB 393 TCLVGFNPGDISVEWTSNGHTSEENYKDTAPVLDSE-----DGSYFIYKLNKMTSKWE 445
QY 646 RHNSYTCETHK 657
DB 446 KIDSFSQNVNRE 457

RESULT 16

S38865

Ig kappa chain - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 15-Jun-2001

C;Accession: S38865

R;Kipp, B.; Becker, W.; Schlaak, M.

submitted to the EMBL Data Library, November 1993

A;Description: Combination of a defined specificity and desired isotype by cloning of an

A;Reference number: S38864

A;Accession: S38865

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-219 <KIP>

A;Cross-references: EMBL:227396; NID:g416538; PIDN:CAA81787.1; PID:g416539

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

Query Match 25.5%; Score 896.5; DB 2; Length 219;

Best Local Similarity 80.2%; Pred. No. 8.7e-40;

Matches 174; Conservative 15; Mismatches 23; Indels 5; Gaps 1;

QY 460 IYMTQPTSLVSGADRVITCKASQSV-----SNDVAVYQKPGQSPKLLISYTSRYA 514

DB 2 LVMTQSPFLSVSLGDSQASISCRSSQLVHTNGNTYLHWYLOKPLSPKLLIYVSNRES 61

QY 515 GVPDRFGSGGYGDTFTLTITSSVQAEADAAYFCODYNSPPTFGGKTKLEIKRADAAPTYS 574

DB 62 GVPDRFGSGGYGDTFTLTITSSVQAEADAAYFCODYNSPPTFGGKTKLEIKRADAAPTYS 121

QY 575 IPPSSEQLTSGGASVVCFLNNFYPKDVNWKIDGSEKQKGVLSWTDQDSDKSTYSMS 634

DB 122 IPPSSEQLTSGGASVVCFLNNFYPKDVNWKIDGSEKQKGVLSWTDQDSDKSTYSMS 181

QY 635 STLTLTKDEYERHNSYTCETHKTSPIVKSFNRNE 671

DB 182 STLTLTKDEYERHNSYTCETHKTSPIVKSFNRNE 218

RESULT 17

JC5810

monoclonal antibody 13-1 light chain - mouse

C;Species: Mus musculus (house mouse)

C;Date: 04-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jan-2000

C;Accession: JC5810

R;Akashi, S.; Kato, K.; Torizawa, T.; Dohmae, N.; Yamaguchi, H.; Kamachi, M.; Harada, A.;

Biochem. Biophys. Res. Commun. 240, 566-572, 1997

A;Title: Structural characterization of mouse monoclonal antibody 13-1 against a porphyrin

A;Reference number: JC5810; MUID:98063277; PMID:9398605

A;Molecule type: protein

A;Residues: 1-218 <AKA>

C;Comment: This catalytic antibody has peroxidase oxidase. It is directed against a porphyrin

C;Superfamily: immunoglobulin V region; immunoglobulin homology

F;15-94/Domain: immunoglobulin homology <IM>

Query Match 25.3%; Score 892; DB 2; Length 218;

Best Local Similarity 79.7%; Pred. No. 1.5e-39;

Matches 173; Conservative 12; Mismatches 28; Indels 4; Gaps 1;

QY 459 SIYMTQPTSLVSGADRVITCKASQSVND---VAVYQKPGQSPKLLISYTSRYA 514

DB 1 NIVLTQSPASLAVSLGQRATISCRASKSVASGYIMHWYLOKPGQPKLLISLASNLES 60

QY 515 GVPDRFGSGGYGDTFTLTITSSVQAEADAAYFCODYNSPPTFGGKTKLEIKRADAAPTYS 574

DB 61 GVPDRFGSGGYGDTFTLTITSSVQAEADAAYFCODYNSPPTFGGKTKLEIKRADAAPTYS 120

QY 575 IPPSSEQLTSGGASVVCFLNNFYPKDVNWKIDGSEKQKGVLSWTDQDSDKSTYSMS 634

DB 121 IPPSSEQLTSGGASVVCFLNNFYPKDVNWKIDGSEKQKGVLSWTDQDSDKSTYSMS 180

QY 635 STLTLTKDEYERHNSYTCETHKTSPIVKSFNRNE 671

DB 181 STLTLTKDEYERHNSYTCETHKTSPIVKSFNRNE 217

RESULT 18

S49220

IG gamma-1 chain - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 21-Jan-2000
C:Accession: S49220
R;Kipp, B.; Becker, W.P.; Schlaak, M.M.
submitted to the EMBL Data Library, September 1994
A:Description: Cloning and expression of a recombinant mouse Fab-fragment recognizing a
A:Reference number: S49220
A:Accession: S49220
A:Molecule type: mRNA
A:Residues: 1-221 <KIP>
A:Cross-references: EMBL:D27502; NID:9541778; PIDN:CAA85732.1; PID:9541779
A:Experimental source: strain Balb/c
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:1-120/Domain: V region #status predicted <VRG>
F:121-221/Domain: C region #status predicted <CRG>
F:139-203/Domain: immunoglobulin homology <IMM>

Query Match 25.3%; Score 890.5; DB 2; Length 221;
Best Local Similarity 77.4%; Pred. No. 1.8e-39;
Matches 171; Conservative 20; Mismatches 29; Indels 1; Gaps 1;
QY 1 EVQLQSGDPLVKGASVKISCKASCSYFTGYMHVVKOSPGKLEWIGRIINPNNGVTLY 60
DB 1 QVQLKESGAEIVKSGASVLSCTASGFKIDTYMEVKORPEQGLEWIGRIDPANGEIKY 60
QY 61 NQKFKDKATLVDSKSTTAYMELRLTSDSAVYICARSTM:TNVYMDYWGQTSVTVSS 120
DB 61 DPRFQGTATITADTSTNTAYLQLSLTSDTAVYCVRRGYGSSQ-EPTWGQGTTLTVSS 119
QY 121 AKTPPSVPLPGSAAQNTSMWTLCLVKGYPPEPTVTWNSGLSSGVHTFPAVLQSD 180
DB 120 AKTPPSVPLPGSAAQNTSMWTLCLVKGYPPEPTVTWNSGLSSGVHTFPAVLQSD 179
QY 181 LYLTLSSSVTPSSTWSEIVTCNVAHPASSTKVDKXIVPRD 221
DB 180 LYLTLSSSVTPSSTWSEIVTCNVAHPASSTKVDKXIVPRD 220

RESULT 19

S42772
IG kappa chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-Jan-2000
C:Accession: S42772
R;Schellekens, G.A.
submitted to the EMBL Data Library, November 1993
A:Reference number: S42771
A:Accession: S42772
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-217 <SCH>
A:Cross-references: EMBL:X75536; NID:9414143; PIDN:CAA53226.1; PID:9414144
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:14-93/Domain: immunoglobulin homology <IMM>

Query Match 25.2%; Score 886.5; DB 2; Length 217;
Best Local Similarity 79.8%; Pred. No. 2.8e-39;
Matches 172; Conservative 14; Mismatches 25; Indels 5; Gaps 1;
QY 461 VMTQTPTSLVSGADRVITTCASQSV-----SNDVAVYQQKPGQSPKLLISYTSRYAG 515
DB 1 VMTQSPFLSLVSLGDAQSICRSSQSLVHTNGNTYLHWYLRKPGQSPKVLIVKSTRPSG 60
QY 516 VDRFSGSGVGTFTLTISVQVEDAAVYFCQDYNSPPTFGGKLEIKRADAAPTYSI 575
DB 61 VDRFSGSGSGTFTFKISRVEAEDLGVYFCSSQSTVTPFTFGSGTKLEIKRADAAPTYSI 120
QY 576 FPPSSEQLTSGGASVVCFLNNFVKDINVKWKIDGSRQNGVLSNWTQDQSKDSTYSMSS 635

Db 121 FPPSSEQLTSGGASVVCFLNNFVKDINVKWKIDGSRQNGVLSNWTQDQSKDSTYSMSS 180

QY 636 TLTLTKDEYERHNSYTCETHTKTSTSPIVKSFNRNE 671
DB 181 TLTLTKDEYERHNSYTCETHTKTSTSPIVKSFNRGE 216

RESULT 20

S68241
IG kappa chain V region (Mab13-1) - mouse (fragment)
N:Alternate names: immunoglobulin light chain
C:Species: Mus musculus (house mouse)
C>Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 20-Jun-2000
C:Accession: S68241; S68214
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
submitted to the EMBL Data Library, March 1994
A:Description: Specific peroxidase activity by formation of an antibody L-chain-porphyrin
A:Reference number: S68241
A:Accession: S68241
A:Molecule type: mRNA
A:Residues: 1-218 <TAK>
A:Cross-references: EMBL:D29670; NID:9473962; PIDN:BAA06141.1; PID:9473963
R;Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A:Title: Thermolabile peroxidase activity with a recombinant antibody L chain-porphyrin
A:Reference number: S68211; MUID:96085223; PMID:7498516
A:Accession: S68214
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 'N', 3-212 <TAW>
A:Cross-references: EMBL:D29670
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin

Query Match 25.0%; Score 880; DB 2; Length 218;
Best Local Similarity 78.7%; Pred. No. 6.2e-39;
Matches 170; Conservative 13; Mismatches 29; Indels 4; Gaps 1;

QY 460 IVMTQTPTSLVSGADRVITTCASQSVND----VAVYQQKPGQSPKLLISYTSRYAG 515
DB 2 LVLTQSPASLAVSLGQRATISCRASKSVASGVYVHWYQQKPGPKLLISLATNLESG 61
QY 516 VDRFSGSGVGTFTLTISVQVEDAAVYFCQDYNSPPTFGGKLEIKRADAAPTYSI 575
DB 62 VPARFSGSGSGTFTLNIHPVEBEDVATYYCQHSRELPLTFGAGTKLEKRAADAAPTYSI 121
QY 576 FPPSSEQLTSGGASVVCFLNNFVKDINVKWKIDGSRQNGVLSNWTQDQSKDSTYSMSS 635
DB 122 FPPSSEQLTSGGASVVCFLNNFVKDINVKWKIDGSRQNGVLSNWTQDQSKDSTYSMSS 181
QY 636 TLTLTKDEYERHNSYTCETHTKTSTSPIVKSFNRNE 671
DB 182 TLTLTKDEYERHNSYTCETHTKTSTSPIVKSFNRGE 217

RESULT 21

IG kappa chain - mouse
C:Species: Mus musculus (house mouse)
C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jan-2000
C:Accession: S25058
R;Fischer, R.; Voss, A.; Niersbach, M.; Munziker, W.; Hirsch, H.J.; Kreuzaler, F.
submitted to the EMBL Data Library, July 1992
A:Description: Production of a Tobacco mosaic virus (TMV) inactivating neotop specific mc
A:Reference number: S25057
A:Accession: S25058
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-235 <FIS>
A:Cross-references: EMBL:X67211; NID:954828; PIDN:CAA47650.1; PID:954829
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:38-111/Domain: immunoglobulin homology <IMM>

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Query Match      24.9%; Score 878.5; DB 2; Length 235;
Best Local Similarity 76.7%; Pred. No. 8.1e-39;
Matches 171; Conservative 19; Mismatches 32; Indels 1; Gaps 1;

QY 449 LSIISLYLTTISVMTQTPTSLVVSAGDRTVITCKASQSVNDVAVYQKQSPKLLISY 508
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 13 ISASVIRGRQVLVQLQSPAINASASPEKVTWTCSSASSVSK-MQWYQKQSGTSPKRWYD 71

QY 509 TSSRYAGVPDRFSGSGYGTDFLTLSVQAEADAAVYFCQDYNPPTFGGQTKLEIKRAD 568
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 72 TSKLASGVPGRFSGSGYGTDFLTLSVQAEADAAVYFCQDYNPPTFGGQTKLEIKRAD 131

QY 569 AAPTIVSIFPPSSQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTDQDSKD 628
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 132 AAPTIVSIFPPSSQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTDQDSKD 191

QY 629 SNYSMSSTLTITKDEYERHNSYTCEATHKTSPIVKSFNNE 671
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 192 STYSMSSTLTITKDEYERHNSYTCEATHKTSPIVKSFNNE 234

RESULT 22
JL0029
Ig kappa chain precursor (RP93) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C>Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 11-Jan-2000
C:Accession: JL0029
R:Chien, N.C.; Pollock, R.R.; Desaymard, C.; Scharff, M.D.
J. Exp. Med. 167, 954-973, 1988
A:Title: Point mutations cause the somatic diversification of IgM and IgG2a antiphosphor
A:Reference number: JL0029; MUID:88171315; PMID:3127529
A:Accession: JL0029
A:Molecule type: mRNA
A:Residues: 1-225 <CHI>
A:Experimental source: strain BALB/c, cell line RP93 hybridoma cell
A:Note: the authors translated the codon CGG for residue 106 as Pro, ACC for residue 132
A:Note: the nucleotide sequence shown is inconsistent with authors' translation because
ect except for four positions shown above
C:Comment: The protein is an anti-phosphorylcholine antibody.
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: immunoglobulin
F:7-225/Product: Ig kappa chain #status predicted <ILC>
F:7-106/Domain: V region #status predicted <VAR>
F:107-119/Domain: J region #status predicted <JIR>
F:120-225/Domain: C region #status predicted <COR>

Query Match      24.9%; Score 876.5; DB 2; Length 225;
Best Local Similarity 76.4%; Pred. No. 9.8e-39;
Matches 168; Conservative 21; Mismatches 26; Indels 5; Gaps 1;

QY 457 TTSIVMTQTPTSLVVSAGDRTVITCKASQSVND-----VAVYQKQSPKLLISYTS 511
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 5 SSDVLMTQIPSLPVSLGDAQSICRSQNIHVHSTGNTYLEWYLPKQSPNLLIYKISN 64

QY 512 RVAGVPDRFSGSGYGTDFLTLSVQAEADAAVYFCQDYNPPTFGGQTKLEIKRADAA 571
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 65 RFGVPDRFSGSGGTDFLSIRVEADLGVYCFQSSHVWTFGGQTKLEIKRADAA 124

QY 572 TVSIFFPPSSQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTDQDSKDY 631
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 125 TVSIFFPPSSQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTDQDSKDY 184

QY 632 SMSSTLTITKDEYERHNSYTCEATHKTSPIVKSFNNE 671
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 185 SMSSTLTITKDEYERHNSYTCEATHKTSPIVKSFNNE 224

RESULT 23
S14237
Ig kappa chain precursor (15C5) - mouse
C:Species: Mus musculus (house mouse)
C>Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: S14237
```

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R:Vandamme, A.M.; Bulens, F.; Bernar, H.; Nelles, L.; Lijnen, R.H.; Collen, D.
Eur. J. Biochem. 192, 767-775, 1990
A:Title: Construction and characterization of a recombinant murine monoclonal antibody di
A:Reference number: S14236; MUID:91006173; PMID:2209622
A:Accession: S14237
A:Molecule type: mRNA
A:Residues: 1-234 <VAN>
A:Cross-references: EMBL:X56394; NID:G51622; PIDN:CAA319805.1; PID:G51623
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:36-110/Domain: immunoglobulin homology <IMM>
```

```
Query Match      24.8%; Score 875; DB 2; Length 234;
Best Local Similarity 78.8%; Pred. No. 1.2e-38;
Matches 167; Conservative 18; Mismatches 27; Indels 0; Gaps 0;

QY 460 IVMTQTPTSLVVSAGDRTVITCKASQSVNDVAVYQKQSPKLLISYTSRYAGVPDR 519
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 22 IKMTQSPSSMYASLGERVTWTCASQDINSYLSIQKPKSPKTLIYRGNLAVGVPGR 81

QY 520 FSGSGYGTDFLTLSVQAEADAAVYFCQDYNPPTFGGQTKLEIKRADAAPTVSIFPPS 579
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 82 FSGSGGQDYSLTISSEYEDGVYCYLAYDEFPPTFGGQTKLEIKRADAAPTVSIFPPS 141

QY 580 SEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTDQDSKDYTSMSSTLT 639
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 142 SEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTDQDSKDYTSMSSTLT 201

QY 640 TKDEYERHNSYTCEATHKTSPIVKSFNNE 671
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 202 TKDEYERHNSYTCEATHKTSPIVKSFNNE 233
```

```
RESULT 24
S01320
Ig kappa chain precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 21-Jan-2000
C:Accession: S01320
R:de Waele, P.; Feys, V.; van de Voorde, A.; Molemans, F.; Fiers, W.
Eur. J. Biochem. 176, 287-295, 1988
A:Title: Expression in non-lymphoid cells of mouse recombinant immunoglobulin directed as
A:Reference number: S01320; MUID:88329081; PMID:3138116
A:Accession: S01320
A:Molecule type: mRNA
A:Residues: 1-234 <DE1>
A:Cross-references: EMBL:X13187; NID:G51784; PIDN:CAA31579.1; PID:G51785
A:Note: this sequence was determined from the differentiated gene
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-234/Product: Ig kappa chain #status predicted <MAT>
F:36-110/Domain: immunoglobulin homology <IMM>
```

```
Query Match      24.8%; Score 874; DB 2; Length 234;
Best Local Similarity 74.9%; Pred. No. 1.4e-38;
Matches 167; Conservative 24; Mismatches 28; Indels 4; Gaps 1;

QY 453 LLYLYT-----SIWMTQTPTSLVVSAGDRTVITCKASQSVNDVAVYQKQSPKLLISY 508
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 11 LLLWLTDARCDIQMTQSPASLSVSGESVTITCRASENIYSLAWYQKQKSPQLLVYV 70

QY 509 TSSRYAGVPDRFSGSGYGTDFLTLSVQAEADAAVYFCQDYNPPTFGGQTKLEIKRAD 568
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 71 ATKLVGVPDRFSGSGGTQYSLKINSLOSEFGSYCFQFWDPTPTFGSGTKLEMKRAD 130

QY 569 AAPTIVSIFPPSSQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTDQDSKD 628
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 131 AAPTIVSIFPPSSQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLNSWTDQDSKD 190

QY 629 STYSMSSTLTITKDEYERHNSYTCEATHKTSPIVKSFNNE 671
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 191 STYSMSSTLTITKDEYERHNSYTCEATHKTSPIVKSFNNE 233
```


RESULT 27

A56169
Ig kappa chain V region (clone 23.2) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 11-Jan-2000
C/Accession: A56169
R/Monfardini, C.; Kieber-Emmons, T.; VonFeldt, J.M.; O'Malley, B.; Rosenbaum, H.; Godill
J. Biol. Chem. 270, 6628-6638, 1995
A/Title: Recombinant antibodies in bioactive peptide design.
A/Reference number: A56169; MUID:95204454; PMID:7896802
A/Accession: A56169
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-210 <NON>
A/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin

Query Match 24.3%; Score 857; DB 2; Length 210;
Best Local Similarity 79.4%; Pred. No. 9.1e-38;
Matches 166; Conservative 13; Mismatches 26; Indels 4; Gaps 1;

QY 460 IVMQTPTSLVLSAGDRVTITCKASQSVND-----VAVYQKQKQSPKLLISYTSRYAG 515

DB 2 IVLTQSPASLTIVSLGQRATISCRASKSVSSGYSYVHWYQKPGQPPKVLIVLASNLESG 61

QY 516 VPDRESSGSGYGFDTLTSSVQAEDAAVYFCQDYNSTPTGGGTGKLEIKADAAPTVSI 575

DB 62 VPPRFGSGSGYGFDTLTINHPVEEEDAAIYCOHSRELPWTFGGGTGKLEIKADAAPTVSI 121

QY 576 FPPSSEQLTSGGASVVCFLNFPYKIDINVKWKIDGSEHQNGVLSWTDQDSKDSYSMS 635

DB 122 FPPSSEQLTSGGASVVCFLNFPYKIDINVKWKIDGSEHQNGVLSWTDQDSKDSYSMS 181

QY 636 TLTLTKDEYERHNSYTCETHKTSPIV 664

DB 182 TLTLTKDEYERHNSYTCETHKTSPIV 210

RESULT 28

S06084
Ig kappa chain precursor - rat
C/Species: Rattus norvegicus (Norway rat)
C/Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 21-Jan-2000
C/Accession: S06084
R/Crowe, J.S.; Smith, M.A.; Cooper, H.J.
Nucleic Acids Res. 17, 7392, 1989
A/Title: Nucleotide sequence of Y3-Ag 1.2.3. rat myeloma immunoglobulin kappa chain cDNA
A/Reference number: S06084; MUID:90016888; PMID:2508067
A/Accession: S06084
A/Molecule type: mRNA
A/Residues: 1-240 <CRO>
A/Cross-references: EMBL:X16129; NID:G56457; PIDN:CAA34256.1; PID:G56458
A/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: heterotetramer; immunoglobulin
F/1-20/Domain: signal sequence #status predicted <SIG>
F/21-240/Product: Ig kappa chain #status predicted <MAT>
F/153-222/Domain: immunoglobulin homology <IMM>

Query Match 24.2%; Score 853; DB 2; Length 240;
Best Local Similarity 69.6%; Pred. No. 1.7e-37;
Matches 165; Conservative 31; Mismatches 31; Indels 10; Gaps 2;

QY 445 SSTSLISLILYTT-----SIVMTQTPTSLVLSAGDRVTITCKASQSV-----SNDVAVY 494

DB 3 SQTQVLSLLWISGTCGDFVMTQSPSLAVSAGETVTINCKSSQSLFYSNGKNYLAWY 62

QY 495 QOKPQSPKLLISYTSRYAGVPRFSGYGTDFTLTSSVQAEADAAVFCQDYNSTPP 554

DB 63 QOKPQSPKLLIYWAETQSGVPRDFISGSGTDFTLTSSVQAEADAAVFCQYETPY 122

QY 555 TFGGKTLEIKRADAAPTVSIFFPSSEQLTSGGASVVCFLNFPYKIDINVKWKIDGSEHQ 614

DB 123 TFGAGTKLEIKRADAAPTVSIFFPSTEQATGASVVCFLNFPYKIDGTER 182

QY 615 NGVLNSWTDQDSKDSYSMSSTLTLTQDEYERHNSYTCETHKTSPIVKSFNRE 671

DB 183 DGVLDSDTDQDSKDSYSMSSTLSLKADYSEHNLTYCEVWHKTSPPVKSFNRE 239

RESULT 29

S68211
Ig heavy chain (Mab13-1) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 29-Jul-1997 #sequence_revision 29-Aug-1997 #text_change 20-Jun-2000
C/Accession: S68211
R/Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A/Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A/Reference number: S68211; MUID:96085223; PMID:7498516
A/Accession: S68211
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-220 <YAK>
A/Cross-references: EMBL:D29669; NID:G473958; PIDN:BAA06140.1; PID:G473959
A/Note: the sequence of residues 1-4, 213-220 and the corresponding nucleotide sequence
C/Superfamily: immunoglobulin C region; immunoglobulin homology
F/136-200/Domain: immunoglobulin homology <IMM>

Query Match 22.9%; Score 808; DB 2; Length 220;
Best Local Similarity 70.2%; Pred. No. 3.3e-35;
Matches 153; Conservative 24; Mismatches 37; Indels 4; Gaps 2;

QY 6 QSGPDLVKGASVKISKASGYSTGYVHWKQSPKGLWIG--RINPNNGVTLYNOK 63

DB 2 ESGGLVRFQNSLKLSTLSTGTFYSNYRWHLRQPGKLEWIAVITVKSNDYGAKYAS 61

QY 64 FDKKATLTVDKSTTAYMELRSLTSDSAVYCAKSTMITNVMYDVGOGTSVTSSAKT 123

DB 62 VRCRFTISRDDSKSVYLQWNLRLREEDTATYCCRTPWV--YAMDCWGGTSTVIVSSAKT 119

QY 124 TPSPVYPLAPGSAATNSMVTGLCLVKGYPFPBPVTVWNSGSLSSGVHFPFPAVLQSDLYT 183

DB 120 TPSPVYPLAPGSAATNSMVTGLCLVKGYPFPBPVTVWNSGSLSSGVHFPFPAVLQSDLYT 179

QY 184 LSSSVTPSTPSTPSETVTCNVAHPASSTKVDKKIVPRD 221

DB 180 LSSSVTPSTPSTPSETVTCNVAHPASSTKVDKKIVPRD 217

RESULT 30

S68213
Ig heavy chain (Mab03-1) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 29-Jul-1997 #sequence_revision 17-Sep-1997 #text_change 21-Jan-2000
C/Accession: S68213
R/Takagi, M.; Kohda, K.; Hamuro, T.; Harada, A.; Yamaguchi, H.; Kamachi, M.; Imanaka, T.
FEBS Lett. 375, 273-276, 1995
A/Title: Thermostable peroxidase activity with a recombinant antibody L chain-porphyrin
A/Reference number: S68211; MUID:96085223; PMID:7498516
A/Accession: S68213
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-213 <YAK>
A/Cross-references: EMBL:D29667
A/Superfamily: immunoglobulin C region; immunoglobulin homology
F/137-201/Domain: immunoglobulin homology <IMM>

Query Match 20.9%; Score 737.5; DB 2; Length 213;
Best Local Similarity 64.7%; Pred. No. 1.4e-31;
Matches 139; Conservative 29; Mismatches 44; Indels 3; Gaps 1;

QY 2 VOLQSQGPDVLPFGASVKISKASGYSTGYVHWKQSPKGLWIGRINPNNGVTLYN 61

DB 2 VOLVESGGGLVPGGSRKLSCAASGTFSSFGHWVWVROAPEKGLEWVAISSGSSIIYA 61

QY 62 QKPKKATLTVKSSSTAYMELASLTSEDSAVYICARSTMTITNYVMDYWGQSTSVTSSA 121
 Db 62 DTWKGRTISDRPNKNTLFLQMTSLSEDTAMVYCARSWLLP---FDYWGQSTTVTSSA 118
 QY 122 KTTTPSVYPLAPGSAAGTSMVTLGLVKGYPEPVTVTWNGSLSSSGVHTTTPAVLQSL 181
 Db 119 KTTTPSVYPLAPGCGTTGSSVTGLVKGYPEPVTVTWNGSLSSSVHTTTPALLQSL 178
 QY 182 YTLSSSVTPSPSTPSETVTCNVAHPASSTKVDKK 216
 Db 179 YTMSSSVTPSPSTPSETVTCNVAHPASSTVDKK 213
 RESULT 31
 PC4155
 Ig gamma-2b chain V-C region Mabb23 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 10-May-1996 #sequence_revision 19-Jul-1996 #text_change 21-Jan-2000
 C:Accession: PC4155
 R:Kwak, J.W.; Choi, B.K.; Lee, D.I.; Kang, Y.K.; Seo, Y.G.; Cho, W.K.; Han, M.H.
 Gene 169, 237-239, 1996
 A:Title: Cloning and characterization of cDNAs coding for heavy and light chains of a m
 A:Reference number: PC4155; MUID:96194809; PMID:8647454
 A:Accession: PC4155
 A:Molecule type: mRNA
 A:Residues: 1-231 <KWA>
 A:Cross-references: GB:U28970; NID:G1262180; PIDN:AA052489.1; PID:G1262181
 A:Note: This protein has unusual amino acid compared with the conserved sequences of mou
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 F:1-231/Product: heavy chain #status predicted <MAR>
 F:98-102/Region: unique D sequence
 F:103-119/Region: V region
 F:139-203/Domain: immunoglobulin homology <IMM>
 Query Match 20.3%; Score 715; DB 2; Length 231;
 Best Local Similarity 60.9%; Pred. No. 2.3e-30;
 Matches 137; Conservative 29; Mismatches 55; Indels 4; Gaps 2;
 QY 1 EVOLQSGDPLVPGASVKISCKASGYFTGYMHVWVKSPGKGLWIGRIINPNNGVTLY 60
 Db 1 EVOLVSGDGLVAPQSLSITCTVSGFSLTDYGVNIRQPPGKGLWIGVIA-GGSITF 59
 QY 61 NQKFKKATLTVKSSSTAYMELASLTSEDSAVYICARSTMTITNYVMDYWGQSTSVTSS 120
 Db 60 NSALKSRSLNSKNSKQVFLKNSLHTDNTAYCYCKHEDYDWDYFVWGAGTTVTSS 119
 QY 121 AKTTPPSVYPLAPGSAAGTSMVTLGLVKGYPEPVTVTWNGSLSSSGVHTTTPAVLQSD 180
 Db 120 AKTTPPSVYPLAPGCGTTGSSVTGLVKGYPEPVTVTWNGSLSSSVHTTTPALLQSG 179
 QY 181 LYTLSSSVTPSPSTPSETVTCNVAHPASSTKVDKXIVPRDSGGP 225
 Db 180 LYTMSSSVTPSPSTPSETVTCNVAHPASSTVDKXIVPRDSGGP 221
 RESULT 32
 JE0244
 Ig kappa chain NIG2 precursor - human
 C:Species: Homo sapiens (man)
 C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
 C:Accession: JE0244
 R:Alim, M.A.; Hara, Y.; Hosain, M.S.; Takeda, K.; Yamagata, F.; Yamaki, S.; Kazi, H.; T
 submitted to JIPID, November 1998
 A:Description: A new subgroup of k type light chains (VkV) identified in cases of AL amy
 A:Reference number: JE0243
 A:Accession: JE0244
 A:Molecule type: protein
 A:Residues: 1-215 <ALI>
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 F:16-90/Domain: immunoglobulin homology <IMM>
 Query Match 19.9%; Score 702.5; DB 2; Length 215;

Best Local Similarity 62.1%; Pred. No. 9.3e-30;
 Matches 133; Conservative 36; Mismatches 42; Indels 3; Gaps 2;
 QY 460 IVMTQTPTSLVAGSAGRVTTTCASQSVNDVAYQKQSPKLLISYTSYAGVDPDR 519
 Db 2 VVLTQSPATLTVSGFERATLSCASQSVHNLAWYQKQSPKLLIYRATSTATGIPAR 61
 QY 520 FSGSGYGTDFTLITSSVOAEDAAVYFCQDYNS--PFTGGGTGKLEIKRAAAPTYSIFP 577
 Db 62 FSGSGGTDFTLITSSVQSEDFALYCCQ--YNTWPLTFTGGGTGKLEIKRTVAAPSVFIIP 120
 QY 578 PSSEQLTSGGASVYVFLNFPKIDINVKWIDGSRONGVNLNWTDDSDKDYSSSTL 637
 Db 121 PSDEQLASGTASVVCLLNFPYKAVQVQVNDALQSGNSQESVTEQDSKDYSSSTL 180
 QY 638 TLTKDEYERHNSYTCEATHTSTSPIVKSFNRNE 671
 Db 181 TLSKADYEKHKVYACEVTHOGLSSPVTKSNRGE 214
 RESULT 33
 S04845
 Ig heavy chain precursor - African clawed frog (fragment)
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 26-Aug-1999
 C:Accession: S04845; S05695
 R:Amemiya, C.T.; Haire, R.N.; Litman, G.W.
 Nucleic Acids Res. 17, 5389, 1989
 A:Title: Nucleotide sequence of a cDNA encoding a third distinct Xenopus immunoglobulin t
 A:Reference number: S04845; MUID:89345103; PMID:2503814
 A:Accession: S04845
 A:Molecule type: mRNA
 A:Residues: 1-549 <AME>
 A:Cross-references: EMBL:X15114
 R:Litman, G.W.
 submitted to the EMBL Data Library, April 1989
 A:Reference number: S05695
 A:Accession: S05695
 A:Molecule type: mRNA
 A:Residues: 'LC', 3-308, 'H', 310-549 <LIT>
 A:Cross-references: EMBL:X15114; NID:G64799; PID:G763031
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: glycoprotein; heterotrimer; immunoglobulin
 F:26-109/Domain: immunoglobulin homology <IMM>
 F:281,294/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 19.9%; Score 700.5; DB 2; Length 549;
 Best Local Similarity 28.0%; Pred. No. 3.8e-29;
 Matches 194; Conservative 107; Mismatches 214; Indels 179; Gaps 23;
 QY 1 EVOLQSGDPLVPGASVKISCKASGYFTGYMHVWVKSPGKGLWIGRIINPNNGVTLY 60
 Db 12 DIELVQSPSEIKSPGESIKUSCKTSGTFTNYLHWLQQVPGKGLWIGRIYFGDADTDY 71
 QY 61 NQKFKKATLTVKSSSTAYMELASLTSEDSAVYICARSTMTITNYVMDYWGQSTSVTSS 120
 Db 72 SSSYQGRCHISTDNPQSTFTFLANLKVEDTAIYCAREGV--GVYFDYWGQGTMTVTS 129
 QY 121 AKTTPPSVYPLAP--GSAATQNSMTVTLGCLVKGYFPFPTVTWNGSLSSSGVHTTFAVL- 177
 Db 130 ATLHAPSVPFPLRPPCGSSS--SDSHVTTCGLSTGLPAPVDVKNWNSGITSLGNKFPVAVLQ 188
 QY 178 QSLDYTLSSSVTPSPSTPSPS--ETVTCNVAHPASSTKVDKXIVPRDSGGPSEKSEINEKD 236
 Db 189 QSGFPASSQQTFLPSDWKAKSEFCNVEHKPTSTKYTKIEQDEPEIEPTVEL--- 244
 QY 237 LRKSEIQGTALGNLQIYYNKAITSSEKSAADQFTNTLLFKGFTGHPWINDLLVDL 296
 Db 245 -----LQG----- 247
 QY 297 GSTAATSEYEGSSVDLYGAYYQACAGTGNKTKACMYGGVTLDHNNRLTEBKVPINLWI 356
 Db 248 -----PCASSKVELLCLITGYA-----PSEIKVHLL 275

A;Description: Isolation and characterisation of sheep kappa light chain cDNA.

A;Reference number: S33161
 A;Accession: S33161
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-230 <POL>
 A;Cross-references: EMBL:X54110; NID:G237103; PIDN:CAA38046.1; PID:gl364221
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin
 F;143-212/Domain: immunoglobulin homology <IMM>

Query Match 19.2%; Score 675; DB 2; Length 230;
 Best Local Similarity 59.4%; Pred. No. 2.7e-28;
 Matches 126; Conservative 37; Mismatches 49; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVAGDRVTITCKASQSVNDVAWYQKQSPKLLISYTSRYAGVDR 519
 DB 18 IQVTSFSSLSASLTERVSTICTSQSVNLYNWYQKQSPKLLIYATRLHTDVFPSR 77
 QY 520 FSGSGYGTDTLTISVQAEADAAVYFCQDYNPPTFGGTTKLEIKRADAAPTIVIFPPS 579
 DB 78 FSGSGGDTYLTISNLEANDATYICLOVESTPLAFGGGTNVEIKRSDAQSVFLKPS 137
 QY 580 SEQLTGGASVWFLNFPKIDNVKWDIGSERQNGVNSWTDQSDKSTYMSSTLT 639
 DB 138 EEQLRTGTVWCLVNDVFPKIDNVKWDVGTQNSFNQNSFTDQSDKSTYSLSTLT 197
 QY 640 TKDEYERHNSYTCETHATKSTSTPIKSFNRNE 671
 DB 198 SSSEYQSHNAYACEVSHKSLPTALVKSPKNE 229

RESULT 38
 S22080

Ig heavy chain precursor (B/MT.4A.17.H5.A5) - bovine
 N;Alternate names: Ig gamma-1 chain C region (clone 8.10)
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
 C;Accession: S22080; S06610; A31303
 R;Sanders, P.G.
 Submitted to the EMBL Data Library, November 1991
 A;Reference number: S22080
 A;Accession: S22080
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-470 <SAN>
 A;Cross-references: EMBL:X62916; NID:G439; PIDN:CAA44699.1; PID:G440
 R;Symons, D.B.A.; Clarkson, C.A.; Beale, D.
 Mol. Immunol. 26, 841-850, 1989
 A;Title: Structure of bovine immunoglobulin constant region heavy chain gamma 1 and gamma 2
 A;Reference number: S06610; MUID:90097956; PMID:2513487
 A;Accession: S06610
 A;Molecule type: DNA
 A;Residues: 142-470 <SYM>
 A;Cross-references: EMBL:X16701
 A;Note: the sequence was determined from the germline gene
 C;Genetics:
 A;Gene: Ig CH gamma-1
 A;Introns: 98/1; 111/1; 221/1
 C;Superfamily: immunoglobulin C region; immunoglobulin homology
 C;Keywords: glycoprotein; heterotetramer; immunoglobulin; membrane protein
 F;161-225/Domain: immunoglobulin homology <IMM>
 F;338/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 19.1%; Score 673.5; DB 2; Length 470;
 Best Local Similarity 28.1%; Pred. No. 7.9e-28;
 Matches 187; Conservative 78; Mismatches 161; Indels 239; Gaps 18;

QY 1 EVQLQQSGPDIVKPGASVKISKASGYSTGYMHWKQSPGKGLWIGRINPNNGVTLY 60
 DB 20 QVQUREGSPVLKPSQILSTCTVSGFSLSYALTWRQAPGKALEWVGIT-SGGTTY 78
 QY 61 NQKFDKATLTVDKSSSTAYAMELSLTSEDSAVYICARST---MITNVMYDVGQGTST 117

DB 79 NPALKSRSLITKNSKQSVLSVSVTPEDTATYYCARSTYGEVGDGAIDAWGQGLVY 138
 QY 118 VSSAKTTPSPVYPLAPGSAQTNSMTLGLCLVKGYFPEPVTTWNSGSLSSGSHVTEPAVL 177
 DB 139 VSSASTTAPKVPYFLSSCCGDKSSSTVTGLCVSYNPEPVTTWNSGALKSGVHTPEAVL 198
 QY 178 QSD-LYTLSSSVTPSPSTPSETVTCNVAHPASSTKVDKKIVPRDGGSPSEKSEINEKD 236
 DB 199 QSSGLYSLSMVTVPGST-SGQFTCNVAHPASSTKVDKAVDPTCKPSPC-----D 248
 QY 237 LRKXSELOGTALGNLKIYYNSKAITSEKSAQDLTNTLLFKGFTTGHWPWNLVLDL 296
 DB 249 CCPPPELPGG-----PSVFIPPKP-----KDTLT-----ISGTPETVTCVVVDV 287
 QY 297 GSTAATSEYEGSSVDLYGAYGYQCAGGTENKTCACMGYVTLHNNRLTEKKVPIINLMI 356
 DB 288 G-----HD-----DPEVKFSWFV 300
 QY 357 DGKO-----TTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGCLYNSDSFGKVGQGLIVFH 412
 DB 301 DDVEVNTATTKPREQNFSTYRV-VSALRIQHODWTGK-----EFKCKVH----- 345
 QY 413 SSEGSTVSYDLFDAQGOVPTLLRIYRDNTTISSTLSISLYLYTTSIVMTQTPTSLNS 472
 DB 346 -NEG-----LPAPIV-----TISRT----- 360
 QY 473 AGDRVTITCKASQSVNDVAWYQKQSPKLLISYTSRYAGVDRFSGSGYGTDTLT 532
 DB 361 -----KGPAREPQ----- 368
 QY 533 ISSVQAEADAAVYFCQDYNPPTFGGTTKLEIKRADAAPTIVIFPSSEOLTSGGASVVC 592
 DB 369 -----VYVLAPQELSKSTVSLTC 388
 QY 593 FLNNFYPKDINVKWKIDGSRQNGVNSWTDQSDKSTYMSSTLTTLTKDEYERHNSYTC 652
 DB 389 MVTGFPDYIAVQRNGQPESEDKYGTTPQLDADSSYFLYSLKLRVDRNSWQEGDTYTC 448
 QY 653 BATHK 657
 DB 449 VVWHE 453

RESULT 39
 S29593

Ig kappa chain (WM65) - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 11-Jan-2000
 C;Accession: S29593
 R;Seymour, R.
 Submitted to the EMBL Data Library, February 1991
 A;Reference number: S29593
 A;Accession: S29593
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-197 <SEY>
 A;Cross-references: EMBL:X57856; NID:G52588; PIDN:CAA40991.1; PID:G52589
 C;Superfamily: immunoglobulin V region; immunoglobulin homology
 C;Keywords: heterotetramer; immunoglobulin

Query Match 18.8%; Score 663.5; DB 2; Length 197;
 Best Local Similarity 72.9%; Pred. No. 8.7e-28;
 Matches 132; Conservative 16; Mismatches 28; Indels 5; Gaps 2;

QY 460 IVMTQPTSLVAGDRVTITCKASQSV--SND---VAWYQKQSPKLLISYTSRYA 514
 DB 17 IVMTQAAPSIPTGESASISCRSKSLHNSGTYLYWFLQRFQSPQLLIYKSNLAS 76
 QY 515 GVPDRFSGSGYGTDTLTISVQAEADAAVYFCQDYNPPTFGGTTKLEIKRADAAPTIVS 574
 DB 77 GVPDRFSGSGYGTDTLTISVQAEADAAVYFCQDYNPPTFGGTTKLEIKRADAAPTIVS 136

QY 575 IFPPSEQLTSGGASVVCFLNNFYKIDINVKWKIDGSRQGVNSWTDQSDKSTYSMS 634
Db 137 IFPPSEQLTSGGASVVCFLNNFYKIDINVKWKIDGSRQGVNSWTDQSDKSTYSMS 196

QY 635 S 635
Db 197 S 197

RESULT 40
S69131
Ig heavy chain (DOT) - human (fragment)
N:Alternate names: anti-riboflavin IgG Fd fragment
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1998 #sequence_revision 22-May-1998 #text_change 21-Jan-2000
C:Accession: S69131
R:Stoppani, M.; Bellotti, V.; Negri, A.; Merlini, G.; Garver, F.; Ferri, G.
Eur. J. Biochem. 228, 886-893, 1995
A:Title: Characterization of the two unique human anti-flavin monoclonal immunoglobulins
A:Reference number: S69130; PMID:95255298; PMID:7737190
A:Accession: S69131
A:Molecule type: protein
A:Residues: 1-241 <STO>
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: blocked amino end; heterotetramer; immunoglobulin; pyroglutamic acid
F:1-241/Product: Ig heavy chain (DOT) (fragment) #status experimental <MAT>
F:140-205/Domain: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 18.8%; Score 661.5; DB 2; Length 241;
Best Local Similarity 59.4%; Pred. No. 1.4e-27;
Matches 130; Conservative 35; Mismatches 51; Indels 3; Gaps 3;

QY 1 EYQLOQSGPDLVKGASVKISKASGYSTGYMHVWVKQSPKGLWIGRINPNNGVTLV 60
Db 1 QVQLVQSGVERKVPQASVRIKASGYAFENYIHWRQAPGLGLEWMGINPQVAG-AVS 59

QY 61 NQFKDKATLVVDKSSSTTAYMELRSLTSEDSAVVYCAR-STMTNYVMYDYGQGTSTVTS 119
Db 60 SEKFRDLVMSDTSANTVSMQLRNLRSDDTGRVFCARVSYDFQSGYGMVWGQGTIVTS 119

QY 120 SAKTTPPVYPLAPGSAQTSMTVLGCLVKGYPPEVPTVWNSGSSGVHTFAVLQS 179
Db 120 SASTKGPSVFPLAPCSRSTSTALGCLVLDYDPEPTVTSWNSGALTSVGHTFAVLQS 179

QY 180 D-LYTLSSSVTPSPSTPSETVTCNVAHPASSTKVDDKI 217
Db 180 SGLYSLSSVTVTPSSNFGTQYTCNVDEKPSNTKVDKTV 218

RESULT 41
A23746
Ig kappa chain V-III (KAU cold agglutinin) - human
C:Species: Homo sapiens (man)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 21-Jan-2000
C:Accession: A23746
R:Leoni, J.; Gniso, J.; Goni, F.; Frangione, B.
J. Biol. Chem. 266, 2836-2842, 1991
A:Title: The primary structure of the Fab fragment of protein KAU, a monoclonal immunoglobulin
A:Reference number: A23746; PMID:91131575; PMID:1993660
A:Accession: A23746
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-215 <LEO>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:16-91/Domain: immunoglobulin homology <IMM>

Query Match 18.7%; Score 659.5; DB 2; Length 215;
Best Local Similarity 62.0%; Pred. No. 1.6e-27;
Matches 132; Conservative 31; Mismatches 49; Indels 1; Gaps 1;

QY 460 IVMTQTPTSLVSGADRVITCKASQSV-SNDVAWYQKPGQPKLLISYTSRRYAGVD 518

Db 2 IVTQSPATLSLSPGERATLISGGASQSVSNVLAWYQKFGQAPRLIYDASSRATGIPD 61
QY 519 RFSGSGGTDTLTITISVQAEADAAYFCQODYNSPPTFGGCTKLEIKRAADAAPTSTFPP 578
Db 62 RFSGSGGTDTLTITISLPEDEFVYGYQYGSPLTFGGGTKEIKRTVAAPSVFIFPP 121
QY 579 SSQLTSGGASVVCFLNNFYKIDINVKWKIDGSRQGVNSWTDQSDKSTYSMSSTLT 638
Db 122 SDEQLKSGTASVGLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSLSSTLT 181
QY 639 LTKDEYERHNSYTCEATHKTSTSPVKSFNRE 671
Db 182 LSKADYEKHKVYAGEVTHQGLSSPVTKSFNRGE 214

RESULT 42
JE0241
Ig kappa chain Am37 precursor - human
C:Species: Homo sapiens (man)
C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jan-2000
C:Accession: JE0241
R:Alim, M.A.; Yamaki, S.; Hossain, M.S.; Takeda, K.; Kojima, M.; Takashi, I.; Shinoda, T.
submitted to JIPID, November 1998
A:Description: Structure relationship of kappa type light chains with AL amyloidosis: Mult
A:Reference number: JE0241
A:Accession: JE0241
A:Molecule type: protein
A:Residues: 1-216 <ALI>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
F:16-92/Domain: immunoglobulin homology <IMM>

Query Match 18.7%; Score 658; DB 2; Length 216;
Best Local Similarity 60.8%; Pred. No. 1.9e-27;
Matches 131; Conservative 30; Mismatches 49; Indels 6; Gaps 3;

QY 460 IVMTQTPTSLVSGADRVITCKASQSV-SNDVAWYQKPGQPKLLISYTSRRYAG 515
Db 2 IVLTQSPDFLAFLSLGERATINCKSSVLYNSKNFLAWYQKFGQ-PKLLI-WANVRESG 59

QY 516 VPRFRSGSGVGTDTLTITISVQAEADAAYFCQODYNSPPTFGGCTKLEIKRAADAAPTSTI 575
Db 60 VPRFRSGSGVGTDTLTITISLQAEVAVYCCQYYSTPYSGQGRLEIKRTVAAPSVFI 119

QY 576 FPSSSQTLSGGASVVCFLNNFYKIDINVKWKIDGSRQGVNSWTDQSDKSTYSMS 635
Db 120 FPSSDQLKSGTASVGLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKSTYSLS 179

QY 636 TLTLTKDEYERHNSYTCEATHKTSTSPVKSFNRE 671
Db 180 TLTLTKADYEKHKVYAGEVTHQGLSSPVTKSFNRGE 215

RESULT 43
S31459
Ig gamma-1 chain - sheep (fragment)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S31459
R:Patric, S.; Nau, F.
submitted to the EMBL Data Library, December 1992
A:Reference number: S31459
A:Accession: S31459
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-472 <PAT>
A:Cross-references: EMBL:X69797
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:277-346/Domain: immunoglobulin homology <IMM>

Query Match 17.6%; Score 619.5; DB 2; Length 472;
Best Local Similarity 25.7%; Pred. No. 4.9e-25;

QY 637 LTLTKDEYERHNSYTCEATHKTSTPIVKSFRNE 671
 Db 195 LSLTKAQYNSHVSIVTCEVH-NSGSAIVQSFNRGD 228

RESULT 49
 S29594
 Ig gamma chain (MM65) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 08-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
 C:Accession: S29594
 R:Seymour, R.
 submitted to the EMBL Data Library, February 1991

A:Reference number: S29593
 A:Accession: S29594
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-178 <SEY>
 A:Cross-references: EMBL:X57857; NID:G52590; PIDN:CAA40992.1; PID:G52591
 C:Keywords: immunoglobulin

Query Match 16.0%; Score 562; DB 2; Length 178;
 Best Local Similarity 73.5%; Pred. No. 1.4e-22;
 Matches 108; Conservative 13; Mismatches 24; Indels 2; Gaps 1;

QY 1 EVQLQSGDPLVPGASVKISKASGYFTGYMHVWVKQSPGKLEWIGRIINPNNGVTLY 60
 Db 14 EVQLQSGDPLVPGASVKISKASGYFTGYMHVWVKQSPGKLEWIGRIINPNNGVTLY 60

QY 61 NQKFKDKATITVDKSSITAYMELSLTSDSAVYCARSTMIINYMDYWGQGTSTVSS 120
 Db 74 DPXFGKATITVDKSSITAYMELSLTSDSAVYCARSTMIINYMDYWGQGTSTVSS 131

QY 121 AKTTPPSVYPLAPGSAQTNSMTLGC 147
 Db 132 AKTTPPSVYPLAPGSAQTNSMTLGC 158

RESULT 50
 I54782
 gene Pvt-1a/Ig-Ck protein - mouse (fragment)
 C:Species: Mus sp. (mouse)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 02-Sep-2000
 C:Accession: I54782
 R:Huppi, K.; Siwarski, D.
 Int. J. Cancer 59, 848-851, 1994

A:Title: Chimeric transcripts with an open reading frame are generated as a result of tr
 A:Reference number: I54782; MUID:95080867; PMID:7989128
 A:Accession: I54782
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-126 <RSS>
 A:Cross-references: GB:S76258; NID:G913277; PIDN:AAB32752.1; PID:G913278
 C:Genetics:
 A:Gene: Pvt-1a/Ig-Ck
 C:Superfamily: pre-B cell omega light chain; immunoglobulin homology

Query Match 15.9%; Score 561; DB 2; Length 126;
 Best Local Similarity 93.0%; Pred. No. 1e-22;
 Matches 107; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 557 GGGTKLEIKRADAAPTIVSIFPPSSEQLTSGGASVCFVFNINPKDINKVKIDGSRQNG 616
 Db 11 GAAAKVKSIAADAAPTIVSIFPPSSEQLTSGGASVCFVFNINPKDINKVKIDGSRQNG 70

QY 617 VLNSWTDQSKDSTYSMSSTLTITKDEYERHNSYTCEATHKTSTPIVKSFRNE 671
 Db 71 VLNSWTDQSKDSTYSMSSTLTITKDEYERHNSYTCEATHKTSTPIVKSFRNE 125

RESULT 51
 P10011
 Ig heavy chain precursor V region (4C11) - mouse (fragment)

C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
 C:Accession: P10011
 R:Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
 Mol. Immunol. 25, 33-40, 1988

A:Title: Structural basis of stimulatory anti-idiotypic antibodies.
 A:Reference number: P10011; MUID:88142863; PMID:3125424
 A:Accession: P10011
 A:Molecule type: mRNA
 A:Residues: 1-151 <CHE>
 A:Experimental source: cell line 4C11
 A:Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylcho
 C:Superfamily: immunoglobulin V region; immunoglobulin homology
 C:Keywords: heterotrimer; immunoglobulin
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-136/Product: Ig heavy chain V region 4C11 #status predicted <VAT>
 F:34-117/Domain: immunoglobulin homology <IMV>
 F:50-54/Region: complementarity-determining 1
 F:69-85/Region: complementarity-determining 2
 F:118-125/Region: complementarity-determining 3
 F:137-151/Domain: C region (fragment) #status predicted <COR>

Query Match 15.9%; Score 560.5; DB 2; Length 151;
 Best Local Similarity 80.3%; Pred. No. 1.3e-22;
 Matches 110; Conservative 7; Mismatches 11; Indels 9; Gaps 2;

QY 1 EVQLQSGDPLVPGASVKISKASGYFTGYMHVWVKQSPGKLEWIGRIINPNNGVTLY 60
 Db 20 EVQLQSGDPLVPGASVKISKASGYFTGYMHVWVKQSPGKLEWIGRIINPNNGVTLY 79

QY 61 NQKFKDKATITVDKSSITAYMELSLTSDSAVYCARSTMIINYMDYWGQGTSTV 117
 Db 80 NEKFKDKATITVDKSSITAYMELSLTSDSAVYCARSTMIINYMDYWGQGTSTV 133

QY 118 VSSAKTTPPSVYPLAPG 134
 Db 134 VSSAKTTPPSVYPLAPG 150

RESULT 52
 G1M5
 Ig gamma-1 chain C region, secreted form - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 31-Mar-1980 #sequence_revision 24-Sep-1981 #text_change 16-Jul-1999
 C:Accession: A02159; A26234; A26236
 R:Honjo, T.; Obata, M.; Yamawaki-Kataoka, Y.; Kataoka, T.; Takahashi, N.; I
 Cell 18, 559-568, 1979

A:Title: Cloning and complete nucleotide sequence of mouse immunoglobulin gamma1 chain g
 A:Reference number: A02159; MUID:80045036; PMID:115593
 A:Accession: A02159
 A:Molecule type: DNA
 A:Residues: 1-324 <HON>
 A:Cross-references: GB:J00453
 A:Note: the sequence was determined from the germline gene
 A:Note: Lys-324 is removed posttranslationally
 R:Obata, M.; Yamawaki-Kataoka, Y.; Takahashi, N.; Kataoka, T.; Shimizu, A.; Mano, Y.; Sei
 Gene 9, 87-97, 1980

A:Title: Immunoglobulin gamma-1 heavy chain gene: structural gene sequences cloned in a l
 A:Reference number: A26234; MUID:80202559; PMID:6769752
 A:Accession: MOPC 31C
 A:Accession: A26234
 A:Molecule type: mRNA
 A:Residues: 76-324 <ORA>
 A:Cross-references: GB:V00775; NID:G51652; PIDN:CAA24153.1; PID:G51653
 R:Rogers, J.; Clarke, P.; Salser, W.
 Nucleic Acids Res. 6, 3305-3321, 1979

A:Title: Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain.
 A:Reference number: A26236; MUID:80012837; PMID:113776
 A:Accession: MOPC 21
 A:Molecule type: mRNA
 A:Residues: 170-275, 'D', '277', 'D', '279-322 <ROG>
 A:Cross-references: GB:V00795; NID:G51830; PIDN:CAA24176.1; PID:G780265

R:Adetugbo, K.
 J. Biol. Chem. 253, 6068-6075, 1978
 A:Title: Evolution of immunoglobulin subclasses. Primary structure of a murine myeloma 9
 A:Reference number: A26237; MUID:78242288; PMID:98524
 A:Contents: annotation; MOPC 21
 A:Note: this is the final paper in a series reporting the protein sequence, the disulfide
 A:Note: there are a number of differences from the sequence shown
 C:Genetics:
 A:Introns: 1/1; 98/1; 111/1; 218/1
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: alternative splicing; duplication; Glycoprotein; heterotetramer; immunoglob
 F:20-84/Domain: immunoglobulin homology <IM1>
 F:98-110/Region: hinge
 F:131-200/Domain: immunoglobulin homology <IM2>
 F:237-304/Domain: immunoglobulin homology <IM3>
 F:27-82,138,198,243-302/Disulfide bonds: #status experimental
 F:102/Disulfide bonds: interchain (to light chain) #status experimental
 F:104,107,109/Disulfide bonds: interchain (to heavy chain) #status experimental
 F:174/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 15.8%; Score 557; DB 1; Length 324;
 Best Local Similarity 28.3%; Pred. No. 5.3e-22;
 Matches 156; Conservative 48; Mismatches 89; Indels 258; Gaps 13;

QY 121 AKTTPSVYPLAPGSAAGTNSMTLGLVKGYPFVTVWNSGSLSSGVTFFPAVLQSD 180
 Db 1 AKTTPSVYPLAPGSAAGTNSMTLGLVKGYPFVTVWNSGSLSSGVTFFPAVLQSD 60
 QY 181 LYTLLSSVTVPSSTWPSSTVTCNVAHPASSTKVDKIVPRDGGPSEKSEINKDLRKK 240
 Db 61 LYTLLSSVTVPSSTWPSSTVTCNVAHPASSTKVDKIVPRDCG----- 103
 QY 241 SELQGTALGNLKIYYNNSKAITSSSEKSAQDLTNTLLFKGFTCHPMYNDLLVDLGSTA 300
 Db 104 CKPCICTVPEVSSVFIFPK-----PKDVLITL----- 132
 QY 301 ATSEYEGSVLDLYGAYGYQCAGGTNTKACMYGGVTLHDNNRLTEKKVPINLWDGKQ 360
 Db 133 -----TP-KVTCVVDIS-----KDDPEVQFSWFVD--- 157
 QY 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGQGLIVF 411
 Db 158 -DVEVHTAQTPREEQFNSTFRSVELPIMHQDLNGKEFKCRVNSAAPPAPIEK----- 211
 QY 412 HSSEGSTVSYDLFDAQGGYPTLLRIYRDNNTTISSTLSISLYLTYTTSIVMTQTPTSLV 471
 Db 212 -----TISK----- 216
 QY 472 SAGDRVTITCKASQSVSNDVAWYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDFTL 531
 Db 217 ----- 216
 QY 532 TISSVQAEAAVYFCQDYNSPPTFGGKLEIKRADAAPTIVSIFPPSSEQLTSGASVV 591
 Db 217 -----KGRKAPQVYTIPTPKQMAKDKVSLT 243
 QY 592 CFLANFYKDNVKKIDGSEKON-----GVLNSWTDDSKDSTYSMSSTLTITKDYER 646
 Db 244 CMITDFPEDITVQWNGQPAENYKNTQPMNT-----NGSYFYVSKLVQKSNWEA 296
 QY 647 HNSYTCEATHK 657
 Db 297 GNTFTCSVLHE 307

RESULT 53
 G1MSM
 Ig gamma-1 chain C region, membrane-bound form - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 17-Dec-1982 #sequence revision 31-Mar-1991 #text_change 16-Jul-1999
 C:Accession: B02159; A02160; B02158

R:Honjo, T.; Obara, M.; Yamawaki-Kataoka, Y.; Kataoka, T.; Kawakami, T.; Takahashi, N.; K
 Cell 18, 559-568, 1979
 A:Title: Cloning and complete nucleotide sequence of mouse immunoglobulin gamma chain ge
 A:Reference number: A02159; MUID:80045036; PMID:1115593
 A:Accession: B02159
 A:Molecule type: DNA
 A:Residues: 1-393 <HON>
 A:Cross-references: GB:J00453
 A:Note: the sequence was determined from the germline gene
 R:Tyler, B.M.; Cowman, A.F.; Gerondakis, S.D.; Adams, J.M.; Bernard, O.
 Proc. Natl. Acad. Sci. U.S.A. 79, 2008-2012, 1982
 A:Title: mRNA for surface immunoglobulin gamma chains encodes a highly conserved transmem
 A:Reference number: A02160; MUID:82197626; PMID:6804950
 A:Accession: A02160
 A:Molecule type: mRNA
 A:Residues: 323-393 <TYL>
 R:Rogers, J.; Choi, E.; Souza, L.; Carter, C.; Word, C.; Kuehl, M.; Eisenberg, D.; Wall,
 Cell 26, 19-27, 1981
 A:Title: Gene segments encoding transmembrane carboxyl termini of immunoglobulin gamma cl
 A:Reference number: A02158; MUID:82115295; PMID:6799207
 A:Accession: B02158
 A:Molecule type: DNA
 A:Residues: 323-366 <ROG>
 A:Note: this sequence is the translation of the first exon of the M segment
 C:Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The ma
 ncode membrane-bound chains in that it contains an alternative 3' end, encoded in separa
 C:Genetics:
 A:Introns: 1/1; 98/1; 111/1; 218/1; 323/1; 366/3
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
 hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 C:Keywords: alternative splicing; duplication; Glycoprotein; heterotetramer; immunoglob
 F:131-200/Domain: immunoglobulin homology <IM>
 F:340-357/Domain: transmembrane #status predicted <TYM>
 F:358-393/Domain: intracellular #status predicted <INT>
 F:174,278/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.8%; Score 557; DB 1; Length 393;
 Best Local Similarity 28.3%; Pred. No. 6.8e-22;
 Matches 156; Conservative 48; Mismatches 89; Indels 258; Gaps 13;

QY 121 AKTTPSVYPLAPGSAAGTNSMTLGLVKGYPFVTVWNSGSLSSGVTFFPAVLQSD 180
 Db 1 AKTTPSVYPLAPGSAAGTNSMTLGLVKGYPFVTVWNSGSLSSGVTFFPAVLQSD 60
 QY 181 LYTLLSSVTVPSSTWPSSTVTCNVAHPASSTKVDKIVPRDGGPSEKSEINKDLRKK 240
 Db 61 LYTLLSSVTVPSSTWPSSTVTCNVAHPASSTKVDKIVPRDCG----- 103
 QY 241 SELQGTALGNLKIYYNNSKAITSSSEKSAQDLTNTLLFKGFTCHPMYNDLLVDLGSTA 300
 Db 104 CKPCICTVPEVSSVFIFPK-----PKDVLITL----- 132
 QY 301 ATSEYEGSVLDLYGAYGYQCAGGTNTKACMYGGVTLHDNNRLTEKKVPINLWDGKQ 360
 Db 133 -----TP-KVTCVVDIS-----KDDPEVQFSWFVD--- 157
 QY 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGQGLIVF 411
 Db 158 -DVEVHTAQTPREEQFNSTFRSVELPIMHQDLNGKEFKCRVNSAAPPAPIEK----- 211
 QY 412 HSSEGSTVSYDLFDAQGGYPTLLRIYRDNNTTISSTLSISLYLTYTTSIVMTQTPTSLV 471
 Db 212 -----TISK----- 216
 QY 472 SAGDRVTITCKASQSVSNDVAWYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDFTL 531
 Db 217 ----- 216
 QY 532 TISSVQAEAAVYFCQDYNSPPTFGGKLEIKRADAAPTIVSIFPPSSEQLTSGASVV 591
 Db 217 -----KGRKAPQVYTIPTPKQMAKDKVSLT 243

C:Accession: PS0017; C25941

R:Brueggemann, M.

Gene 74, 473-482, 1988

A:Title: Evolution of the rat immunoglobulin gamma heavy-chain gene family.

A:Reference number: PS0017; MUID:89232738; PMID:3149946

A:Accession: PS0017

A:Molecule type: DNA

A:Residues: 1-326 <BRU>

R:Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H.

Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986

A:Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibody

A:Reference number: A25941; MUID:86287397; PMID:3016742

A:Accession: C25941

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 220-326 <BR2>

C:Genetics:

A:Introns: 98/1; 113/1; 220/1

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: immunoglobulin

F:20-84/Domain: immunoglobulin homology <IMM>

Query Match 15.6%; Score 550; DB 2; Length 326;
Best Local Similarity 27.7%; Pred. No. 1.2e-21;
Matches 150; Conservative 64; Mismatches 90; Indels 238; Gaps 14;

QY 121 AKTTPSVYPLAPGSAAGTNSMTLGLVKGYPPEPVTVWNSGSLSSGVHTFPFVAVLQSD 180
DB 1 AETAPSVYPLAPGALKNSMTLGLVKGYPPEPVTVWNSGALSSGVHTFPFVAVLQSG 60

QY 181 LYTSSSVTVPSSTWPSSTVTCNVAHPASSTKVDKIVPRDGGPSEKSEINEKDLRKK 240
DB 61 LYLTSSVTVPSSTWPSSTVTCNVAHPASSTKVDKIVPRCNGGDKPC----- 109

QY 241 SELOQTALGNLKOIYYNSKAITSEKSAQDLNTLLFKGFTGHFWNDLLVDLGSTA 300
DB 110 -----TCTGSEVSS-----VFIFPPKPKDVL----- 130

QY 301 ATSEYEGSSVDLYGAYGYQCAGGTENKTACMGVGTLDNNRLTEKKVPINLWIDG-- 358
DB 131 -----TITL-----TP-KVTCVVVDIS-----QDDPEVHFSWFDDVE 162

QY 359 ---KQTTVPIDKVTISKKEVTVOELDQARHYLHGKFGLYNSDSFGKVGQRLIVFHSSE 415
DB 163 VHTAQTRPPEEQFNSTFR--SVSELPILHQDLNGR----- 196

QY 416 GSTVSYDLFDAQGYPDTLRIYRDNTTISTSLISLYLYTTSIVMTQTSLIVSAGD 475
DB 197 ----- 196

QY 476 RVITTCASQSVSNDVAMVYQKQKPGSPKLLISYTSRYAGVDPDRFSGSGYGTDTLTISS 535
DB 197 --TPRCV-----TSAAPFSPIEKTISK 217

QY 536 VQAEADAAYFCQDYNPPTFGGTTKLEIKRADAAPTVSIFFPSSEQLTSGGASVVCFLN 595
DB 218 PE-----GRTQV-----PHVYTMSTPKEMTQNEVSIITCMVK 249

QY 596 NFYPKDINVKWKIDGSRQNGVLSNWTQDSDKSTYSMSSTLTLTDKDYERHNSYTCEAT 655
DB 250 GFYPDPDIYVEWMNGQPOEN--YKNTPTMTDT--DGSYFLYSLKLVNKKVKEKQQGNTFTCSVL 307

QY 656 HK 657
DB 308 HE 309

RESULT 57

PS0019

Ig gamma-2a chain C region - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 16-Jul-1999

C:Accession: PS0019; D25941

RESULT 58

S29690

Ig heavy chain VDJ region - rat (fragment)

C:Species: Rattus norvegicus (Norway rat)

C>Date: 06-Jan-1995 #sequence_revision 30-Jan-1998 #text_change 20-Jun-2000

C:Accession: S25690

R:Dammers, P.M.; Bos, N.A.; Kroese, F.G.M.

R:Brueggemann, M.
Gene 74, 473-482, 1988
A:Title: Evolution of the rat immunoglobulin gamma heavy-chain gene family.
A:Reference number: PS0017; MUID:89232738; PMID:3149946
A:Accession: PS0019
A:Molecule type: DNA
A:Residues: 1-322 <BRU>
R:Brueggemann, M.; Free, J.; Diamond, A.; Howard, J.; Cobbold, S.; Waldmann, H.
Proc. Natl. Acad. Sci. U.S.A. 83, 6075-6079, 1986
A:Title: Immunoglobulin heavy chain locus of the rat: striking homology to mouse antibody
A:Reference number: A25941; MUID:86287397; PMID:3016742
A:Accession: D25941
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 216-322 <BR2>
C:Genetics:
A:Introns: 98/1; 109/1; 216/1
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: immunoglobulin
F:20-84/Domain: immunoglobulin homology <IMM>

Query Match 15.3%; Score 539; DB 2; Length 322;
Best Local Similarity 28.2%; Pred. No. 4.5e-21;
Matches 153; Conservative 55; Mismatches 92; Indels 242; Gaps 15;

QY 121 AKTTPSVYPLAPGSAAGTNSMTLGLVKGYPPEPVTVWNSGSLSSGVHTFPFVAVLQSD 180
DB 1 AETAPSVYPLAPGALKNSMTLGLVKGYPPEPVTVWNSGALSSGVHTFPFVAVLQSG 60

QY 181 LYTSSSVTVPSSTWPSSTVTCNVAHPASSTKVDKIVPRDGGPSEKSEINEKDLRKK 240
DB 61 LYLTSSVTVPSSTWPSSTVTCNVAHPASSTKVDKIVPRC----- 102

QY 241 SELOQTALGNLKOIYYNSKAITSEKSAQDLNTLLFKGFTGHFWNDLLVDLGSTA 300
DB 103 -----NPCGCTGSEVSS-----VFIFPPKTKDVL----- 126

QY 301 ATSEYEGSSVDLYGAYGYQCAGGTENKTACMGVGTLDNNRLTEKKVPINLWIDG-- 358
DB 127 -----TITL-----TP-KVTCVVVDISQND-----PEVRFSEWFDDE 158

QY 359 ---KQTTVPIDKVTISKKEVTVOELDQARHYLHGKFGLYNSDSFGKVGQRLIVFHSSE 415
DB 159 VHTAQTHAEKQSNSTLR--SVSELPVHVDWLNK-----TFCKVN----- 199

QY 416 GSTVSYDLFDAQGYPDTLRIYRDNTTISTSLISLYLYTTSIVMTQTSLIVSAGD 475
DB 200 -----SGAFFAPI----- 207

QY 476 RVITTCASQSVSNDVAMVYQKQKPGSPKLLISYTSRYAGVDPDRFSGSGYGTDTLTISS 535
DB 208 -----EKSIS-----KPEGTPT----- 219

QY 536 VQAEADAAYFCQDYNPPTFGGTTKLEIKRADAAPTVSIFFPSSEQLTSGGASVVCFLN 595
DB 220 -----GPQVVTMAPPKEMTQSQVSITCMVK 245

QY 596 NFYPKDINVKWKIDGSRQNGVLSNWTQDSDKSTYSMSSTLTLTDKDYERHNSYTCEAT 655
DB 246 GFYPDPDIYVEWMNGQPOEN--YKNTPTMTDT--DGSYFLYSLKLVNKKVKEKQQGNTFTCSVL 303

QY 656 HK 657
DB 304 HE 305

PNC0444
 Ig heavy chain V region precursor - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #
 A:Accession: PNC0444
 R:X.Kalyuzh, B.; Betrl, G.; Shao, H.; Diamantstein, T.;
 Gene 122, 321-328, 1992
 A>Title: A general method for chimerization of monoclonal
 A:Reference number: PNC0444; PMID:9313640; PMID:1339
 A:Accession: PNC0444
 A:Molecule type: mRNA
 A:Residues: 1-150 <KAL>
 A:Cross-references: GB:L02346

C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-150/Product: Ig heavy chain V region #status predicted <MAT>
F:20-117/Domain: variable region <VRG>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 15.0%; Score 527; DB 2; Length 150;
Best Local Similarity 79.7%; Pred. No. 7.2e-21;
Matches 106; Conservative 4; Mismatches 21; Indels 2; Gaps 1;

QY 1 EVLQOQSGPDLVKPGASVKISKASGYSTGYMHVWQSPGKLEWIGRINPNNGVTLY 60
DB 20 EVLQOQFGAELVKPGTSVKISKASGYIFTDYNMHWKSHGKSLWIGDIDPFDSSY 79
QY 61 NQKFKDKATLTVDKSSITAYMELRLSTSDSAVYICARSTMITNTYMDYWGQSTVTVSS 120
DB 80 NQKFKGKATLTVDKSSNTAYMELRLSTSDTAVYICARGGF--PYGMDYWGQSTVTVSS 137
QY 121 AKTTPPSVYPLAP 133
DB 138 AKTTPPSVYPLAP 150

RESULT 62
A46507
Ig alpha chain - chicken
C:Species: Gallus gallus (chicken)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 26-Aug-1999
C:Accession: A46507
R:Mansikka, A.
J. Immunol. 149, 855-861, 1992
A:Title: Chicken IGA H chains. Implications concerning the evolution of H chain genes.
A:Reference number: A46507; MUID:92340889; PMID:1634774
A:Accession: A46507
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-585 <MAN>
A:Cross-references: GB:S40610; NID:g251907; PID:g251908
A>Note: sequence inconsistent with the nucleotide translation
A>Note: sequence extracted from NCBI backbone (NCBI:109906, NCBI:109907)
C:Superfamily: immunoglobulin C region; immunoglobulin homology
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 14.7%; Score 516.5; DB 2; Length 585;
Best Local Similarity 24.4%; Pred. No. 1.4e-19;
Matches 174; Conservative 99; Mismatches 228; Indels 211; Gaps 25;

QY 2 VQLQOQSGPDLVKPGASVKISKASGYSTGYMHVWQSPGKLEWIGRINPNNGVTLYN 61
DB 21 VTLDESGLQTPGGLSLVCKASGFTFSSYSMGMRQAPGKLEWVAGIDDDGSGTGYG 80
QY 62 QKFKDKATLTVDKSSITAYMELRLSTSDSAVYICARSTMITNTYV--MDYWGQSTVTY 118
DB 81 PAVQGRATISRDNGOSTVRLQNLRAEDTATYCKASCGGACASIDAWHGTEIV 140
QY 119 SSAKTTPSVYPLAPGSAQNSMWTGLCKVGYFPFPTVTMNSGL--SSGVHTTTPAV 176
DB 141 SSASASRPTLYQLPLSDCPDPNVTGCLVTSFELPFPVTMTTGAADATATVSLPVA 200
QY 177 LQSDLYTLSSSVTPSSWTPSETVTCNVAHPASTKDKIIVPRSDSGPSEKSEINEKD 236
DB 201 TTGGTYSLTALTVPRELQGNFVFCRAQHAATGADV-KETIGDGVCP----- 248
QY 237 LRKXSELOGTALGNLQIYYNSKAITSSSEKADQFTNTLLFGFTGHPFWNDLLVLD 296
DB 249 -----IFTSKVTLSDPTQDFERRVLV-----CLVEGL 278
QY 297 GSTAATSEYEGSSVDLYGAYGYOCAGGTENKTA-----CMYGGVTLHDNRLTEKK 349
DB 279 PSAGAAQWLQDNSE-----TPAPESDESGCDSTESGYTQWSRVNVTKRS- 325
QY 350 VPINLWIDKGQTTVPIDKVKTSKKEVTVQELDLQARHLHGKFLGYNLSDSGFGKVGQGLI 409

DB 326 -----WEGGAQ-----FGCRVTHGAL 341
QY 410 VHSSEGSTVSYDLFDAQGOYPTLLRIYRDNTTISSTLSISLYLTYTTGIVMTQPTSL 469
DB 342 --KEPTATVSTDC-DATPQ-----LQVSL-----LPFILEEL 371
QY 470 LVSGADRVTITCKASQSVND---VAVYQKQPOQSKPLIISYTSRYAGVDPDRFSGSYG 526
DB 372 LVS--HNATVTCVVSNAADAGVSVWSRSSG--GLDVSQTEDRQA----- 414
QY 527 TDTLTLSISVCAEDAAVYFCQDDYNSPPTFGGCTKLE-----IKRADA---APTYS 574
DB 415 -DRYTVRSF-----LRVCAEENWGGETFGCSVRREEGVVVAEESIRKETDTPLHAPSVY 467
QY 575 IFPPSEQLT-SGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQD----- 625
DB 468 VFPPPAEELSLOETATLTWCASSFLP-----SSILLTWTQQNPISPNQY 512
QY 626 -----SKDST-YMSSTLTILTKDEYERHNSYCEATHK-TSTSPIVKSNRN 670
DB 513 LIFPEKOGDFYSLYSKLVSVEDWQRGDVFQVGVGHGDIPLNFHKSIDKN 564

RESULT 63
A49982
Ig heavy chain V region (BA7.1) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C:Accession: A49982
R:Lin, C.; Kleber-Emmons, T.; Villalobos, A.P.; Foster, M.H.; Wahlgren, C.; Kleyman, T.R.
J. Biol. Chem. 269, 2805-2813, 1994
A:Title: Topology of an amiloride-binding protein.
A:Reference number: A49982; MUID:94132051; PMID:8300613
A:Accession: A49982
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-120 <LIN>
A:Cross-references: GB:I24802; NID:g452096; PID:AAA98740.1; PID:g452097
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 14.6%; Score 514; DB 2; Length 120;
Best Local Similarity 81.7%; Pred. No. 2.6e-20;
Matches 98; Conservative 6; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVLQOQSGPDLVKPGASVKISKASGYSTGYMHVWQSPGKLEWIGRINPNNGVTLY 60
DB 1 EVLQOQSGPELVKPGASVKISKASGYSTGYIHWKSHVKSLEWIGHISPYNGATTY 60
QY 61 NQKFKDKATLTVDKSSITAYMELRLSTSDSAVYICARSTMITNTYMDYWGQSTVTVSS 120
DB 61 NQNFKDTASLTVDKSSITAYMELRLSTSDSAVYICARPNYCHYTMIDYWGQSTVTVSS 120

RESULT 64
A49633
Ig lambda-like chain, V-C region - nurse shark
C:Species: Ginglymostoma cirratum (nurse shark)
C:Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 21-Jan-2000
C:Accession: A49633
R:Greenberg, A.S.; Steiner, L.; Kasahara, M.; Flajnik, M.F.
Proc. Natl. Acad. Sci. U.S.A. 90, 10603-10607, 1993
A:Title: Isolation of a shark immunoglobulin light chain cDNA clone encoding a protein re
A:Reference number: A49633; MUID:94068449; PMID:8248152
A:Accession: A49633
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-238 <GRE>
A:Experimental source: spleen
A>Note: sequence extracted from NCBI backbone (NCBI:141012, NCBI:141013)
C:Superfamily: immunoglobulin V region; immunoglobulin homology

F:36-110/Domain: immunoglobulin homology <IMM>

Query Match 14.6%; Score 513.5; DB 2; Length 238;
Best Local Similarity 48.6%; Pred. No. 6.4e-20;
Matches 105; Conservative 38; Mismatches 68; Indels 5; Gaps 3;

QY 460 IVMTQPTSLYLSAGDRVITCKASQSYSDVAVYQOQKPGQSPKLLISYTSRYAGVDR 519
DB 22 INTQSPPLVSLGGLGTATITCTASQSYSNLAWYQOQKPGQSPKLLIYAATNRYTCVSR 81

QY 520 FSGSGYGTFTLTISVQAEAAVFCQDYNPP---TFGGTGLKLEIKRADAAPTISIF 576
DB 82 FSGSGSGTFTLTISNVQNEVDVYVQSAVYSYGRLLAFGKGTGLRLSRDRSQPKLTLL 141

QY 577 PPSSEQL-TSGASVVCFLNFPKIDINVKWIDSERQNGVLSNWTQDSDKSYNSVS 635
DB 142 PPSDQVQTKGTATLVCLANHFYDELQVQWKKQGAVIDSGVQTS-NYLRSASDSTYSVSS 200

QY 636 TLTLTKDEYERHNSYCEATHTKTSTSPVKSFNRE 671
DB 201 LTLTSGSDHESNAPFSCALHTVLSPLSKISRSE 236

RESULT 65
PL0012
Ig heavy chain precursor V region (F6-3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
C:Accession: PL0012
R:Cheng, H.L.; Sood, A.K.; Ward, R.E.; Kieber-Emmons, T.; Kohler, H.
Mol. Immunol. 25, 33-40, 1988
A:Title: Structural basis of stimulatory anti-idiotypic antibodies.
A:Reference number: PL0011; MUID:88142863; PMID:3125424
A:Accession: PL0012
A:Molecule type: mRNA
A:Residues: 1-166 <CHE>
A:Experimental source: cell line F6-3
C:Comment: This protein is an anti-idiotypic antibody which induces an anti-phosphorylch
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-32/Domain: signal sequence #status predicted <SIG>
F:33-151/Product: Ig heavy chain V region 4C11 #status predicted <MAT>
F:47-130/Domain: immunoglobulin homology <IMM>
F:63-67/Region: complementarity-determining 1
F:82-98/Region: complementarity-determining 2
F:131-140/Region: complementarity-determining 3
F:152-166/Domain: C region (fragment) #status predicted <COR>

Query Match 14.5%; Score 510.5; DB 2; Length 166;
Best Local Similarity 73.9%; Pred. No. 5.9e-20;
Matches 99; Conservative 9; Mismatches 25; Indels 1; Gaps 1;

QY 1 EVOLQSGPDLVKGASVKISCKASGYSTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
DB 33 QVOLQSGPELVKPGASVKISCKASGYRFTDYMHVWVKQSGKSLWIGSTNPYIDTNY 92

QY 61 NQKFKDKATLTVDKSSSTAYMELRLTSDSAVYVCARSTMTINYMDYWGQTSVTSS 120
DB 93 KENFKGRATVTVDKSSSTAYMELRLTSDSAVYVCAREGGFGN-SLDYWGQTSVNVSS 151

QY 121 AKTTPPSVYPLAPG 134
DB 152 AKTTPPSVYPLAPG 165

RESULT 66
A27609
Ig heavy chain precursor V region (I29) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 15-Dec-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999
C:Accession: A27609
R:Klein, D.; Nietupski, J.; Sirlin, S.; Stavnezer, J.
J. Immunol. 140, 1676-1684, 1988

A:Title: I.29 lymphoma cells express a nonmutated V-H gene before and after H chain switch
A:Reference number: A27609; MUID:88154467; PMID:3126234
A:Accession: A27609
A:Molecule type: DNA
A:Residues: 1-139 <KLE>
A:Cross-References: EMBL:M19401; NID:G195441; PIDN:AAA38303.1; PID:G5533992
C:Genetics:
A:Introns: 16/1
A:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-139/Product: Ig heavy chain V region I29 #status predicted <VAR>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 14.4%; Score 506; DB 2; Length 139;
Best Local Similarity 80.8%; Pred. No. 8e-20;
Matches 97; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 1 EVOLQSGPDLVKGASVKISCKASGYSTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
DB 20 EVOLQSGPELVKPGASVKISCKASGYRFTDYMHVWVKQSGKSLWIGSTNPYIDTNY 79

QY 61 NQKFKDKATLTVDKSSSTAYMELRLTSDSAVYVCARSTMTINYMDYWGQTSVTSS 120
DB 80 NQKFKGRATLTVDKSSSTAYMELRLTSDSAVYVCARYSYVYAMDYWGQTSVTSS 139

RESULT 67
I37267
Ig heavy chain V region (I29) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 16-Aug-1996
C:Accession: I37267
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A:Title: Heavy and light chain variable region sequences and antibody properties of anti-
A:Reference number: A38740; MUID:91177923; PMID:1706720
A:Accession: I37267
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-128 <RUF>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-102/Domain: immunoglobulin homology <IMM>

Query Match 14.3%; Score 503; DB 2; Length 128;
Best Local Similarity 79.7%; Pred. No. 1e-19;
Matches 98; Conservative 7; Mismatches 14; Indels 4; Gaps 1;

QY 2 VOLQSGPDLVKGASVKISCKASGYSTGYMHVWVKQSPGKLEWIGRINPNNGVTLYN 61
DB 6 VOLQSGPELVKPGASVKISCKTSGYTFEYTHVWVKQSHGKSLWIGGINPNNGGTSYN 65

QY 62 QKFKDKATLTVDKSSSTAYMELRLTSDSAVYVCARSTMTIT----NYMDYWGQTSVT 117
DB 66 QKFKGRATLTVDKSSSTAYMELRLTSDSAVYVCARGLTTVVAKSYFYFDYWGQGTILT 125

QY 118 VSS 120
DB 126 VSS 128

RESULT 68
P30057
Ig heavy chain precursor V region (PAR) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 20-Jun-2000
C:Accession: P30057
R:Yaoita, Y.; Takahashi, M.; Azuma, C.; Kanai, Y.; Honjo, T.
J. Biochem. 104, 337-343, 1988
A:Title: Biased expression of variable region gene families of the immunoglobulin heavy c
A:Reference number: P30057; MUID:89197817; PMID:2467902
A:Accession: P30057

A:Molecule type: DNA
A:Residues: 1-135 <VAO>
A:Cross-references: GB:D00307; NID:9220448; PIDN:BA00213.1; PID:9220449
A:Note: the authors translated the codon AAG for residue 32 as Asn and GAC for 92 as Gly
C:Comment: the gene encoding this protein was isolated from a hybridoma that produces an Ig heavy chain precursor V region - ladyfish
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:1-13/Domain: signal sequence #status predicted <SIG>
F:20-135/Product: Ig heavy chain V region PAR #status predicted <MAT>
F:34-117/Domain: immunoglobulin homology <IMM>

Query Match 14.3%; Score 502; DB 2; Length 135;
Best Local Similarity 82.5%; Pred. No. 1.2e-19;
Matches 99; Conservative 6; Mismatches 11; Indels 4; Gaps 1;

Qy 1 EVQLQSGPDLVKPGASVKISKASGYSFTGYMHVWVKQSPKGLGWIGRINPNNGVTLV 60
Db 20 EVQLQSGPDLVKPGASVKISKASGYSFTGYMHVWVKQSPKGLGWIGRINPNNGVTLV 79
Qy 61 NQKFKGKATLVDKSSSTAYMELRLTSEDSAVVYCARSTMTINVMYDYGQGSVTVSS 120
Db 80 NQKFKGKATLVDKSSSTAYMELRLTSEDSAVVYCARSTMTINVMYDYGQGSVTVSS 135

RESULT 69
A34891
Ig heavy chain precursor V region - ladyfish
C:Species: Elops saurus (ladyfish)
C:Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 21-Jul-2000
C:Accession: A34891
R:Amemiya, C.T.; Litman, G.W.
Proc. Natl. Acad. Sci. U.S.A. 87, 811-815, 1990
A:Title: Complete nucleotide sequence of an immunoglobulin heavy-chain gene and analysis
A:Reference number: A34891; MUID:90138916; PMID:2105490
A:Accession: A34891
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-568 <AME>
A:Cross-references: GB:M26182; NID:9213134; PID:AAA49238.1; PID:G213135
C:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:33-116/Domain: immunoglobulin homology <IMM>

Query Match 14.1%; Score 495.5; DB 2; Length 568;
Best Local Similarity 22.8%; Pred. No. 1.6e-18;
Matches 159; Conservative 109; Mismatches 225; Indels 203; Gaps 24;

Qy 4 LQSQGPDLVKPGASVKISKASGYSFTGYMHVWVKQSPKGLGWIGRINPNNGVTLVXOK 63
Db 22 LTESPAVKKFGESKLTCTAGSTFNSYNGWIRQAPGKGLWATLKYNABEYYSQS 81
Qy 64 FKDKATLVDKSSSTAYMELRLTSEDSAVVYCARSTMTINVMYDYGQGSVTVSSAKT 123
Db 82 VKGRFTISRDNSKQLVQLQNSLRADTAIVYCAR--VYGYAFDYWGRTMTVTTTGEQ 139
Qy 124 TPSPVYPLAGSAQTSMVTLGCLVKGYPPEPTVTWNSGSL--SGVHTFPVAVLQSDLY 182
Db 140 ASPVFPVL--SCATSGYVINGGIGKYLPSDTFSWSDSTDLTDLYQLPSPVLSGGKY 197
Qy 183 TLSSSVTPSPSTWPTVTCNVHPASTKVDKXIVPRDGGPSEKSEINEKDLRKSE 242
Db 198 D-----RVSH-----ARVTEGDFKSAE 215
Qy 243 LQ-GLALNKLQIYYNSKATISSE--KSADOFILNTLLPKGFTGHPWINDLLVLDLST 299
Db 216 FKCTTELGKK--TPVVIKPEPPKPPKPPVLSIMT-----PSQFEITLN----- 258
Qy 300 AATSEYEGSSVDLYGAYGYOCAGGTENKTACMYGGVTLDDNNRLTEKKVPIINLWI-DG 358
Db 259 -KTATFACLAIDFFPKGHSFK-----WLRDG 283
Qy 359 KQTVTPDKVTKSKETVTVQELDQARHYLHGKFLGNSFGKVGQRLIVFHSSEGST 418
Db 359 KQTVTPDKVTKSKETVTVQELDQARHYLHGKFLGNSFGKVGQRLIVFHSSEGST 418

Db 284 KEVTDGIATLTCEQCK-----GDKSFTASSFLQASQW 317
Qy 419 VSYD-----LFDAGQVDPDLLRIYRDNNTTISSTLSISLYLTTSIVMTQTPTSLVSA 473
Db 318 KRLDGTFTCFIQEGEITE-----QVYKSSAECSPEAQIDAKISPTPEELFLQ- 367
Qy 474 GDRVTITCKASQSVS--NDVAV--YQKDPQ-----SPKILISYTSRYAGVPDRFSG 522
Db 368 -QRTLTICKITGDVGRNVTVWVGSEVRVGQDFEQRMISKLLIDYE----- 413
Qy 523 SGYGTDTLTLTSSVQAEDAAVYFCQDYNPP-----FGGQTKLEIKRADAAPT 573
Db 414 -----EMKNRTYCTCKVEHSDLPSPLATSYRREGCKWQ-----SPTV 451
Qy 574 SIPEPSEQLTSGASVFLANNFYPKDINVKKIDGSRQNGVLSWTDQDSKDSYISM 633
Db 452 FILAP-AEQNLSTVLICYAKDFEPEQLISLWLDQPVETDV--PTTEVVKTEGTSYV 508
Qy 634 SSTLTITKQBYERHNSVTCEATHKTSPIVKSFNR 669
Db 509 FSQLTIPASDWDGVSVCVHETVWESVVKTIIVR 544

RESULT 70
C37267
Ig heavy chain V region (Py69) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
C:Accession: C37267
R:Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A:Title: Heavy and light chain variable region sequences and antibody properties of anti-
A:Reference number: A38740; MUID:91177923; PMID:1706720
A:Accession: C37267
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-128 <RUF>
C:Superfamily: immunoglobulin V region; immunoglobulin homology
C:Keywords: heterotetramer; immunoglobulin
F:19-102/Domain: immunoglobulin homology <IMM>

Query Match 14.1%; Score 495; DB 2; Length 128;
Best Local Similarity 77.2%; Pred. No. 2.7e-19;
Matches 95; Conservative 9; Mismatches 15; Indels 4; Gaps 1;

Qy 2 VOLQQSGPDLVKPGASVKISKASGYSFTGYMHVWVKQSPKGLGWIGRINPNNGVTLV 61
Db 6 VOLQQSGPDLVKPGASVKISKASGYSFTGYMHVWVKQSPKGLGWIGRINPNNGVTLV 55
Qy 62 QKFKGKATLVDKSSSTAYMELRLTSEDSAVVYCAR-----STMITNYMDYWGQTSVT 117
Db 65 QKFKGKATLVDKSSSTAYMELRLTSEDSAVVYCARPGYGNVYTSYVFDYWGQTTLT 125
Qy 118 VSS 120
Db 126 VSS 128

RESULT 71
PS0024
Ig heavy chain precursor V region (6A4) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Nov-1996
C:Accession: PS0024
R:Marget, M.; Eckhardt, A.; Ehret, W.; von Specht, B.U.; Duchene, M.; Domdey, H.
Gene 74, 335-345, 1988
A:Title: Cloning and characterization of cDNAs coding for the heavy and light chains of a
A:Reference number: PS0023; MUID:89232725; PMID:3149944
A:Accession: PS0024
A:Molecule type: mRNA
A:Residues: 1-139 <MAR>
A:Experimental source: strain BALB/c
C:Comment: This chain is obtained from an IgG2a monoclonal antibody against Pseudomonas

C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin; pyroglytamic acid
F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-139/Domain: Ig heavy chain V region #status predicted <IGV>
F;24-117/Domain: immunoglobulin homology <IM>
F;30/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted

Query Match 14.0%; Score 492; DB 2; Length 139;
Best Local Similarity 77.5%; Pred. No. 4.3e-19;
Matches 93; Conservative 8; Mismatches 19; Indels 0; Gaps 0;

QY 1 EVLOQSGDLPKPGASVKISKASGYSTGYMEHWKQSGKLEWIGRINPNNGVLY 60
DB 20 QVLOQSGAELKPGASVXNSKASGYSTGYMEHWKQSGKLEWIGRINPNNGVLY 79
QY 61 NQKFKDKATLTVDKSTTAYMEIRLSLTSDSAVVYCARSTMTINTYMDYWGQGTSTVTVSS 120
DB 80 NQNFKDKATLTADKSSSTAYMQLSLTSDSAVVYCTRSYNYVEGMDYWGQGTSTVTVSS 139

RESULT 72
G2MSAM
IG gamma-2a chain C region, secreted form (allele a) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Sep-1980 #sequence revision 01-Sep-1981 #text_change 16-Jun-2000
C;Accession: A02152; A32657; A32658
R;Sikorav, J.B.; Auffray, C.; Rougeon, F.
Nucleic Acids Res. 8, 3143-3155, 1980
A;Title: Structure of the constant and 3' untranslated regions of the murine Balb/C gamma
A;Reference number: A02152; MUID:81076554; PMID:6777755
A;Accession: A02152
A;Molecule type: mRNA
A;Residues: 1-330 <SIG>
A;Cross-references: GB:V00798; NID:951835; PIDN:CAA24178.1; PID:g1333984
R;Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T.
Nucleic Acids Res. 9, 1365-1381, 1981
A;Title: The complete nucleotide sequence of mouse immunoglobulin gamma 2 A gene and ev
A;Reference number: A32657; MUID:81198976; PMID:6262729
A;Accession: A32657
A;Molecule type: DNA
A;Residues: 1-330 <YAM>
A;Cross-references: GB:J00470
A;Note: the sequence was determined from the germline gene
R;Oillo, R.; Auffray, C.; Morchamps, C.; Rougeon, F.
Proc. Natl. Acad. Sci. U.S.A. 78, 2442-2446, 1981
A;Title: Comparison of mouse immunoglobulin gamma-2A and gamma-2B chain genes suggests
A;Reference number: A32658; MUID:81223894; PMID:6787604
A;Accession: A32658
A;Molecule type: DNA
A;Residues: 1-330 <OLL>
A;Note: the sequence was determined from the germline gene
A;Note: Lys-330 is removed posttranslationally
R;Bourgeois, A.; Fougereau, M.; Rocca-Serra, J.
Eur. J. Biochem. 43, 423-435, 1974
A;Title: Determination of the primary structure of a mouse IgG2a immunoglobulin: amino-a
A;Reference number: A32659; MUID:74175517; PMID:4831970
A;Contents: annotation; myeloma protein MOPC 173
A;Note: this is one paper in a series reporting the sequence; for additional references,
R;de Preval, C.; Fougereau, M.
Eur. J. Biochem. 30, 452-462, 1972
A;Title: Determination of the primary structure of a mouse gammaG2a immunoglobulin. Iden
A;Reference number: A32660; MUID:73056887; PMID:4565406
A;Contents: annotation; MOPC 173, disulfide bonds
C;Genetics:
A;Introns: 1/1; 98/1; 114/1; 224/1
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob
F;20-84/Domain: immunoglobulin homology <IM>
F;98-113/Region: hinge
F;137-206/Domain: immunoglobulin homology <IM2>

F;243-310/Domain: immunoglobulin homology <IM3>
F;15/Disulfide bonds: interchain (to light chain) #status experimental
F;27-204,250-308/Disulfide bonds: #status experimental
F;107,110,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F;180/Binding site: carbonyl (Asn) (covalent) #status predicted

Query Match 14.0%; Score 491.5; DB 1; Length 330;
Best Local Similarity 26.4%; Pred. No. 1.3e-18;
Matches 151; Conservative 43; Mismatches 110; Indels 267; Gaps 13;

QY 121 AKTTPSVYPLAPGSAQAQNSMTLGLVKGYPPPEVTVTWNSGSLSSGVHFFPAVLQSD 180
DB 1 AKTAPSVYPLAPVCGDTTGTSSVTLGLVKGYPPPEVTVTWNSGSLSSGVHFFPAVLQSD 60
QY 181 LYTLSSTVTPSSTWPESTVTCNVAPASSTKVKKIVPRDSGCPSEKSEINEKDLRKK 240
DB 61 LYTLSSTVTPSSTWPESTVTCNVAPASSTKVKKIVPRDSGCPSEKSEINEKDLRKK 108
QY 241 SELQGTALGNLKIYYNNSKAITSEKSDAQFLNTLLFKGFTGHPWYNDLLVGLSTA 300
DB 109 ----- 108
QY 301 ATSEYEGSSVDLYGAYGYOCAGTGNKTACTACMGYGVTLHDNNLTTEKKVPINLWIDGKQ 360
DB 109 -----PKCPAPN-----LUGGPSVF----- 124
QY 361 TTVPIDKVTSKKEVTVQELDLQARHVLHGKFLYNSDSFGKVGQRLIVHFHSEGSTVS 420
DB 125 -----IFPPKIKDVLMI---SLSPITV 143
QY 421 YDLFDAQGYPDLLRLRYRNTTISLSISLYLYTTSISWTQTPTSLLSVSGDRAVTT 480
DB 144 CVVVDVSEDDPD-----VOISFVANNVEHTAQOT----- 174
QY 481 CKASQSVNDVAVYQKQKQSGPKLLISYTSRYAGVDPDRSGSGYGTDFLTITSSVQAE 540
DB 175 -----HREDYNSTLRV----- 186
QY 541 AAVYFCQDYNSTPPTFGGKLEIKRAD-----AAPTIVIFPPSSEQLT 584
DB 187 SALPIQHQQDWNGKEF-----KCKVNNKDLPAPIERTISKPKSVRAPQVTVLPPEEEMT 242
QY 585 SGGASVVCFLNFPKPKDKINVKKIDGSEKQ-----GVLSWTDQDSKDYSSMSSTLT 639
DB 243 KKQVTLTCMTDFMPEDIIYVETWNGKTELYNKNTPEVLDS-----DOSYFMYSKLRV 295
QY 640 TKDEYERHNSYTCBATHK-TSTSPIVKSFNR 669
DB 296 EKKWVERNSYSCSVHVEGLNHHHTTKFSR 326

RESULT 73
G2MSAM
IG gamma-2a chain C region, membrane-bound form - mouse
C;Species: Mus musculus (house mouse)
C;Date: 19-Feb-1984 #sequence revision 31-Mar-1991 #text_change 16-Jul-1999
C;Accession: A02154; B32657; I57809
R;Yamawaki-Kataoka, Y.; Nakai, S.; Miyata, T.; Honjo, T.
Proc. Natl. Acad. Sci. U.S.A. 79, 2623-2627, 1982
A;Title: Nucleotide sequences of gene segments encoding membrane domains of immunoglobuli
A;Reference number: A02154; MUID:8222190; PMID:6283537
A;Accession: A02154
A;Molecule type: DNA
A;Residues: 329-399 <YAM>
A;Cross-references: GB:J00471
A;Note: the sequence was determined from the germline gene
R;Yamawaki-Kataoka, Y.; Miyata, T.; Honjo, T.
Nucleic Acids Res. 9, 1365-1381, 1981
A;Title: The complete nucleotide sequence of mouse immunoglobulin gamma 2 A gene and evol
A;Reference number: A32657; MUID:81198976; PMID:6262729
A;Accession: B32657
A;Molecule type: DNA
A;Residues: 1-329, 'K' <YA2>

R;Hall, B.; Milcarek, C.
Mol. Immunol. 26, 819-826, 1989
A>Title: Sequence and polyadenylation site determination of the murine immunoglobulin gene
A;Reference number: I57809; MUID:90097953; PMID:2513486
A;Accession: I57809
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 373-399 <RES>
A;Cross-references: GB:M35032; NID:g194478; PIDN:AAA37919.1; PID:g387217
C;Comment: The sequence of residues 1-328 was assumed to be identical with the corresponding
C;Comment: Cell lines producing IgG contain two mRNA species for Ig gamma chains. The ma
hat it contains an alternative 3' end, encoded in separate exons, that is homologous wit
C;Genetics:
A;Introns: 1/1; 98/1; 114/1; 224/1; 329/1; 372/1
A;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IGA and IGM, the subunits associate into la
C;Superfamily: immunoglobulin C region; immunoglobulin homology
C;Keywords: alternative splicing; duplication; glycoprotein; heterotetramer; immunoglob
F;137-206/Domain: immunoglobulin homology <IMM>
F;346-363/Domain: transmembrane #status predicted <TM>
F;364-399/Domain: intracellular #status predicted <INT>
F;180/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 14.0%; Score 491.5; DB 1; Length 399;
Best Local Similarity 26.4%; Pred. No. 1.7e-18;
Matches 151; Conservative 43; Mismatches 110; Indels 267; Gaps 13;

QY 121 AKTTPSVYPLAPGSAATNSMTLGLVKGYPPEPVTVTWNSGLSGVHTFFAVLQSD 180
Db 1 AKTAPSVYPLAPVCGDTTGSVTLGCLVKGYPPEPVTVTWNSGLSGVHTFFAVLQSD 60

QY 181 LYTSSSVTPSSWPSTTCNVAHPASSTKVDKIVPRDSGGPSEKSEINEKDLRKK 240
Db 61 LYTSSSVTPSSWPSSQITCNVAHPASSTKVDKIEPR---GPTIKPCP----- 108

QY 241 SELQTAIGNLKQIYYNKAITSSEKSAQDFLNTLLFKGFFGHPWYNDLLVDLGSTA 300
Db 109 ----- 108

QY 301 ATSEYEGSVDLGAYGYCAGGTPNKTAQMGVGVTLHDNNRLTEKKVPEINLWIDGKQ 360
Db 109 -----PKCPAPN-----LLGSPSVF----- 124

QY 361 TTVPIDKVKTSKEVTVQELDQARHYLHGKFGLYNSDSFGKQVQGLIVFHSSEGSTVS 420
Db 125 -----IPPKIKDVLMI---SLSPIT 143

QY 421 YDLFDAQOQYDTLRIYRDNTTISSTLSLSLYTTSIVMTQTPFSLLSAGDRVIT 480
Db 144 CVVDVSEDDP-----VQISWFVNVEVHTAQOT----- 174

QY 481 CKASQSVSNDVAMVYQKQPGQSPKLLISYTSRYAGVDFRFGSGYGTDFTLTSSVQAE 540
Db 175 -----HREDYNSTLRVV--- 186

QY 541 AAVYFCQDYNSTPFGGTTKLEIKRAD-----AAPTVISFPSPSOLT 584
Db 187 SALPIQHODWVSGKEF-----CKVNNKDLPAPIERTISKPKGSVRAPQVYVLPPEEEMT 242

QY 585 SGGSVVCFLNFPKQINVKWKIDGGERQV-----GVLSNWTQDQSKDSTYSNSSLTL 639
Db 243 KKQVTLICWVDWPDIDYVETWNGKLTNLYKNKTEPVLD-----DGSYFMYSLRV 295

QY 640 TKDSEYERHNSVTCATHK-TSTSPIVKSFNR 669
Db 296 EKQNVERNYSVCSVHEGLNHHHTTKFSFR 326

RESULT 74

S20639

Ig heavy chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Jul-1999

C;Accession: S20639
R;Losman, M.; Fasy, T.M.; Novick, K.E.; Monestier, M.
submitted to the EMBL Data Library, February 1992
A;Description: Relationships among antinuclear antibodies from autoimmune MRL mice reacti
A;Reference number: S20639
A;Accession: S20639
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-125 <LOS>
A;Cross-references: EMBL:X65004; NID:g52598; PIDN:CAA46137.1; PID:g52599
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 13.9%; Score 489.5; DB 2; Length 125;
Best Local Similarity 76.0%; Pred. No. 5e-19;
Matches 95; Conservative 8; Mismatches 15; Indels 7; Gaps 1;

QY 1 EVQLQSGDPLVKPGASVKISCKASGYSTGYVMHWVKSPGKLEWIGRIINPNNGVTLY 60
Db 1 EVQLQSGDPLVKPGASVKISCKASGYSTGYVMHWVKSPGKLEWIGRIINPNNGVTLY 60

QY 61 NQKFKDKATLTVDKSTTAYMELSLTSDSAVYCARSTMITNYY-----MDYWGQG 113
Db 61 NEKFKGKATLTDSKSSSTAYMELSLTSDSAVYCARRVYNNVYLRSSLYAMDYWGQ 120

QY 114 TSVTV 118

Db 121 TSVTV 125

RESULT 75

S41394

Ig heavy chain V region - mouse

C;Species: Mus musculus (house mouse)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Jun-2000

C;Accession: S41394

R;Margartte, C.; Gilbert, D.; Brard, F.; Tron, F.

submitted to the EMBL Data Library, January 1994

A;Description: Structural characterization of an (NZB X NZW)F1 mouse-derived Igm anti-DNP

A;Reference number: S41393

A;Accession: S41394

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-120 <MAR>

A;Cross-references: EMBL:Z29586; NID:g452354; PIDN:CAA82703.1; PID:g1334080

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;15-98/Domain: immunoglobulin homology <IMM>

Query Match 13.9%; Score 488; DB 2; Length 120;
Best Local Similarity 76.7%; Pred. No. 5.7e-19;
Matches 92; Conservative 11; Mismatches 17; Indels 0; Gaps 0;

QY 1 EVQLQSGDPLVKPGASVKISCKASGYSTGYVMHWVKSPGKLEWIGRIINPNNGVTLY 60
Db 1 EVQLQSGAELVKPGASVKLSCKASGYTFTSYVMHWVKRPGQGLEWIGEIDPSDSTYY 60

QY 61 NQKFKDKATLTVDKSTTAYMELSLTSDSAVYCARSTMITNYYMDYWGQTSVTYSS 120
Db 61 NQKFKGKATLTVDKSSSTAYMQLTSDSAVYCARRYGSRVMDYWGQTSVTYSS 120

Search completed: August 12, 2004, 13:33:05

Job time : 27.2583 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 12, 2004, 13:22:49 ; Search time 14.7627 Seconds
(without alignments)
2370.233 Million cell updates/sec

Title: US-09-900-766-1

Perfect score: 3522

Sequence: 1 EVQLQQSPDLVKPGASVKI.....EATHKTSPIVKSFNRNES 672

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1107	31.4	257	1	ETXE STAAU
2	948	26.9	257	1	ETXA STAAU
3	611	17.3	258	1	ETXD STAAU
4	557	15.8	324	1	GC1_MOUSE
5	557	15.8	393	1	GC1M_MOUSE
6	556	15.8	106	1	KAC_MOUSE
7	550	15.6	326	1	GC1_RAT
8	539	15.3	322	1	GCA_RAT
9	491.5	14.0	330	1	GCA_MOUSE
10	491.5	14.0	399	1	GCAM_MOUSE
11	481.5	13.7	117	1	HV12_MOUSE
12	481	13.7	139	1	HV07_MOUSE
13	480.5	13.6	117	1	HV13_MOUSE
14	480	13.6	118	1	HV51_MOUSE
15	479	13.6	336	1	GCB_MOUSE
16	479	13.6	405	1	GCEM_MOUSE
17	472	13.4	106	1	KACA_RAT
18	467	13.3	335	1	GCAB_MOUSE
19	458.5	13.0	120	1	HV03_MOUSE
20	457	13.0	106	1	KACB_RAT
21	454	12.9	137	1	HV11_MOUSE
22	450.5	12.8	140	1	HV02_MOUSE
23	446	12.7	333	1	GCB_RAT
24	437.5	12.4	138	1	HV48_MOUSE
25	437.5	12.4	329	1	GCC_RAT
26	433	12.3	120	1	HV50_MOUSE
27	425	12.1	117	1	HV09_MOUSE
28	423	12.0	149	1	HV54_MOUSE
29	422	12.0	117	1	KV51_MOUSE
30	420.5	11.9	136	1	HV15_MOUSE
31	417	11.8	117	1	HV04_MOUSE
32	415	11.8	117	1	HV10_MOUSE
33	414	11.8	117	1	HV49_MOUSE

34	413	11.7	117	1	HV05_MOUSE
35	413	11.7	329	1	GC2_CAVPO
36	406.5	11.5	133	1	KV4B_HUMAN
37	406	11.5	134	1	KV4C_HUMAN
38	404	11.5	117	1	HV05_MOUSE
39	401	11.4	329	1	GC3_MOUSE
40	401	11.4	398	1	GC3M_MOUSE
41	397	11.3	330	1	GC1_HUMAN
42	396.5	11.3	121	1	HV01_MOUSE
43	396.5	11.3	327	1	GC4_HUMAN
44	395	11.2	114	1	KV4A_HUMAN
45	395	11.2	136	1	KV5B_MOUSE
46	392	11.1	117	1	HV52_MOUSE
47	385	10.9	147	1	HV1C_HUMAN
48	378	10.7	326	1	GC2_HUMAN
49	375	10.6	108	1	KV1M_HUMAN
50	372.5	10.6	129	1	KV3H_HUMAN
51	370	10.5	117	1	HV1G_HUMAN
52	369	10.5	109	1	KV1H_HUMAN
53	368.5	10.5	109	1	KV3D_HUMAN
54	368	10.4	129	1	KV1M_HUMAN
55	364.5	10.3	109	1	KV3F_HUMAN
56	364.5	10.3	129	1	KV3L_HUMAN
57	362	10.3	117	1	HV1B_HUMAN
58	361.5	10.3	109	1	KV3B_HUMAN
59	361.5	10.3	113	1	KV2G_MOUSE
60	361	10.2	109	1	KV4D_HUMAN
61	360	10.2	108	1	KV5M_MOUSE
62	360	10.2	128	1	KV3K_HUMAN
63	358	10.2	108	1	KV5K_MOUSE
64	358	10.2	121	1	KV4O_HUMAN
65	357.5	10.2	129	1	KV3M_HUMAN
66	357	10.1	108	1	KV1S_HUMAN
67	356	10.1	108	1	KV5P_MOUSE
68	356	10.1	323	1	GC_RABIT
69	355	10.1	108	1	KV1P_HUMAN
70	355	10.1	108	1	KV5L_MOUSE
71	354	10.1	108	1	KV1Y_HUMAN
72	354	10.1	108	1	KV5N_MOUSE
73	353	10.0	108	1	KV1N_HUMAN
74	353	10.0	108	1	KV5O_MOUSE
75	352	10.0	108	1	KV5U_MOUSE
76	351	10.0	108	1	KV1E_HUMAN
77	351	10.0	114	1	KV1A_MOUSE
78	348	9.9	108	1	KV1G_HUMAN
79	347	9.9	108	1	KV1R_HUMAN
80	345.5	9.8	107	1	KV1D_HUMAN
81	345	9.8	108	1	KV1V_HUMAN
82	345	9.8	131	1	KV3I_MOUSE
83	344	9.8	108	1	KV1C_HUMAN
84	344	9.8	111	1	KV3L_MOUSE
85	344	9.8	129	1	KV1X_HUMAN
86	343	9.7	111	1	KV3J_MOUSE
87	343	9.7	111	1	KV3M_MOUSE
88	343	9.7	111	1	KV3C_MOUSE
89	342.5	9.7	109	1	KV3E_HUMAN
90	342	9.7	111	1	KV3N_MOUSE
91	342	9.7	111	1	KV3T_MOUSE
92	341.5	9.7	117	1	HV42_MOUSE
93	341	9.7	106	1	KAC_HUMAN
94	341	9.7	108	1	KV1K_HUMAN
95	340.5	9.7	109	1	KV1T_HUMAN
96	340	9.7	111	1	KV3Q_MOUSE
97	339	9.6	108	1	KV1O_HUMAN
98	339	9.6	111	1	KV3R_MOUSE
99	338.5	9.6	108	1	KV3A_HUMAN
100	337	9.6	108	1	KV1A_HUMAN

ALIGNMENTS

RESULT 1

```

ETXE STAAU          STANDARD;          PRT;    257 AA.
ID  ETXE STAAU          STANDARD;          PRT;    257 AA.
AC  P1293;
DT  01-JAN-1990 (Rel. 13, Created)
DT  01-JAN-1990 (Rel. 13, Last sequence update)
DT  15-MAR-2004 (Rel. 43, Last annotation update)
DE  Enterotoxin type E precursor (SEE).
GN  ENTE.
OS  Staphylococcus aureus.
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCSI_TaxID=1280;
RN  [1]
RP  SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.
RC  STRAIN=MOB265;
RX  MEDLINE=88257005; PubMed=3384800;
RA  Couch J.L., Soltis M.T., Betley M.J.;
RT  "Cloning and nucleotide sequence of the type E staphylococcal
    enterotoxin gene.";
RL  J. Bacteriol. 170:2954-2960(1988).
RN  [2]
RP  3D-STRUCTURE MODELING.
RX  MEDLINE=96022987; PubMed=7552730;
RA  Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
RT  "Residues defining V beta specificity in staphylococcal
    enterotoxins.";
RL  Nat. Struct. Biol. 2:680-686(1995).
CC  -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
    staphylococcal food poisoning syndrome. The illness characterized
    by high fever, hypotension, diarrhea, shock, and in some cases
    death.
CC  -!- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
    for the toxin interaction with MHC class II (By similarity).
CC  -!- SUBCELLULAR LOCATION: Secreted.
CC  -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
    family.
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
    between the Swiss Institute of Bioinformatics and the EMBL outstation -
    the European Bioinformatics Institute. There are no restrictions on its
    use by non-profit institutions as long as its content is in no way
    modified and this statement is not removed. Usage by and for commercial
    entities requires a license agreement (See http://www.isb-sib.ch/announcement/
    or send an email to license@isb-sib.ch).
CC  -----
CC  EMBL: M21319; AAA26617.1;
CC  DR  PIR: A28179; A28179.
CC  DR  PDB: LSEE; 15-OCT-95.
CC  DR  InterPro: IPR008992; Bact_endotox.
CC  DR  InterPro: IPR006177; Bctf1_tox.
CC  DR  InterPro: IPR006123; Staph/Strep_toxin.
CC  DR  InterPro: IPR006126; Staph/Strep_tox.
CC  DR  InterPro: IPR006173; Staph_tox_OB.
CC  DR  Pfam: PF02876; Staph_Strep_tox_C7_1.
CC  DR  Pfam: PF01123; Staph_Strep_toxin; 1.
CC  DR  PRINTS: PR00279; BACTRTOXIN.
CC  DR  PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
CC  DR  PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
CC  DR  Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
    3D-structure.
CC  1 27
CC  FT CHAIN          1 27  ENTEROTOXIN TYPE E.
CC  FT METAL          28 257  ZINC (BY SIMILARITY).
CC  FT METAL          249 249  ZINC (BY SIMILARITY).
CC  FT METAL          251 251  ZINC (BY SIMILARITY).
CC  FT METAL          33 35  ZINC (BY SIMILARITY).
CC  FT HELIX          39 41
CC  FT HELIX          42 42
CC  FT STRAND         46 47
CC  FT TURN           48 51
CC  FT HELIX          52 54
CC  FT HELIX          59 64
CC  FT STRAND         66 67
CC  FT TURN           69 69
CC  FT STRAND         69 69

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FT TURN          73 74
FT STRAND        75 79
FT TURN          83 84
FT STRAND        90 94
FT TURN          98 104
FT HELIX         105 106
FT TURN          109 113
FT STRAND        115 116
FT TURN          118 119
FT STRAND        128 132
FT STRAND        135 137
FT TURN          139 140
FT STRAND        142 142
FT STRAND        152 152
FT STRAND        154 155
FT TURN          156 157
FT STRAND        163 163
FT STRAND        171 171
FT STRAND        173 175
FT TURN          176 190
FT HELIX         191 191
FT TURN          203 211
FT STRAND        219 221
FT STRAND        227 227
FT HELIX         234 239
FT TURN          242 244
FT STRAND        245 247
FT TURN          249 257
FT STRAND        257 257
SQ SEQUENCE 257 AA; 29358 MW; 27EDA94B97770CE3 CRC64;

Query Match          31.4%; Score 1107; DB 1; Length 257;
Best Local Similarity 89.7%; Pred. No. 1.1e-61;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Caps 0;

QY  226 SEKSEENEXDLRKKSLOGLTALCNLKOIYYNSKATTSSEKSDAQDLTNTLLFKGFFTG 285
DB  25 SEKSEENEXDLRKKSLOGLTALCNLKOIYYNSKATTSSEKSDAQDLTNTLLFKGFFTG 84
QY  286 HPWYNLLVLDLGSAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMGVGTLLHNNRLT 345
DB  85 HPWYNLLVLDLGSAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMGVGTLLHNNRLT 144
QY  346 BEKVPINLWIDGKQTTVPIDKVKTSKEVTQVELDLQARHYLHGKFGLYNSDSFGKVK 405
DB  145 BEKVPINLWIDGKQTTVPIDKVKTSKEVTQVELDLQARHYLHGKFGLYNSDSFGKVK 204
QY  406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISTSLISLYLYTT 458
DB  205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISTSLISLYLYTT 257

RESULT 2
ETXA STAAU          STANDARD;          PRT;    257 AA.
ID  ETXA STAAU          STANDARD;          PRT;    257 AA.
AC  P13163;
DT  01-JAN-1990 (Rel. 13, Created)
DT  01-JAN-1990 (Rel. 13, Last sequence update)
DT  15-MAR-2004 (Rel. 43, Last annotation update)
DE  Enterotoxin type A precursor (SEA).
GN  ENTA OR MW1889.
OS  Staphylococcus aureus (strain MW2), and
    Staphylococcus aureus.
OC  Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX  NCSI_TaxID=196620, 1280;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=MW2;
RX  MEDLINE=22040717; PubMed=12044378;
RA  Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA  Nagai Y., Iwano N., Asano K., Naimi T., Kuroda H., Cui L.,
RA  Yamamoto K., Hiramatsu K.;
RT  "Genome and virulence determinants of high virulence community-
    acquired MRSA.";
RT  acquired MRSA.";

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RL Lancet 359:1819-1827(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FRI337;
RX MEDLINE=88086892; PubMed=3335483;
RA Betley M.J., Mekalanos J.J.;
RT "Nucleotide sequence of the type A staphylococcal enterotoxin gene.";
RL J. Bacteriol. 170:34-41(1988).
RN [3]
RP SEQUENCE OF 25-257.
RX MEDLINE=87222293; PubMed=3584106;
RI Huang T.-Y., Hughes J.L., Bergdoll M.S., Schantz E.J.;
RT "Complete amino acid sequence of staphylococcal enterotoxin A.";
RL J. Biol. Chem. 262:7006-7013(1987).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95354648; PubMed=7628431;
RA Schach E.M., Zaitseva I., Zaitsev V.N., Dohlisten M., Kalland T.,
RT Schlievert P.M., Ohlendorf D.H., Svensson L.A.;
RT "Crystal structure of the superantigen staphylococcal enterotoxin
type A.";
RL EMBO J. 14:3292-3301(1995).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=97113025; PubMed=8943278;
RA Sundstroem M., Hallen D., Svensson A., Schach E., Dohlisten M.,
RA Abrahamson L.;
RT "The Co-crystal structure of staphylococcal enterotoxin type A with
Zn2+ at 2.7-A resolution. Implications for major histocompatibility
complex class II binding.";
RL J. Biol. Chem. 271:32212-32216(1996).
RN [6]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=96022987; PubMed=7552730;
RA Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
RT "Residues defining V beta specificity in staphylococcal
enterotoxins.";
RL Nat. Struct. Biol. 2:680-686(1995).
RN [7]
RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX MEDLINE=9734373; PubMed=9191070;
RA Schach E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
RT "A structural and functional comparison of staphylococcal
enterotoxins A and C2 reveals remarkable similarity and
dissimilarity.";
RL J. Mol. Biol. 269:270-280(1997).
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
staphylococcal food poisoning syndrome. The illness characterized
by high fever, hypotension, diarrhea, shock, and in some cases
death.
CC -!- COPACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
for the toxin interaction with MHC class II.
CC -!- SUBUNIT: Monomer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
family.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AP004828; BAB95754.1; -;
DR EMBL; M18970; AAA26681.1; -;
DR PIR; A28664; A28664.
DR PDB; 1BSF; 11-JUL-96.
DR PDB; 1SXT; 19-NOV-97.
DR PDB; 1DYQ; 21-FEB-02.
DR PDB; 1I4G; 21-MAR-01.

DR PDB; 1I4H; 21-MAR-01.
DR PDB; 1L05; 18-DEC-02.
DR PDB; 1SEA; 15-OCT-95.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph_Strep_toxin.
DR InterPro; IPR006126; Staph_Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
KW 3D-structure; Complete proteome.
FT SIGNAL 1 24 ENTEROTOXIN TYPE A.
FT CHAIN 25 257
FT DISULFID 120 130
FT METAL 211 211 ZINC.
FT METAL 249 249 ZINC.
FT METAL 251 251 ZINC.
FT CONFLICT 242 242 T -> S (IN REF. 3).
FT HELIX 28 31
FT TURN 32 33
FT HELIX 39 41
FT TURN 44 45
FT HELIX 46 55
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FT STRAND 59 65
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FT STRAND 218 221
FT TURN 222 223
FT HELIX 230 233
FT HELIX 234 237
FT TURN 238 239
FT STRAND 242 244
FT STRAND 248 255
SQ SEQUENCE 257 AA; 29669 MW; ADEBF5BCAIF14677 CRC64;
Query Match 26.9%; Score 948; DB 1; Length 257;
Best Local Similarity 76.4%; Pred. No. 7.3e-52;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
QY 226 SEKSEBINEKDLRKKSSELOGTALGNLKKQIYYYNKRAITSSEKSAQOFLNTLLPKGFPTG 285
DB 25 SEKSEBINEKDLRKKSSELOGTALGNLKKQIYYYNKRAITSSEKSHQFLQHTLLPKGFPTD 84
QY 286 HPWYNDLLVDLGLSTAAITSEYEGSSVDLYCAYGYOCAGTTPKTKACMYGCVTLHNNRLT 345

Db 85 HSWNDLLVDFDSKIDVYKKGKVDLYGAYGYCAGGTPNKTAQMYGGVTLHDNNRLT 144
 QY 346 EEKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGIYNSDSFGGKVQ 405
 Db 145 EEKVPINLWDGKQNTVPLETKNKVNTVOELDLQARHYLHGKFGIYNSDSFGGKVQ 204
 QY 406 RGLIVHSSEGSTVSYDLFDAQGYPTDILLIYRDNNTTSSLSISLYTT 458
 Db 205 RGLIVHSTSPSVNYDLFGAQGYNTLLIYRDNKNTINSENHIDIYLYTS 257

RESULT 3
 ETXD STAAU
 ID ETXD STAAU STANDARD; PRT; 258 AA.
 AC P20723;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Enterotoxin type D precursor (SED).
 GN ENT.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacilliales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89359112; PubMed=2549000;
 RA Bayles K.W., Iandolo J.J.;
 RT "Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin D";
 RL J. Bacteriol. 171:4799-4806(1989).
 RN [2]
 RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
 RC STRAIN=ATCC 23235;
 RX MEDLINE=97157473; PubMed=9003758;
 RA Sundstroem M., Abrahamson L., Antonsson P., Mehindate K., Mourad W.,
 RA Dohlsten M.;
 RT "The crystal structure of staphylococcal enterotoxin type D reveals Zn2+-mediated homodimerization";
 RL EMBO J. 15:6832-6840(1996).
 CC -1- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases death.
 CC -1- SUBUNIT: Homodimer; zinc-dependent.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.

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 CC -----
 DR EMBL; M28521; AAB06195.1; -
 DR PIR; A33953; A33953.
 DR HSP; P13163; ISXT.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bctr1_tox.
 DR InterPro; IPR006123; Staph/Strep toxin.
 DR InterPro; IPR006126; Staph/Strep tox.
 DR InterPro; IPR006173; Staph tox OB.
 DR Pfam; PF02876; Staph tox C.
 DR Pfam; PF01123; Staph tox toxin; 1.
 DR PRINTS; PR00279; BACTRTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN 1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN 2; 1.
 DR Enterotoxin; Toxin; Signal; Superantigen; Zinc.
 FT SIGNAL 1 25
 FT CHAIN 26 258 ENTEROTOXIN TYPE D.
 FT METAL 212 212 ZINC.

FT METAL 250 250 ZINC.
 FT METAL 252 252 ZINC.
 FT VARIANT 114 114 P -> A (IN STRAIN ATCC 23235).
 SQ SEQUENCE 258 AA; 29746 MW; 4F7C6A28D42597FD CRC64;
 Query Match 17.3%; Score 611; DB 1; Length 258;
 Best Local Similarity 51.1%; Pred. No. 5.2e-31;
 Matches 118; Conservative 35; Mismatches 78; Indels 0; Gaps 0;
 QY 226 SEKSEENEDLRKSELOQTALGNLKLQIYYNSKAITSEKSAQOFLNTLLFKGFFTG 285
 Db 26 NENIDSVKEKELHKKSELSTALNNKHSYADKNPIIGENKSTGDOFLENTLLYKKFFTD 85
 QY 286 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYCAGGTPNKTAQMYGGVTLHDNNRLT 345
 Db 86 LINFEDLLINFNSKEMAKHFKSKVDYPIRYGICYGGEIDRTACTYGGVTPEHGKILK 145
 QY 346 EEKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGIYNSDSFGGKVQ 405
 Db 146 ERKKIPINLWINGVQKEVSLDKVQTKKNTVOELDLQARHYLHGKFGIYNSDSFGGKVQ 205
 QY 406 RGLIVHSSEGSTVSYDLFDAQGYPTDILLIYRDNNTTSSLSISLYLY 456
 Db 206 RGKIEFDSGSKVSYDLFQVKGDFEKLRIYSDNKNLTSTHEHLHIDIVLY 256

RESULT 4

GCI MOUSE
 ID GCI MOUSE STANDARD; PRT; 324 AA.
 AC P01868;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE 19 gamma-1 chain C region secreted form.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80045036; PubMed=115593;
 RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
 RA Takahashi N., Mano Y.;
 RT "Cloning and complete nucleotide sequence of mouse immunoglobulin gamma 1 chain gene";
 RL Cell 18:559-568(1979).
 RN [2]
 RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
 RX MEDLINE=8020559; PubMed=6769752;
 RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
 RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
 RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences cloned in a bacterial plasmid";
 RL Gene 9:187-97(1980).
 RN [3]
 RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
 RX MEDLINE=80012837; PubMed=113776;
 RA Rogers J., Clarke P., Salser W.;
 RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin heavy chain";
 RL Nucleic Acids Res. 6:3305-3321(1979).
 RN [4]
 RP SEQUENCE (MYELOMA PROTEIN MOPC 21).
 RX MEDLINE=78242286; PubMed=98524;
 RA Adetugbo K.;
 RT "Evolution of immunoglobulin subclasses. Primary structure of a murine myeloma gamma1 chain";
 RL J. Biol. Chem. 253:6068-6075(1978).
 RN [5]
 RP DISULFIDE BONDS (MOPC 21).
 RX MEDLINE=73008889; PubMed=5073237;
 RA Svasti J., Milstein C.;
 RT "The disulphide bridges of a mouse immunoglobulin G1 protein.";

RL Biochem. J. 126:837-850(1972).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Secreted;
 CC IsoId=P01868-1; Sequence=Displayed;
 CC Note-May be the major isoform;
 CC Name=Membrane-bound;
 CC IsoId=P01869-1; Sequence=External;
 CC -----
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 CC -----
 DR EMBL; V00793; CAA24172.1; -
 DR EMBL; V00793; CAA24173.1; -
 DR EMBL; V00793; CAA24174.1; -
 DR EMBL; V00793; CAA24175.1; -
 DR EMBL; V00795; CAA24176.1; -
 DR PIR; A02159; GIMS.
 DR GlycoSuiteDB; P01868; -
 DR MGD; MGI:96446; Igh-4.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_C1.
 DR InterPro; IPR003066; Ig_MHC.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00407; IGc1; 2.
 DR PROSITE; PS00835; IG LIKE; 3.
 DR PROSITE; PS00290; IG MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Alternative splicing.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 110 HINGE.
 FT DOMAIN 111 217 CH2.
 FT DOMAIN 218 324 CH3.
 FT DISULFID 27 82
 FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 138 198
 FT CARBOHYD 174 174 N-LINKED (GLCNAC...).
 FT FTID=CAR_000055.
 FT DISULFID 244 302
 FT MOD_RES 324 324 REMOVED POST-TRANSLATIONALLY.
 FT CONFLICT 276 276 N -> D (IN REF. 3).
 FT CONFLICT 278 278 N -> D (IN REF. 3).
 SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1P2C93 CRC64;
 Query Match 15.8%; Score 557; DB 1; Length 324;
 Best Local Similarity 28.3%; Pred. No. 1.6e-27;
 Matches 156; Conservative 48; Mismatches 89; Indels 258; Gaps 13;
 QY 121 AKTTPPSVYPLAPGSAATNSMTGLVGVFPFVTVWNSGLSSGVHTFPVAVLQSD 180
 Db 1 AKTTPPSVYPLAPGSAATNSMTGLVGVFPFVTVWNSGLSSGVHTFPVAVLQSD 60
 QY 181 LYTLSSVTVPSSTWPSSTVTCNVAHPASSTKVDKVIKVRDGGFSEKSEINKEKDLRK 240
 Db 61 LYTLSSVTVPSSTWPSSTVTCNVAHPASSTKVDKVIKVRDGGFSEKSEINKEKDLRK 103
 QY 241 SELQGTALGNLKQIYYNSKAITSEKSAQDFLNTLLFKGFTTGHWPYNLLVLDLSTA 300
 Db 104 CKPCLCTVPSVSSVIFPPK-----PKDVLITL----- 132
 QY 301 ATSEYEGSVLDYGAAYGYQCAGSTPNKACVGGVTLHNNRLTEKKKVPINLWDGKQ 360
 Db 133 -----TP-KVTCWWDIS-----KDDPEVQFSWFVD--- 157

RESULT 5

GCIM_MOUSE
 ID GCIM_MOUSE STANDARD; PRT; 393 AA.
 AC P01869;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig gamma-1 chain C region, membrane-bound form.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=80045036; PubMed=115593;
 RA Honjo T., Ohta M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
 RA Takahashi N., Mano Y.;
 RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
 gamma 1 chain gene";
 RL Cell 18:559-568(1979).
 RN [2]
 RP SEQUENCE OF 323-393 FROM N.A.
 RX MEDLINE=82197626; PubMed=6804950;
 RA Tyler B.M., Cowman A.P., Gerondakis S.D., Adams J.M., Bernard O.;
 RT "mRNA for surface immunoglobulin gamma chains encodes a highly
 RT conserved transmembrane sequence and a 28-residue intracellular
 RT domain";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2008-2012(1982).
 RN [3]
 RP SEQUENCE OF 323-366 FROM N.A.
 RX MEDLINE=82115295; PubMed=6799207;
 RA Rogers J., Choi E., Souza L., Carter C., Word C.J., Kuehl M.,
 RA Eisenberg D., Wall R.;
 RT "Gene segments encoding transmembrane carboxyl termini of
 RT immunoglobulin gamma chains";
 RL Cell 26:19-27(1981).
 RN [4]
 RP SEQUENCE OF 1-44 FROM N.A.
 RX MEDLINE=82222190; PubMed=6283537;
 RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
 RT "Nucleotide sequences of gene segments encoding membrane domains of
 RT immunoglobulin gamma chains";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Membrane-bound;
 CC IsoId=P01869-1; Sequence=Displayed;


```

RT "DNA sequence of the constant gene region of the mouse immunoglobulin
RL kappa chain.";
RN Nucleic Acids Res. 9:971-981(1981).
RP [7]
RX MEDLINE=86329081; PubMed=3138116;
RA de Waele P., Feys V., van de Voorde A., Molemans F., Fiers W.;
RT "Expression in non-lymphoid cells of mouse recombinant immunoglobulin
RT directed against the tumour marker human placental alkaline
RL phosphatase.";
RL Eur. J. Biochem. 176:287-295(1988).
CC !- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC
CC EMBL; V00807; CAA24189.1; -.
DR PIR; B90262; K1MS.
DR PDB; 1AIF; 01-FEB-97.
DR PDB; 1FSK; 02-OCT-00.
DR PDB; 1KB5; 08-APR-98.
DR PDB; 1KCR; 11-MAY-02.
DR PDB; 1KCS; 11-MAY-02.
DR PDB; 1KCU; 11-MAY-02.
DR PDB; 1KCV; 11-MAY-02.
DR PDB; 25C8; 09-JUL-99.
DR MGD; MGI:96495; Igk-C.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig 1.
DR SMART; SM00407; Igcl; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT NON TER 1
FT DOMAIN 5 102 IG-LIKE.
FT DISULFID 26 86
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
SQ SEQUENCE 106 AA; 11778 MW; 4351PF5EP49AE9S CRC64;

Query Match 15.8%; Score 556; DB 1; Length 106;
Best Local Similarity 100.0%; Pred. No. 3.9e-28;
Matches 105; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 567 ADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRONGVLSWTDQDS 626
Db 1 ADAAPTYSIFPPSSSEQLTSGGASVVCFLNNFYPKIDINVKWKIDGSRONGVLSWTDQDS 60

QY 627 KDSTYSMSSTLTLDKDEYERHNSYTCETHAKTKTSTSPVKSFNNE 671
Db 61 KDSTYSMSSTLTLDKDEYERHNSYTCETHAKTKTSTSPVKSFNNE 105

RESULT 7
GCL_RAT STANDARD; PRT; 326 AA.
AC P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-1 chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0017; PS0017.
DR HSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig 3.
DR SMART; SM00407; Igcl; 2.
DR PROSITE; PS50835; IG LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON TER 1
FT DOMAIN 1 97 CHI.
FT DOMAIN 98 112 HINGE.
FT DOMAIN 113 219 CH2.
FT DOMAIN 220 326 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT CARBOHYD 176 176
SQ SEQUENCE 326 AA; 35946 MW; 013BAB45EP49B9DA CRC64;

Query Match 15.6%; Score 550; DB 1; Length 326;
Best Local Similarity 27.7%; Pred. No. 4.3e-27;
Matches 150; Conservative 64; Mismatches 90; Indels 238; Gaps 14;

QY 121 AKTTPSVYPLAPGSAQTNSMVTGLCLVKGYFPEPVTVWNSGSLSSGHTFPAVLQSD 180
Db 1 AETAPSVYPLAPGTALKNSMVTGLCLVKGYFPEPVTVWNSGSLSSGHTFPAVLQSG 60

QY 181 LYLTSSTVTPSTWPESETVTCNVAHPASSTKVDKIVPRDGGSGPSEKEEINEKDLRKK 240
Db 61 LYLTSSTVTPSTWPESETVTCNVAHPASSTKVDKIVPRDGGSGPSEKEEINEKDLRKK 109

QY 241 SELQGTALGNLKIYYNNSKAITSSSEKSDAQFLTNLLFKGFTGHFWYNDLLDLGSGTA 300
Db 110 -----ICTGSEVSS-----VFIPPKFDVL----- 130

QY 301 ATSEYEGSSVDLYGAYGYOCAGGTPNKTACMYGVTLHDNNRLTEEEKVPINLMDG-- 358
Db 131 -----TITL-----TP-KVTCVVVDIS-----QDDPEVHFSWFVDVVE 162

QY 359 ---KQPTVIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQGLIVPHSSE 415
Db 163 VHTAQTRPPEQFNSTFR--SVSELPILHQDWLNGR----- 196

QY 416 GSTVSYDLEFDAQGQVPTLLR-YRDNNTTISSTLSLSLYTYTTSIVMTQTSLLVSAGD 475
Db 197 ----- 196

QY 476 RVITTCASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDPDRSGSGYGDFTLTIS 535
Db 197 --TFRCV-----TSAAPPSPIEKISK 217

QY 536 VQAEADAAYFCQDYNSTPPTFGGKLEIKRADAAPTYSIFPPSSSEQLTSGGASVVCFLN 595
Db 218 PE-----GRQV-----PHVYVMSPTKEEMTQNEVSTICWVK 249

QY 596 NFYPKIDINVKWKIDGSRONGVLSWTDQDSKDSTYSMSSTLTLDKDEYERHNSYTCET 655
Db 250 GYPPDIYVEWQMGQDEN-YKNTPTTMDT-DGSYFLYSLKLVKVKKEKQQGTTCSTVL 307

QY 656 HK 657
Db 308 HE 309

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RESULT 8
GCA_RAT      STANDARD;      PRT;      322 AA.
ID  P20760;
AC  P20760;
DT  01-FEB-1991 (Rel. 17, Created)
DT  01-FEB-1991 (Rel. 17, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  Ig gamma-2A chain C region.
OS  Rattus norvegicus (Rat).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX  NCBI_TaxID=10116;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=89232738; PubMed=3149946;
RA  Brueggemann M.;
RT  "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL  Gene 74:473-482(1988).
CC  -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
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CC  -----
CC  ENBL: M13804; AAA41376.1; ALT_INIT.
DR  PIR; PS0019; PS0019.
DR  HSP; P01842; 7FAB.
DR  InterPro; IPR007110; Ig-like.
DR  InterPro; IPR003597; Ig_c1.
DR  InterPro; IPR003006; Ig_MHC.
DR  Pfam; PF00047; Ig_2.
DR  SMART; SM00407; IGc1; 2.
DR  PROSITE; PS00835; IG_LIKE; 3.
DR  PROSITE; PS00290; IG_MHC; 1.
KW  Immunoglobulin domain; Immunoglobulin C region; Repeat.
FT  NON_TER 1 1
FT  DOMAIN 6 98 IG-LIKE 1.
FT  DOMAIN 115 212 IG-LIKE 2.
FT  DOMAIN 221 317 IG-LIKE 3.
FT  DISULFID 27 82
FT  DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT  DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT  DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT  DISULFID 136 196
FT  DISULFID 242 300
FT  CARBOHYD 172 172 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ  SEQUENCE 322 AA; 35186 MW; E8EAL36A9DE01EDB CRC64;

Query Match 15.3%; Score 539; DB 1; Length 322;
Best Local Similarity 28.2%; Pred. No. 2e-26;
Matches 153; Conservative 55; Mismatches 92; Indels 242; Gaps 15;

QY 121 AKTTPSVYPLAGSAAQTNSWTLGCLVKGYPEPVVTWNSGSLSSGVHTFPVAVLQSD 180
D 1 AETTPSVYPLAGTALKNSWTLGCLVKGYPEPVVTWNSGSLSSGVHTFPVAVLQSG 60
QY 181 LYLTSSTVTPSSWTPSETVTCNVAHPASSTKVDKIVPRDSGGPSEKSEINEKDLRKK 240
D 61 LYLTSSTVTPSSWSSQAVTCNVAHPASSTKVDKIVPREK----- 102
QY 241 SELQGTALGNLKIYYNSKAISSSEKSAQDFLTNLLFGPPTGHPWYNDLLVDLGSTA 300
D 103 -----NPGCGTGEVSS-----VFIFPKTKDVL----- 126
QY 301 ATSEYEGSSVDLYGAVYGYCAGTGNKTKACMGVTLHDNNRLTEKKVPINLWIDG-- 358
D 127 -----TITL-----TP-KVTCVVVDISQND-----PEVRSWFIDVVE 158

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QY 359 ---KQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDPGKQVQRLIVFHSSE 415
D 159 VHTAQTHAPEKQSNILR--SVSELPVIVHRDLWLGK-----TFCKYV----- 199
QY 416 GSTVSYDLFDAQGYPDLLRIYRDNTTISSTLSISLYLTTSIVMTQPTPTSLLSAGD 475
D 200 -----SGAFFAPI----- 207
QY 476 RVTTICKASQSVNDVAMVYQQKFGQPKLLISYTSRYAGVDPDRFSGSGYGTDTFTLTSS 535
D 208 -----EKXIS-----KPEGTPR----- 219
QY 536 VQAEAAVYFCQDYNSPFPFGGKLEIKRAAAPTVSIFPPSSSEQLTSGGASVVCFLN 595
D 220 -----GPOVYTMAPPKEMTQSQVSIICMVK 245
QY 596 NFYPKDINVKKIDGSRQVNLNSWTDQSDKSTYSMSSTLTLTDEYERHNSYTCBAT 655
D 246 GFYPDPDIYTEKXNGQPOEN-YKNTPTMDT-DGSYFLYSLKLVAKKETWQOGNTFTCSVL 303
QY 656 HK 657
D 304 HE 305

RESULT 9
GCAA_MOUSE  STANDARD;      PRT;      330 AA.
ID  P01863;
DT  21-JUL-1986 (Rel. 01, Created)
DT  21-JUL-1986 (Rel. 01, Last sequence update)
DT  10-OCT-2003 (Rel. 42, Last annotation update)
DE  Ig gamma-2A chain C region, A allele.
OS  Mus musculus (Mouse).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX  NCBI_TaxID=10090;
RN  [1]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=81076554; PubMed=6777755;
RA  Sikorav J.-L., Auffray C., Rougeon F.;
RT  "Structure of the constant and 3' untranslated regions of the murine
RL  Balb/c gamma 2a heavy chain messenger RNA.";
RL  Nucleic Acids Res. 8:3143-3155(1980).
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=81198976; PubMed=6262729;
RA  Yamawaki-Katsoka Y., Miyata T., Honjo T.;
RT  "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
RT  and evolution of heavy chain genes: further evidence for intervening
RT  sequence-mediated domain transfer.";
RL  Nucleic Acids Res. 9:1365-1381(1981).
RN  [3]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=81228694; PubMed=6787604;
RA  Ollio R., Auffray C., Morchamps C., Rougeon F.;
RT  "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
RT  suggests that exons can be exchanged between genes in a multigenic
RT  family.";
RL  Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
RN  [4]
RP  MYELOMA PROTEIN MOPC 173.
RX  MEDLINE=74175517; PubMed=4831970;
RA  Bourgois A., Fougereau M., Rocca-Serra J.;
RT  "Determination of the primary structure of a mouse IgG2a
RT  immunoglobulin: amino-acid sequence of the Fc fragment. Implications
RT  for the evolution of immunoglobulin structure and function.";
RL  Eur. J. Biochem. 43:423-435(1974).
RN  [5]
RP  DISULFIDE BONDS.
RX  MEDLINE=73056887; PubMed=4565406;
RA  de Preval C., Fougereau M.;
RT  "Determination of the primary structure of a mouse gamma G2a

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RT	immunoglobulin. Identification of the disulfide bridges.";	
RL	Eur. J. Biochem. 30:452-462(1972).	
CC	-1- SIMILARITY: Contains 3 immunoglobulin-like domains.	
CC	-----	
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CC	-----	
EMBL	V00798; CAA24178.1; --	
DR	PIR; A02152; G2MSA.	
DR	PDB; 1E4X; 12-JUL-01.	
DR	PDB; 1E4X; 12-JUL-01.	
DR	PDB; 1MNU; 06-MAY-99.	
DR	InterPro; IPR007110; Ig-like.	
DR	InterPro; IPR003597; Ig cl.	
DR	InterPro; IPR0031006; Ig_MHC.	
DR	Pfam; PF000047; ig; 2.	
DR	SMART; SM00407; Igc1; 2.	
DR	PROSITE; PS00835; IG_LIKE; 3.	
DR	PROSITE; PS00250; IG_MHC; 1.	
KW	Immunoglobulin domain; Immunoglobulin C region; 3D-structure; Repeat.	
FT	NON TER 1 1	
FT	DOMAIN 6 98 IG-LIKE 1.	
FT	DOMAIN 121 220 IG-LIKE 2.	
FT	DOMAIN 229 325 IG-LIKE 3.	
FT	DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).	
FT	DISULFID 27 82	
FT	DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).	
FT	DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).	
FT	DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).	
FT	DISULFID 144 204	
FT	DISULFID 250 308	
FT	MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.	
SQ	SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;	
	Query Match 14.0%; Score 491.5; DB 1; Length 330;	
	Best Local Similarity 26.4%; Pred. No. 1.8e-23;	
	Matches 151; Conservative 43; Mismatches 110; Indels 267; Gaps 13;	
QY	121 AKTTPSVYPLPGSAAQNSWVTLGCLVKGYPPPEVTVWNSGLSSGVHTFPAYLQSD 180	
DB		
1	AKTAPSVYPLAPVCGDITGSSVTLGCLVKGYPPPEVTVWNSGLSSGVHTFPAYLQSD 60	
QY	181 LYTSSSVVPSSTPSETVTCNVAHPASSTKVDKIVPRDGGPSEKSEENEXDLRKK 240	
DB		
61	LYTLSSSVTVSTWFSQITCNVAHPASSTKVDKKIEPR---GPITKPCP----- 108	
QY	241 SELQGTALGNLKQIYYNYSKAITSEKSAQDFLTNTLLFKGFTGHPWYNDLLVDLGSTA 300	
DB	109 -----	
QY	301 ATSEYBGSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTEKKVPINLMDGKQ 360	
DB	109 -----PCKCPAPN-----LLGGPSVF----- 124	
QY	361 TTVPIDKVAKTSKEVTVQBLDQARHYLHGKFGLYNSDSFGKQVORGLIVFHSSEGSTVS 420	
DB	125 -----IPPKIKVDLMI---SLSPIVT 143	
QY	421 YDLFDAQGYPDTLRIYRDNTTISTSLISLYLTTISIVMTQPTSLILVSGADRVTT 480	
DB	144 CVVVDVSEDDP-----VOISWFWNNVEVHQAQTQ----- 174	
QY	481 CKASQSVNSDVAWYQKPGQSPKLLISYTSRYAGVDPDRFGSGVGTDFTLTISSVQABD 540	
DB	175 -----HREDYNSILRVV----- 186	
QY	541 AAVYFCQDYNSPPTFGGQTKLEIKRAD-----AAPTVISIFPPSEQLT 584	

Db 187 SALPIQHDMWSGKEF-----KCKVNNKDLFAPLERTISKPGSVRAPOQVYVLPPEEEMT 242
 QY 585 SGASVVCFLNNFYPKDINVKWKIDGSEQN-----GVLSNWTDDQDSKOSTYSMSFTLTL 639
 Db 243 KQVILTCTWTFMPEDIIYVETWNGKTLNKNTEPVLDS-----DGSYFMYSKLRV 295
 QY 640 TKDEYERHNSYTCETHK-TSTSPIVKSFNR 669
 Db 296 EKNWYERNYSYCSVVHGLHNNHTTKSPSR 326

 RESULT 10
 GC3M_MOUSE
 ID GC3M_MOUSE STANDARD; PRT; 399 AA.
 AC P01865;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig gamma-2A chain C region, membrane-bound form.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8222190; PubMed=6283537;
 RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
 RT "Nucleotide sequences of gene segments encoding membrane domains of
 RT immunoglobulin gamma chains.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
 CC -!- ALTERNATIVE PRODUCTS;
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=Membrane-bound;
 CC IsoId=P01865-1; Sequence=Displayed;
 CC Name=Secreted;
 CC IsoId=P01864-1; Sequence=External;
 CC Note=Probably the major isoform;
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
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 CC or send an email to license@isb-sib.ch).
 CC
 EMBL; J00471; AAB59661.1; ALT_INIT.
 FIR; A02154; G2MGAM.
 DR PDB; 1KB5; 08-APR-98.
 DR PDB; 1YEE; 15-OCT-97.
 DR MGD; MGI:96443; Igh-1.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; IG_c1
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; Ig; 2.
 DR SMART; SM00407; IGc1; 2.
 DR PROSITE; PS50835; IG LIKE; 3.
 DR PROSITE; PS00290; IG MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Transmembrane; Alternative splicing; 3D-structure; Repeat.
 FT NON_TER 1 1
 FT DOMAIN 6 98 IG-LIKE 1.
 FT DOMAIN 121 220 IG-LIKE 2.
 FT DOMAIN 229 325 IG-LIKE 3.
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 82
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 142 204
 FT DISULFID 250 308
 FT TRANSMEM 346 363 POTENTIAL.

FT DOMAIN 364 399 CYTOPLASMIC (POTENTIAL).
 FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 399 AA; 44020 MW; 4C38138BFAED3FF0 CRC64;
 Query Match 14.0%; Score 491.5; DB 1; Length 399;
 Best Local Similarity 26.4%; Pred. No. 2.4e-23;
 Matches 151; Conservative 43; Mismatches 110; Indels 267; Gaps 13;
 QY 121 AKTTPSVYPLAPGSAQAQNSMTGLCLVKGYPFPVTVWNSGLSSGVHTFPVAVLQSD 180
 Db 1 AKTTPSVYPLAPGSAQAQNSMTGLCLVKGYPFPVTVWNSGLSSGVHTFPVAVLQSD 60
 QY 181 LYTSLSSVTVPSSTWSEVTVTCNVAHPASSTVKDKIVPRDGGPSEKSEBINEKDLKK 240
 Db 61 LYTSLSSVTVPSSTWSEVTVTCNVAHPASSTVKDKIEPR---GPIKPCP----- 108
 QY 241 SELQGTALGNLKIYYNNSKAITSEKSDAQFLTNLLFKGFTGHPWYNDLLVLGSTA 300
 Db 109 ----- 108
 QY 301 ATSEYEGSSVDLYGAYGYQCAGGTNKTACMYGVTLLHNNLLEKVKPINLWDGKQ 360
 Db 109 -----PKCPAPN-----LLGSPSVF----- 124
 QY 361 TTVPIDKVKTSKEVTVQELDLQARHLHGKFLGYNLSDSFGGKVGORGLIVFHSSEGSTVS 420
 Db 125 -----IFPKIKDVLMI---SLSPIVT 143
 QY 421 YDLFDAQGYDPTLLRIYRDNNTSISLSLYLTVTSIVMTQPTSLLSVAGDRVIT 480
 Db 144 CVVDVSDDDPD-----VQISWVFNNEVHTAQQT----- 174
 QY 481 CKASQSVSNDVANYQKPGSPKLLISYSSRYAGVDFRFGSGGYGTDFTLTISSVQAE 540
 Db 175 -----HREDYNSILRVV----- 186
 QY 541 AAVYFQDDYNSPTFTGGGTLKBIKAD-----AAPTYSIFPPSSEQT 584
 Db 187 SALPIQHDDWMSKEF-----CKVNNKDLPAPIERTISKPKGSRAPQVYVLPPEEEMT 242
 QY 585 SGASVVCFLNYPKIDINVKWKIDSERQN-----GVLSNWDQDSDKSTYSMSLTLL 639
 Db 243 KKQVTLTCMTDMPEDPIYVEWNNKGTLYNKTEPVLDS-----DGSYFMSKLKV 295
 QY 640 TKDEYERHNSYTCETHK-TSTSPVVKFSNR 669
 Db 296 EKNWVERNSYSCSVVHEGLNHHHTKSFSR 326
 RESULT 11
 HV12_MOUSE STANDARD; PRT; 117 AA.
 AC P01756;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region WOPC 104E.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
 RX MEDLINE=83075344; PubMed=6816276;
 RA Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H.,
 RA Hood L.E.;
 RT "Complete amino acid sequence of a mouse mu chain: homology among
 heavy chain constant region domains.";
 RL Biochemistry 21:5415-5424 (1982).
 CC -!- MISCELLANEOUS: THE SEQUENCE OF THE LIGHT CHAIN OF THIS IGM MYELOMA
 CC PROTEIN HAS ALSO BEEN DETERMINED.
 CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.

DR PIR; A02039; MEMS4E.
 DR HSP; P01789; IMCP.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Glycoprotein.
 DOMAIN 1 116 IG-LIKE
 FT DISULFID 22 96 BY SIMILARITY.
 FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (COMPLEX).
 FT NON TER 117
 SQ SEQUENCE 117 AA; 12983 MW; 3CF8ACE4BE447B41 CRC64;
 Query Match 13.7%; Score 481.5; DB 1; Length 117;
 Best Local Similarity 78.3%; Pred. No. 1.8e-23;
 Matches 94; Conservative 8; Mismatches 15; Indels 3; Gaps 1;
 QY 1 EVQLQQSGPDLVPGASVKISKASGYSTFYGMHWKSPGKLEWIGRINPNNGVTLY 60
 Db 1 EVQLQQSGPDLVPGASVKISKASGYSTFYGMHWKSPGKLEWIGRINPNNGVTLY 60
 QY 61 NQPKFKATLTVDKSSSTAYMELSLTSEDSAVYCYCARSTMTINVMYDYGQSTVTSS 120
 Db 61 NQPKFKATLTVDKSSSTAYMELSLTSEDSAVYCYCARSTMTINVMYDYGQSTVTSS 117
 RESULT 12
 HV07_MOUSE STANDARD; PRT; 139 AA.
 ID HV07_MOUSE
 AC P01751; P01752;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region B1-8/186-2 precursor.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6;
 RX MEDLINE=81234548; PubMed=6788376;
 RA Bothwell A.L.M., Paskind M., Reith M., Imanishi-Kari T., Rajewsky K.,
 RA Baltimore D.;
 RT "Heavy chain variable region contribution to the NpB family of
 antibodies: somatic mutation evident in a gamma 2a variable region.";
 RL Cell 24:625-637 (1981).
 CC -!- MISCELLANEOUS: THE B1-8 MU CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
 CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
 CC (NPB ANTIBODIES).
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 or send an email to license@isb-sib.ch).
 CC EMBL; J00529; AAA38170.1; -.
 DR PIR; A90809; MEMS18.
 DR PDB; 1A6U; 27-MAY-98.
 DR PDB; 1A6W; 15-JUL-98.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal; 3D-structure.
 FT SIGNAL 1 19
 FT CHAIN 20 139 IG HEAVY CHAIN V REGION B1-8/186-2.
 FT DOMAIN 20 49 FRAMEWORK-1.

```
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 58 FRAMEWORK-2
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 124 D SEGMENT.
FT DOMAIN 125 139 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 139 139
SQ SEQUENCE 139 AA; 15419 MW; 1B57DD4FDC09F465 CRC64;

Query Match
Best Local Similarity 13.7%; Score 481; DB 1; Length 139;
Matches 89; Conservative 14; Mismatches 17; Indels 0; Gaps 0;

QY 1 EVQLQSGPDLVKPGASVKISKASGYFTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60
Db 20 QVQLQPGAEVLKPGASVKLSKASGYFTFTSWHWVQKQPGKLEWIGRIDPNSGGTKY 79
QY 61 NQKFKDKATLTVDKSSSTAYMELRLSTSDSAVYVCARSTMITNYMDYWGQGTSTVVS 120
Db 80 NEKFKGKATLTVDKPSSTAYMQLSLSTSDSAVYVCARYDYGYSSYFDYWGQGTTLTVSS 139
```

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RESULT 13
HV13_MOUSE
ID HV13_MOUSE STANDARD; PRT; 117 AA.
AC P01757;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region J558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=80078170; PubMed=6765983;
RA Schilling J., Clevering B., Davie J.M., Hood L.;
RT "Amino acid sequence of homogeneous antibodies to dextran and DNA
RT rearrangements in heavy chain V-region gene segments.";
RL Nature 283:35-40(1980).
CC -!- MISCELLANEOUS: THE SEQUENCES OF 10 HYBRIDOMA PROTEINS THAT ALSO
CC BIND DEXTRAN DIFFER FROM THAT SHOWN AT 1-7 POSITIONS, MANY OF
CC WHICH OCCUR IN THE D AND J SEGMENTS.
CC -!- MISCELLANEOUS: THIS PROTEIN BINDS DEXTRAN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A26242; MEMS75.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 116 IG-LIKE.
FT DISULFID 22 96 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 13024 MW; 292E2AF4BE447E41 CRC64;
```

```
Query Match
Best Local Similarity 13.6%; Score 480.5; DB 1; Length 117;
Matches 94; Conservative 7; Mismatches 16; Indels 3; Gaps 1;

QY 1 EVQLQSGPDLVKPGASVKISKASGYFTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60
Db 1 EVQLQSGPELVKPGASVKSKASGYFTFTDYMVWKQSHGKLEWIGINPNNGTSTY 60
QY 61 NQKFKDKATLTVDKSSSTAYMELRLSTSDSAVYVCARSTMITNYMDYWGQGTSTVVS 120
Db 61 NQKFKGKATLTVDKSSSTAYMQLSLSTSDSAVYVCARDY---WYFDWVGAGITTVSS 117
```

```
RESULT 14
HV51_MOUSE
ID HV51_MOUSE STANDARD; PRT; 118 AA.
AC P06330;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region AC38 205.12.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84192519; PubMed=6201362;
RA Dildrop R., Bovens J., Stekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; A02040; MEMS38.
DR HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 104 D SEGMENT.
FT DOMAIN 105 118 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON TER 118 118
SQ SEQUENCE 118 AA; 12934 MW; 94F7BEB4C762A018 CRC64;

Query Match
Best Local Similarity 13.6%; Score 480; DB 1; Length 118;
Matches 95; Conservative 6; Mismatches 17; Indels 2; Gaps 1;

QY 1 EVQLQSGPDLVKPGASVKISKASGYFTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60
Db 1 EVQLQSGPELVKPGASVKISKASGYFTFTDYMVWKQSHGKLEWIGINPNNGTSTY 60
QY 61 NQKFKDKATLTVDKSSSTAYMELRLSTSDSAVYVCARSTMITNYMDYWGQGTSTVVS 120
Db 61 NQKFKGKATLTVDKSSSATYMLRLSTSDSAVYVCARGYDPPF--DVMGTGTTTVSS 118

RESULT 15
GCB_MOUSE
ID GCB_MOUSE STANDARD; PRT; 336 AA.
AC P01866;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ig gamma-2B chain C region secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ALLELE A).
RX MEDLINE=80120716; PubMed=6766534;
RA Yamawaki-Kataoka Y., Kataoka T., Takahashi N., Obata M., Honjo T.;
RT "Complete nucleotide sequence of immunoglobulin gamma2b chain gene
RT cloned from newborn mouse DNA.";
RL Nature 283:786-789(1980).
RN [2]
RP SEQUENCE FROM N.A. (MPC 11).
RX MEDLINE=80081501; PubMed=117548;
RA Tucker P.W., Marcu K.B., Slightom J.L., Blattner F.R.;
RT "Structure of the constant and 3' untranslated regions of the murine
RT gamma 2b heavy chain messenger RNA.";
RL Science 206:1299-1303(1979).
```


Notes-May be the major isoform;
 CC -!- PTM: DISULFIDE BONDS BY HOMOLOG WITH OTHER IG GAMMA CHAINS.
 CC -!- MISCELLANEOUS: The sequence of residues 1-335 is assumed to be
 CC identical with the corresponding region of the secreted form.
 CC -!- MISCELLANEOUS: The a allele sequence is shown.
 CC -!- SIMILARITY: Contains 3 immunoglobulin-like domains.
 CC
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 CC
 CC EMBL; J00462; AAB59659.1; ALT_INIT.
 CC
 CC PIR; C02154; G2MSBM.
 CC PDB; 1CIC; 11-YAR-03.
 CC MGD; MG1:96445; Igh-3.
 CC InterPro; IPR007110; Ig-like.
 CC InterPro; IPR003597; Ig_c1.
 CC Pfam; PF00047; Ig; 3.
 CC SMART; SM00407; IgC1; 2.
 CC PROSITE; PS50835; IG-LIKE; 3.
 CC PROSITE; PS00290; IG-MHC; 1.
 CC Immunoglobulin domain; Immunoglobulin C region; Transmembrane;
 CC Alternative splicing; 3D-structure; Repeat.
 CC NON TER 1
 CC DOMAIN 6 98 IG-LIKE 1.
 CC DOMAIN 127 226 IG-LIKE 2.
 CC DOMAIN 235 331 IG-LIKE 3.
 CC DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
 CC DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
 CC DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 CC DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
 CC DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
 CC DISULFID 118 118 INTERCHAIN (WITH A HEAVY CHAIN).
 CC DISULFID 150 210 POTENTIAL.
 CC DISULFID 256 314 CYTOPLASMIC (POTENTIAL).
 CC TRANSMEM 352 369
 CC DOMAIN 370 405
 CC SEQUENCE 405 AA; 44330 MW; 89B3CF0A9B6D49FA CRC64;
 Query Match 13.6%; Score 479; DB 1; Length 405;
 Best Local Similarity 27.6%; Pred. No. 1.4e-22;
 Matches 151; Conservative 47; Mismatches 110; Indels 240; Gaps 14;
 QY 121 AKTTPSVYPLAPGSAAGTNSMTLGLVKGVEPEPTVTWNSGLSGVHTFPAVLQSD 180
 DB 1 AKTTPSVYPLAPGCGDTGSSVTLGLVKGYPFESVTWNSGLSSVHTFPALLQSG 60
 QY 181 LYTSSSVTPSSTWPSSTVTCNVAHPASSTKVDKIVPRSDSGFSEKSEINE- ---KD 236
 DB 61 LYTSSSVTPSSTWPSSTVTCNVAHPASSTKVDKIVPRSDSGFSEKSEINE- --- 114
 QY 237 LRK--KSELOFAGNLKQIYYNSKAITSEKSAQDFLNTLLFKGFFGHPYNDLV 294
 DB 115 CHKCPAPNLEG--GPSVFIIPPNIKDV- ---LMI 142
 QY 295 DLGTAATSEYEGSDVLYGAYGYQCAGGTPNKATCMYGGVTLHDNNRLTEKKVPINL 354
 DB 143 SL-----TP----- 146
 QY 355 WIDGKQITVPIDKVKTSKVEVTVDLQARHYLHGKFLYNSDSFGKVGQGLIVPHSS 414
 DB 147 ----KVTCCVVVD-----VSEDDPDVQISWFVNN-----VEVHTA 176
 QY 415 EGSTVSVDLFDAQGYPDTLRLIRVDRNTTISSTLSISLVLYTTSIVMTQTPTSLVSA 474
 DB 177 QTQTHREDY-----NSTRVVS----- 193
 QY 475 DRVTITKASOSVNDVAVQKPGQSKLLISYTSRYAGVPRDFSGGYGTDFTLTIS 534

Db 194 -----TLPIQ 198
 QY 535 SVQAEAAVYFCQDYNSPPTFGGKLEIKRADAAFTVIFPPSSQLTSGASVVCFL 594
 DB 199 HQDWMSGKFKCKVNNKDLSPITRTISKIKGLVRAPOVVILPPPAQLSRKDVSLTCLV 258
 QY 595 NNFPKPDINVKWKIDGSERON-----GVLSNWDQSDKSTYSMSSTLTITKDEYERHNS 649
 DB 259 VGFNPGDISVEWTSNGHTTEENYKDTAPVLDS-----DGSYFIYKLNKMKTSKWKETDS 311
 QY 650 YTCEATHK 657
 DB 312 FSCNVRHE 319
 RESULT 17
 KACA RAT STANDARD; PRT; 106 AA.
 AC P01836;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DE 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig kappa chain C region, A allele.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DA;
 RX MEDLINE=82082587; PubMed=6273908;
 RA Sheppard H.W., Gutman G.A.;
 RT "Allelic forms of rat kappa chain genes: evidence for strong
 RT selection at the level of nucleotide sequence."
 RL Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
 DR PIR; A02118; KIRTA.
 DR HSSP; P01842; 2MCG.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; IG_MHC.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00407; IgC1; 1.
 DR PROSITE; PS50835; IG-LIKE; 1.
 DR PROSITE; PS00290; IG-MHC; 1.
 DR Immunoglobulin domain; Immunoglobulin C region.
 FT NON TER 1
 FT DOMAIN 5 102 IG-LIKE.
 FT DISULFID 26 86
 FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
 SQ SEQUENCE 106 AA; 11732 MW; B7E120D9700DD66 CRC64;
 Query Match 13.4%; Score 472; DB 1; Length 106;
 Best Local Similarity 83.8%; Pred. No. 6.1e-23;
 Matches 88; Conservative 11; Mismatches 6; Indels 0; Gaps 0;
 QY 567 ADAAPTYSIFPPSSQLTSGASVVCFLNNFYFKDINVKWKIDGSRQNGVLSNWDQDS 626
 DB 1 ADAAPTYSIFPPSMEQLTSGGATVCFVNVFPRDISVKKIDGSEQRDGVLDSDQDS 60
 QY 627 KOSTYSMSSTLTITKDEYERHNSYCEATHKTSSTPIVKSFNRE 671
 DB 61 KOSTYSMSSTLTITKVEYERHNLTCVVVHKTSSSPVVKSFNRE 105
 RESULT 18
 GCAB MOUSE STANDARD; PRT; 335 AA.
 ID GCAB_MOUSE
 AC P01864;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)

Ig gamma-2A chain C region secreted form (B allele).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1];
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=82037861; PubMed=6170065;
RA Schreier P.H., Bothwell A.L.M., Mueller-Hill B., Baltimore D.;
RT "Multiple differences between the nucleic acid sequences of the
RT Igg2a and Igg2ab alleles of the mouse.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4495-4499 (1981).
RN [2];
RP SEQUENCE.
RX MEDLINE=82037777; PubMed=6794027;
RA Dognin M.J., Lauwereys M., Stroberg A.D.;
RT "Multiple amino acid substitutions between murine gamma 2a heavy
RT chain FC regions of Iga and Igb allotypic forms.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:4031-4035 (1981).
CC -1- SUBCELLULAR LOCATION: Secreted (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Secreted;
CC IsoId=P01864-1; Sequence=Displayed;
CC Note=Probably the major isoform;
CC Name=Membrane-bound;
CC IsoId=P01865-1; Sequence=External;
CC -1- MISCELLANEOUS: The sequence differs from that of the a allele,
CC from BALB/c mice, at 15% of the positions.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; J00479; -; NOT_ANNOTATED_CDS.
CC PIR; A02153; G2MSAB.
DR PDB; 1BOG; 23-VAR-99.
DR PDB; 1HH6; 26-JAN-01.
DR PDB; 1HH5; 24-JUL-03.
DR PDB; 1HH6; 08-FEB-01.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGc1; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Alternative splicing;
KW 3D-structure; Repeat.
FT NON_TER 1 1
FT DOMAIN 6 98 IG-LIKE 1.
FT DOMAIN 126 225 IG-LIKE 2.
FT DOMAIN 234 330 IG-LIKE 3.
SQ SEQUENCE 335 AA; 36596 MW; FA332792CBB13C6 CRC64;
Query Match 13.3%; Score 467; DB 1; Length 335;
Best Local Similarity 25.5%; Pred. No. 6.1e-22;
Matches 149; Conservative 40; Mismatches 110; Indels 286; Gaps 13;
QY 121 AKTTTPSPVYPLAPGSAQTNSMTLGLVKGYPPEPTVTWNSGSLSSGVHTTTPAVLQSD 180
DB 1 AKTTAPSVYPLVPGCGTGTSSVTLGLVKGYPPEPTVTWNSGSLSSGVHTTTPAVLQSG 60
QY 181 LYTLLSSVTVPSSTWPSGETVTCNVAHPASSTKYVDKIVPRDGGPSEKSEINEKDLRKK 240
DB 61 LYTLLSSVTVPSSTWPSQTITCNVAHPASSTKYVDKIEPR----- 100

241 SELQGTALGNLKOIYYNSKAITSSSEKADQFLTNTLLFKGFTGHPWYNLLVLDLSTA 300
101 ----- 100
QY 301 ATSEYEGSSVDLYGAYVYQCAGGTENKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
DB 101 ----- 106
QY 361 TTVPIDKVTSKKEVTVQELDLQARHVLHGKFLGNSDSFGKVGQGLIVFHSSEGSTVS 420
DB 107 PCPPHQRVPPCAA-----PDLGGP----- 126
QY 421 YDLFDAQGGVPTLLRIYRDNNTTSSLSLSLYLTTSIVMTQTPTSLVSAGDRVTIT 480
DB 127 -SVIFPPKIKDVL-----ISLSPWVTCVV----- 152
QY 481 CKASQSVSNDVAVYQKPGQSPKLLISYTSRYAGVPDRFSGSGYGTDFLTLTSSVQAED 540
DB 153 -----DPDVQISW-----FYNNVEVHT 174
QY 541 AAVYFCQDYNSTPTFGGKLEIKRAD-----A 569
DB 175 AQTQTHREDYNS--TLRVSAFLIQHODWMSGKFKVNNRALPSPIEKTISKPSGVR 232
QY 570 APTVSIFFPSSSEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQNGVLSWTDQDSKDS 629
DB 233 APQVYVLPFAEEMTKKEPSLTOMITGLPAEIAVDWTSNGRTEQN-YKNATATVLDS-DG 290
QY 630 TYSVSSLTTLTKDEYRHNSYTCETHKT-----STSPIVKSFR 669
DB 291 SYFMYSKLRVQKSTWERSLFGACSVVHEVLNHLTLTKTISRSLGK 335
RESULT 19
HV03_MOUSE STANDARD; PRT; 120 AA.
ID HV03_MOUSE
AC P01747;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region 36-65.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1];
RP SEQUENCE FROM N.A.
RX MEDLINE=83131846; PubMed=6186498;
RA Siekevitz M., Gefter M.L., Brodeur P., Riblet R.,
RA Marshak-Rothstein A.;
RT "The genetic basis of antibody production: the dominant anti-arsenate
RT idotype response of the strain A mouse.";
RL Eur. J. Immunol. 12:1023-1032 (1982).
CC -1- MISCELLANEOUS: FROM ANALYSIS OF THE SIZES OF SEVERAL OTHER
CC DIFFERENTIATED GENES THAT HYBRIDIZE TO THIS ONE, THE AUTHORS
CC CONCLUDE THAT ALL OF THESE V REGIONS HAVE REARRANGED TO THE SAME J
CC SEGMENT, JH2.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC HSP; P01789; IMCP.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; Ig; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Hybridoma.
FT DOMAIN 1 111 IG-LIKE.
FT NON_TER 120 120
SQ SEQUENCE 120 AA; 13307 MW; FF04B4A167B654AF CRC64;
Query Match 13.0%; Score 458.5; DB 1; Length 120;
Best Local Similarity 72.5%; Pred. No. 5e-22; Indels 1; Gaps 1;
Matches 87; Conservative 15; Mismatches 17;


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QY 2 VLOQSGPDLVKPGASVKISKASGYSTGYMHWKSPGKLEWIGRIINPNNGVTLYN 61
Db 1 VLOQSGAELVAGSVKMSCKASGYSTFTSYGNVWKQRPQGQLEWIGVINGPGNYTKYN 60
QY 62 QKFKDKATLTVDKSSTAYMEIRSLTSDSAVYVCARSTMI--TNYVMYWGQISVTYSS 120
Db 61 EAFKQKTLTVDKSSSTAYMQLRSLTSDSAVYFCARSYYGGSYYFYDWGQGITLTLYSS 120

RESULT 20
KACB RAT
ID KACB RAT STANDARD; PRT; 106 AA.
AC P01835;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain C region, B allele.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCB_TaxID=10116;
RN NCB_TaxID=10116;
RP SEQUENCE FROM N.A.
RC STRAIN=Louvain;
RX MEDLINE=82082587; PubMed=6273908;
RA Sheppard H.W., Gurman G.A.;
RT "Allelic forms of rat kappa chain genes: evidence for strong
RT selection at the level of nucleotide sequence.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7064-7068(1981).
RN [2]
RP SEQUENCE (BENCE-JONES PROTEIN S211).
RX MEDLINE=75212238; PubMed=807630;
RA Starace V., Querinjean P.;
RT "The primary structure of a rat kappa Bence Jones protein:
RT phylogenetic relationships of V- and C-region genes.";
RL J. Immunol. 115:59-62(1975).
RC -|- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A93901; KIRTB.
DR HSP; P01842; 2MCG.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_C1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00407; IG_C1; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT DOMAIN 1 1 IG-LIKE.
FT NON_TER 1 1
FT DISULFID 26 86 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 D -> N (IN REF. 2).
FT CONFLICT 2 2 N -> K (IN REF. 2).
FT CONFLICT 30 30 MISSING (IN REF. 2).
FT CONFLICT 48 48
FT CONFLICT 79 79 E -> Q (IN REF. 2).
FT CONFLICT 87 87 E -> Q (IN REF. 2).
FT CONFLICT 98 98 V -> VM (IN REF. 2).
FT CONFLICT 100 100 S -> N (IN REF. 2).
SQ SEQUENCE 106 AA; 11601 MW; 4CPA7CA820DICA36 CRC64;

Query Match 13.0%; Score 457; DB 1; Length 106;
Best Local Similarity 80.0%; Pred. No. 5.2e-22;
Matches 84; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 567 ADAAPTIVIFPPSSQLTSGGASVVCFLNNFVKDINVKWKIDGSRQGVLSNWTQDS 626
Db 1 ADAAPTIVIFPPSTFQLTAGASVVCFLNNFVKDINVKWKIDGSRQGVLSNWTQDS 60

QY 627 KDSYVMSSTLTLDKDEYERNNSYTCETHKTSPIVKSFNNE 671
Db 61 KDSYVMSSTLTLDKADYESHNLVTCVHVHKTSSSPVVKSFNNE 105

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RESULT 21
HV11 MOUSE
ID HV11 MOUSE STANDARD; PRT; 137 AA.
AC P01755;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region S43 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCB_TaxID=10090;
RN NCB_TaxID=10090;
RP SEQUENCE FROM N.A.
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -|- MISCELLANEOUS: THE GAMMA-2A CHAIN MRNA WAS CLONED FROM A HYBRIDOMA
CC MAKING ANTIBODIES TO THE HAPTEN (4-HYDROXY-3-NITROPHENYL)ACETYL
CC (NPB ANTIBODIES).
CC -----
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CC -----
DR EMBL; J00539; AAA38172.1; -.
DR PIR; A02038; G2MS43.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 137 IG HEAVY CHAIN V REGION S43.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 122 D SEGMENT.
FT DOMAIN 123 137 JH2 SEGMENT.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 137 137
SQ SEQUENCE 137 AA; 15200 MW; ADD5881BF44B8EC9 CRC64;

Query Match 12.9%; Score 454; DB 1; Length 137;
Best Local Similarity 70.0%; Pred. No. 1.1e-21;
Matches 84; Conservative 15; Mismatches 19; Indels 2; Gaps 1;

QY 1 EVLOQSGPDLVKPGASVKISKASGYSTGYMHWKSPGKLEWIGRIINPNNGVTLY 60
Db 20 QVQLQQPGAEFVKPGASVKLSCKASGYTFTSYLHMHWNQRPGRGLEWIGRIDFNSGGTTY 79
QY 61 NQKFKDKATLTVDKSSTAYMEIRSLTSDSAVYVCARSTMI--TNYVMYWGQISVTYSS 120
Db 80 NEHFRSKATLTVDKSSTAYMQLSLSLTSDSAVYVCARL--GRYFDYWGQGITLTLYSS 137

RESULT 22
HV02 MOUSE
ID HV02 MOUSE STANDARD; PRT; 140 AA.
AC P01746;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)

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10-OCT-2003 (Rel. 42, Last annotation update)
Ig heavy chain V region 93G7 precursor.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
STRAIN=A/J;
MEDLINE=82152818; PubMed=6801765;
RA Sims J., Rabbitts T.H., Estess P., Slaughter C., Tucker P.W.,
Capra J.D.;
"Somatic mutation in genes for the variable portion of the
immunoglobulin heavy chain";
Science 216:309-311(1982).
-/- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC
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CC
CC EMBL; J00493; AAA38128.1; -.
DR PIR; A94264; HVM5G7.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Hybridoma; Signal.
FT SIGNAL 1 19
FT CHAIN 20 140 IG HEAVY CHAIN V REGION 93G7.
FT DOMAIN 20 139 IG-LIKE.
FT NON TER 140 140
FT SEQUENCE 140 AA; 15514 MW; 25A4CB8B31DASCE8 CRC64;

Query Match 12.8%; Score 450.5; DB 1; Length 140;
Best Local Similarity 71.9%; Pred. No. 1.9e-21;
Matches 8; Conservative 14; Mismatches 19; Indels 1; Gaps 1;

QY 1 EVQLQSGPDLVPGASVKISCKASGYFTGYMHVWYKSPGKLEWIGRINPNNGVTLY 60
DB 20 EVQLQSGAELVRAGSSVKMSCKASGYFTFTSYGINVWYKQPGQLEWIGYINPGYINY 79

QY 61 NQKFKATLTVDKSTTAYWEIRSLTSDSAVYVCARSTMI-TNYVMDYWGQGTSTVTS 119
DB 80 NEKPKGKTLTVDKSSSTAYWQLRSLTSDSAVYFCARSHYGGSYDFDYWGQGTFLTVS 139

QY 120 S 120
DB 140 S 140

RESULT 23
GCB_RAT STANDARD; PRT; 333 AA.
AC P20761;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig gamma-2B chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OC NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89232738; PubMed=3149946;
RA Brueggemann M.;

"Evolution of the rat immunoglobulin gamma heavy-chain gene family";
Gene 74:473-482(1988).
-/- SIMILARITY: Contains 3 immunoglobulin-like domains.
DR PIR; P01842; 7FAB.
DR HSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_cl.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00407; IGcl; 2.
DR PROSITE; PS50835; IG LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Repeat.
FT NON TER 1 1
FT DOMAIN 6 96 IG-LIKE 1.
FT DOMAIN 124 223 IG-LIKE 2.
FT DOMAIN 232 328 IG-LIKE 3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
FT SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

Query Match 12.7%; Score 446; DB 1; Length 333;
Best Local Similarity 25.3%; Pred. No. 1.2e-20;
Matches 140; Conservative 54; Mismatches 131; Indels 228; Gaps 14;

QY 121 AKTTPSVYPLAPGSAQAQTNMTGLGLVKGYPPEVTVTNWSSLSGSGVHTTPAVLQSD 180
DB 1 AQTTAPSVYPLAPGCGDTTSTVTLGLVKGYPPEVTVTNWSSLSGSDVHTTPAVLQSG 60

QY 181 LYTLSSTVTPSWPSETVTCNVHPASSTKVDKIVPRDSDGSPSEKSEINEKDLRKK 240
DB 61 LYTLTSSVT--SSTWPSQVTCNVHPASSTKVDKVKVERENG----- 101

QY 241 SELOGTALGNLQIYYNKAITSSEKSAQOFLTNLTFKGFTHGWYNDLLVDLGSTA 300
DB 102 ----- 101

QY 301 ATSEYEGSSVDLYGAYGYQCAGGTENKTAQMYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
DB 102 -----IGHKC-----FTCPIC-----HKCPVELLGPS 125

QY 361 TTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKQVQGLIVFHSSEGSTVS 420
DB 136 VFI-----FPPKPKDILLI---SQNAKVT 146

QY 421 YDLFDAQOQYEDTLRIYRDNNTTISSTLSLSLYLYTTSIVMTQTPTSLLSVAGDRVT-- 478
DB 147 CVVVDVSEEPDVOFSWFMVNNVEVHTAQTPREQYINSTP---RVVSALPIQHDWMSGK 203

QY 479 -ITCKASQSVSNDVAWYQCKEFGQSPKLLISYTSRSYAGVDPDPGSGGYGTDTLTISVQ 537
DB 204 EFKCKVN-----NKALPSP---IEKTSKPKGLVRK----- 231

QY 538 AEDAAVYFCQDDYNSPPTFGGKTKLEIKRADAATVSIFFPSSPOLTSGGASVVCFLNNF 597
DB 232 -----PQVYVMGPTEQLTEQTVSLTCLTSGF 258

QY 598 YPKDINVKWKIDGSEQRQNGVLNSWTDQDSKDYTSMSSTLTLTDEYERHNSVTCETHK 657
DB 259 LPNDIGVETWNGHIEKN-YKNTFPMVDS-DGSFFMYSKLNVSRSDRSRAPFVCSVTHE 316

QY 658 -TSTSPIVKSFNR 669
DB 317 GLHNHHVEKSISR 329

RESULT 24

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HV48 MOUSE
ID HV48 MOUSE STANDARD; PRT; 138 AA.
AC P03980;
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region TEPC 1017 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_TaxID=10090;
SEQUENCE FROM N.A.
RX MEDLINE=84248078; PubMed=6429663;
RA Gilliam A.C., Shen A., Richards J.E., Blattner F.R., Mushinski J.F.,
RA Tucker P.W.;
RT "Illegitimate recombination generates a class switch from C mu to C
RT delta in an IgD-secreting plasmacytoma.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:4164-4168(1984).
DR PIR; A02033; HVMST7.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00406; igv; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 138 IG HEAVY CHAIN V REGION TEPC 1017.
FT DOMAIN 21 49 FRAMEWORK-1.
FT DOMAIN 21 49 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 50 54 FRAMEWORK-2.
FT DOMAIN 55 68 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 127 COMPLEMENTARITY-DETERMINING-4.
FT DOMAIN 128 138 FRAMEWORK-4.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 138 138
SQ SEQUENCE 138 AA; 15576 MW; 748157E4C6907B8E CRC64;

Query Match 12.4%; Score 437.5; DB 1; Length 138;
Best Local Similarity 68.3%; Pred. No. 1.2e-20;
Matches 82; Conservative 20; Mismatches 17; Indels 1; Gaps 1;

QY 1 EVLOQSGDLVKGASVKISKASGYSTGYMHVWVQSGKGLWIGRINPNNGVTLY 60
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
20 QVLOQPGAEVKGASVQLSCASGHTFTNYIHWVQRFGQGLEWIGINPNDRSNY 79
QY 61 NQKPKKATLTVDKSTTAYMELRLTSGDSAVVYCARSTMTNVMVDYWGQGSTVTVSS 120
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
80 NEKFKKATLTVDKSSSTAYVQLSLLTPEEPVAVVYCARSDGYDWFV-YWQGGTLVTFS 138

RESULT 25
GCC RAT STANDARD; PRT; 329 AA.
AC P20762;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DE Ig gamma-2C chain C region.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
SEQUENCE FROM N.A.
RX MEDLINE=88166903; PubMed=3127222;
RA Brueggeman M., Delmasro-Gallifre P., Waldmann H., Calabi F.;
RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
RT region cDNA: extensive homology to mouse gamma 3.";
RL Eur. J. Immunol. 18:317-319(1988).

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CC -----
DR EMBL; X07189; CAA30169.1; -.
DR FIR; S00847; S00847.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 2.
DR SMART; SM00407; Igc1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 222 CH2.
FT DOMAIN 223 329 CH3.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 143 203
FT DISULFID 249 307
SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;

Query Match 12.4%; Score 437.5; DB 1; Length 329;
Best Local Similarity 26.1%; Pred. No. 4e-20;
Matches 140; Conservative 47; Mismatches 125; Indels 225; Gaps 16;

QY 121 AKTTPSVPLAFGSAQAQNSMWTGLCLVKGYPPPTVTVNSGSLSSGVHTTFAVLQSD 180
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 ARTAFSVPLVFGSGTSGSLVTLGLVKGYPPPTVTVKNSGSLSSGVHTTFAVLQSG 60

QY 181 LYLSSSVTPSTWPTSETVTCNVHPASSTKVDKIVPRDSGGPGEKEINEKDLKK 240
Db :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 LYLSSSVTPSTWSTWSQVTCVAHPATKSNLKRIEPR-----RPPRPP 107

QY 241 SEIQGTALGNLKIYYNKAITSSEKADQFLNTLTFKGFTHFWNLIVDLGSTA 300
Db :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
108 TDI-----CSCDDNLGRPSVF--IFPPKP--KDILM----- 134

QY 301 ATSEYEGSSVDLYGAYGYQCAGTPTNKACMYGGVTLHDNRLTEKKVPINLWIDGKQ 360
Db :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
135 -----ITL-----TP-KVTCVVVDVS-----EPEPDVQFS-WF---- 160

QY 361 TTVPIDKVKTSKKEVTVQELDLQARHYLHGKFLGYNDSFGGKVGQRLIVFHSSEGSTVS 420
Db :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
161 -----VDNVRVFTAQTQPEEQLNGTFRVVSTLHIHQDWMWSGK----- 199

QY 421 YDLFDAQQGYPDTLLRIYRDNTTISSTLSISLYLVTTSIVMTQTPTSLVSAGDRVIT 480
Db -----EFK 202

QY 481 CKASQSVNDVAMVQOKPGQSPKLLISYTSRVAGVPDRFSGSGYGTDTLTLSVQAED 540
Db :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
203 CKVN-----NKDLPSP--IEKTIKPRG----- 223

QY 541 AAVYFCQDYNPPTFGGKTKLEIKRAADAAPTIVSIPPSSEQLTSGASVGCFLANNFYPK 600
Db :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
224 -----KARTPQVYTIPTPPPEQMSKNKVSILTCTWTSFYPA 257

QY 601 DINWKWKIDSGEONGVLNSWTDQDSKDYTSMSSTLTILTKDEYERHNSYTCETHK 657
Db :||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
258 SISVERNGR-ELEQDYKNTLPVLDLSDSYFLYSLKSLSVDTSDSMWRGDIYTCVSVHE 312

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RESULT 26
HV50 MOUSE STANDARD; PRT; 120 AA.
AC P06379;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain v region AC38 15.3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=84182519; PubMed=6201362;
RA Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
RT "A V region determinant (idiotope) expressed at high frequency in B
RT lymphocytes is encoded by a large set of antibody structural genes.";
RL EMBO J. 3:517-523(1984).
DR PIR; D90809; HVM561.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; P00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
KW Immunoglobulin v region.
FT DOMAIN 1 98 V SEGMENT.
FT DOMAIN 99 105 D SEGMENT.
FT DOMAIN 106 120 J SEGMENT.
FT DISULFID 22 96 BY SIMILARITY.
FT NON TER 120 120
SQ SEQUENCE 120 AA; 13311 MW; 914453P426709834 CRC64;

Query Match 12.3%; Score 433; DB 1; Length 120;
Best Local Similarity 67.5%; Pred. No. 1.9e-20;
Matches 81; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 1 EVQLQSGPDLVPGASVKISCKASGYFTGYMHWVKQSPGKLEWIGRIINPNNGVTLY 60
DB 1 QVQLQSGTGLVPGASVNLSCASGYFTSYWHWIRQRPGQGLEWIGINPSNGTNY 60
QY 61 NQKFKDKATLTVDKSSSTAYMELRLSTSDSAVYCARSTMTIYNYMDYWGQGTSTVTVSS 120
DB 61 NEKFKSKATLTVDKSSSATYMQLTSTPDSAVYCARWDYEDRYFDVWGVTGTTVTVSS 120

RESULT 27
HV09 MOUSE STANDARD; PRT; 117 AA.
AC P01753; P11271;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain v region 186-1 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -!- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPb ANTIBODIES.
CC PIR; D90809; HVM561.
CC HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.

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DR InterPro; IPR003596; Ig_v.
DR Pfam; P00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PSS0835; IG-LIKE; 1.
KW Immunoglobulin v region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 186-1.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12890 MW; 16191A088CB17F5A CRC64;

Query Match 12.1%; Score 425; DB 1; Length 117;
Best Local Similarity 79.6%; Pred. No. 5.7e-20;
Matches 78; Conservative 11; Mismatches 9; Indels 0; Gaps 0;

QY 1 EVQLQSGPDLVPGASVKISCKASGYFTGYMHWVKQSPGKLEWIGRIINPNNGVTLY 60
DB 20 QVQLQSGTGLVPGASVNLSCASGYFTSYWHWIRQRPGQGLEWIGINPSNGTNY 79
QY 61 NQKFKDKATLTVDKSSSTAYMELRLSTSDSAVYCAR 98
DB 80 NEKFKSKATLTVDKSSSTAYMQLHSLTSDSAVYCAR 117

RESULT 28
KV5A MOUSE STANDARD; PRT; 149 AA.
AC P01633;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain v-v region MPC11 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE OF 1-71 FROM N.A.
RX MEDLINE=83001944; PubMed=6288267;
RA Kelley D.E., Coleclough C., Perry R.P.;
RT "Functional significance and evolutionary development of the
RT 5'-terminal regions of immunoglobulin variable-region genes.";
RL Cell 29:681-689(1982).
RN [2]
RP SEQUENCE OF 41-149 FROM N.A.
RX MEDLINE=80176554; PubMed=6245773;
RA Rabbitts T.H., Hamlyn P.H., Matthysens G., Roe B.A.;
RT "The variability, arrangement, and rearrangement of immunoglobulin
RT genes.";
RL Can. J. Biochem. 58:176-187(1980).
RN [3]
RP SEQUENCE OF 30-149.
RX MEDLINE=78186617; PubMed=418775;
RA Smith G.P.;
RT "Sequence of the full-length immunoglobulin kappa-chain of mouse
RT myeloma MPC 11.";
RL Biochem. J. 171:337-347(1978).
CC -!- MISCELLANEOUS: THE MATURE CHAIN HAS 12 ADDITIONAL RESIDUES AT ITS
CC AMINO END, DUE TO A TANDEM DUPLICATION OF 36 NUCLEOTIDES AFTER THE
CC CODON FOR RESIDUE 36. RESIDUE 42 CORRESPONDS TO THE AMINO-TERMINAL
CC RESIDUE OF TYPICAL KAPPA CHAINS.
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DR Pfam; PF00047; ig; 1.
DR SMART; SW00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 108A.
FT DOMAIN 20 >117 IG-LIKE.
FT NON_TER 117
SQ SEQUENCE 117 AA; 12972 MW; 428CB44DF25D1BC2 CRC64;

Query Match 12.0%; Score 422; DB 1; Length 117;
Best Local Similarity 84.7%; Pred. No. 8.7e-20;
Matches 83; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 1 EVLOQSGDPLVKPGASVKISKASGYSTGYTMHWVKSPGKGLIEWIRPNNGVTLY 60
Db 20 EVLOQSGPELVKPGASVKISKASGYTFTDYNHWVKSHGKSLIEWIGVIYPYNGGTG 79
QY 61 NOKFKDKATLTVDKSTTAYMELSLTSDSAVYYCAR 98
Db 80 NOKFKSKATLTVDNSSTAYMELSLTSDSAVYYCAR 117

RESULT 30
HV15 MOUSE
ID HV15 MOUSE STANDARD; PRT; 136 AA.
AC P01759;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V region BCL1 precursor.
DE OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8222262; PubMed=6806821;
RA Knapp M.R., Liu C.-P., Newell N., Ward R.B., Tucker P.W., Strober S.,
RA Blattner F.R.;
RT "Simultaneous expression of immunoglobulin mu and delta heavy chains
RT by a cloned B-cell lymphoma: a single copy of the VH gene is shared
RT by two adjacent CH genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:2996-3000(1982).
CC !- SIMILARITY: Contains 1 immunoglobulin-like domain.

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CC EMBL; J00494; AAA38130.1; -.
CC PIR; A02042; HVMSB1.
CC HSP; P01772; 2F84.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003596; Ig_V.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG LIKE; 1.
CC Immunoglobulin V region; Signal.
CC SIGNAL 1 19
CC CHAIN 20 136 IG HEAVY CHAIN V REGION BCL1.
CC DOMAIN 20 135 IG-LIKE.
CC NON_TER 136
CC SEQUENCE 136 AA; 15078 MW; 6827CFBC6DB3F35E CRC64;

Query Match 11.9%; Score 420.5; DB 1; Length 136;
Best Local Similarity 70.0%; Pred. No. 1.3e-19;
Matches 84; Conservative 11; Mismatches 22; Indels 3; Gaps 2;

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OS 1 EVOLQOQSPDLVKGASVKISCKASGYFTGYMHVWQSPGKGLWIGRINPNNGVTLY 60
OC :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
OC 20 QVQLQOQSGEVVRPGVSVKISKSGSYFTDVAHWHVQSHAKSLEWIGVISTYNGNTSY 79
OX :|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J
RC MEDLINE=81234548; PubMed=6788376;
RX Bothwell A.L.M., Paskind M., Rech M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RA "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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CC -----
DR PIR; J00533; AAA38602.1; -.
DR HSP; C90809; HVMS45.
DR HSP; P01810; 2FBJ.
DR MGB; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 58 FRAMEWORK-2.
FT DOMAIN 59 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 11.8%; Score 417; DB 1; Length 117;
Best Local Similarity 78.6%; Pred. No. 1.8e-19;
Matches 77; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 1 EVOLQOQSPDLVKGASVKISCKASGYFTGYMHVWQSPGKGLWIGRINPNNGVTLY 60
Db 20 QVQLQOQSGTELVKPGASVKLSCKASGYFTSYWVHWKQPGQGLEWIGNPFGNGTNY 79

RESULT 31
HV04_MOUSE
ID HV04_MOUSE STANDARD; PRT; 117 AA.
AC P01748;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region 23 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J.
RC MEDLINE=81234548; PubMed=6788376;
RX Bothwell A.L.M., Paskind M., Rech M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RA "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
CC -----
DR PIR; A02030; HVMS23.
DR HSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 23.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 58 FRAMEWORK-2.
FT DOMAIN 59 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12772 MW; C530F829C906F69B CRC64;

Query Match 11.8%; Score 417; DB 1; Length 117;
Best Local Similarity 78.6%; Pred. No. 1.8e-19;
Matches 77; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

Qy 1 EVOLQOQSPDLVKGASVKISCKASGYFTGYMHVWQSPGKGLWIGRINPNNGVTLY 60
Db 20 QVQLQOQSGTELVKPGASVKLSCKASGYFTSYWVHWKQPGQGLEWIGNPFGNGTNY 79

RESULT 32
HV10_MOUSE
ID HV10_MOUSE STANDARD; PRT; 117 AA.
AC P01754; P11270;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-JUL-1999 (Rel. 11, Last annotation update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig heavy chain V region 145 precursor.
GN IGH-VJ558.

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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RP STRAIN=C57BL/6J.
RC MEDLINE=81234548; PubMed=6788376;
RX Bothwell A.L.M., Paskind M., Rech M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RA "Heavy chain variable region contribution to the Npb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
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CC -----
DR PIR; J00533; AAA38602.1; -.
DR PIR; C90809; HVMS45.
DR HSP; P01810; 2FBJ.
DR MGB; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region; Signal.
KW SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 145.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 58 FRAMEWORK-2.
FT DOMAIN 59 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12921 MW; D37D8A3F543E996 CRC64;

Query Match 11.8%; Score 415; DB 1; Length 117;
Best Local Similarity 78.6%; Pred. No. 2.4e-19;
Matches 77; Conservative 11; Mismatches 10; Indels 0; Gaps 0;

Qy 1 EVOLQOQSPDLVKGASVKISCKASGYFTGYMHVWQSPGKGLWIGRINPNNGVTLY 60
Db 20 QVQLQOQSGAELVKGASVKLSCKASGYFTSYWVHWKQPGQGLEWIGRIDPNSGGTKY 79

RESULT 33
HV49_MOUSE
ID HV49_MOUSE STANDARD; PRT; 117 AA.
AC P06328;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH558 B4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN SEQUENCE FROM N.A.
RP MEDLINE=8509340; PubMed=2578321;
RX Yancopoulos G.D., Alt F.W.;
RA

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RT "Developmentally controlled and tissue-specific expression of
 RT unarranged VH gene segments.";
 RL Cell 40:271-281(1985).

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CC -----
 CC EMBL; M13788; AAA38506.1; --
 CC PIR; A02035; MHMSB4.
 CC HSSP; P01810; 2FBJ.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_v.

DR Pfam; PF00047; Ig; 1.

DR SMART; SM00406; IGV; 1.

DR PROSITE; PS50835; IG LIKE; 1.

KW Immunoglobulin V region; Signal.

FT SIGNAL 1 19

FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH58 B4.

FT DOMAIN 20 49 FRAMEWORK-1.

FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 55 68 FRAMEWORK-2.

FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 86 117 FRAMEWORK-3.

FT DISULFID 41 115 BY SIMILARITY.

FT NON_TER 117 117

FT SEQUENCE 117 AA; 12834 MW; B8862PAC67ABD345 CRC64;

Query Match 11.8%; Score 414; DB 1; Length 117;
 Best Local Similarity 78.4%; Pred No. 2.7e-19;
 Matches 76; Conservative 10; Mismatches 11; Indels 0; Gaps 0;

QY 2 VQLQSGDPLVKPGASVKISKASGYSTGYMHWKQSPGKLEWIGRINPNNGVTLYN 61

Db 21 VQLQPGAEVLKPGASVKLSKASGYTFTSYMHWKQSPGKLEWIGRINPNNGVTLYN 80

QY 62 QKFKDXTLTVDKSTTAYMELSLTSEDSAVYYCAR 98

Db 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

QY 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

Db 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

QY 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

Db 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

QY 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

Db 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

QY 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

Db 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

QY 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

Db 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

QY 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

Db 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

QY 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

Db 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

QY 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

Db 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

QY 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

Db 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

QY 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

Db 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

QY 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

Db 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

QY 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

Db 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

QY 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

Db 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

QY 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

Db 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

QY 81 EKFKSKATLTVDKSSSTAYMQLSSLTSEDSAVYYCTR 117

DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal.

FT SIGNAL 1 19

FT CHAIN 20 117 IG HEAVY CHAIN V REGION 102.

FT DOMAIN 20 49 FRAMEWORK-1.

FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.

FT DOMAIN 55 68 FRAMEWORK-2.

FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.

FT DOMAIN 86 117 FRAMEWORK-3.

FT DISULFID 41 115 BY SIMILARITY.

FT NON_TER 117 117

FT SEQUENCE 117 AA; 12867 MW; 740A65DD851FCA8C CRC64;

Query Match 11.7%; Score 413; DB 1; Length 117;
 Best Local Similarity 80.2%; Pred No. 3.1e-19;
 Matches 77; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 2 VQLQSGDPLVKPGASVKISKASGYSTGYMHWKQSPGKLEWIGRINPNNGVTLYN 61

Db 21 VQLQPGAEVLKPGASVKSVKASGYTFTSYMHWKQSPGKLEWIGRINPNNGVTLYN 80

QY 62 QKFKDXTLTVDKSTTAYMELSLTSEDSAVYYCA 97

Db 81 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

QY 62 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

Db 81 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

QY 62 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

Db 81 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

QY 62 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

Db 81 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

QY 62 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

Db 81 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

QY 62 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

Db 81 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

QY 62 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

Db 81 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

QY 62 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

Db 81 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

QY 62 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

Db 81 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

QY 62 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

Db 81 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

QY 62 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

Db 81 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

QY 62 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

Db 81 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

QY 62 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

Db 81 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

QY 62 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

Db 81 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

QY 62 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

Db 81 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

QY 62 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

Db 81 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

QY 62 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

Db 81 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

QY 62 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

Db 81 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

QY 62 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

Db 81 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

QY 62 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

Db 81 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

QY 62 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

Db 81 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

QY 62 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

Db 81 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

QY 62 QKFKGKATLTVDKSSSTAYMQLSSLTSEDSAVYYCA 116

RT "Structure of heavy chain from strain 13 guinea pig
 RT immunoglobulin-G(2). 3. Amino acid sequence of the region around the
 RT half-cysteine joining heavy and light chains.";
 RL Biochemistry 10:18-25(1971).
 RN [3]
 RP SEQUENCE OF 69-133 AND 312-329.
 RX MEDLINE=71058486; PubMed=5538616;
 RA Turner K.J., Cebra J.J.;
 RT "Structure of heavy chain from strain 13 guinea pig
 RT immunoglobulin-G(2). II. Amino acid sequence of the carboxyl-terminal
 RT and hinge region cyanogen bromide fragments.";
 RL Biochemistry 10:9-17(1971).
 RN [4]
 RP SEQUENCE OF 134-226.
 RX MEDLINE=75036072; PubMed=4429665;
 RA Tracey D.E., Cebra J.J.;
 RT "Primary structure of the CH2 homology region from guinea pig IgG2
 RT antibodies.";
 RL Biochemistry 13:4796-4803(1974).
 RN [5]
 RP SEQUENCE OF 227-311.
 RX MEDLINE=75036073; PubMed=4609467;
 RA Trischmann T.M., Cebra J.J.;
 RT "Primary structure of the CH3 homology region from guinea pig IgG2
 RT antibodies.";
 RL Biochemistry 13:4804-4811(1974).

```

RN DISULFIDE BONDS.
RP MEDLINE=71058474; PubMed=4922544;
RX Oliveira B., Lamm M.E.;
RA "interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
RT Biochemistry 10:26-31(1971).
CC -!- MISCELLANEOUS: This chain was isolated from pooled serum of strain
CC 13 inbred guinea pigs.
DR PIR; A94553; GZGP.
DR HSSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00407; IGL; 2.
DR PROSITE; PS50835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON TER 1 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 79
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 142 202
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
FT DISULFID 248 308
SQ SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 11.7%; Score 413; DB 1; Length 329;
Best Local Similarity 23.6%; Pred. No. 1.3e-18;
Matches 136; Conservative 61; Mismatches 104; Indels 276; Gaps 17;

QY 120 SAKTTPSVPLAPGSAOATNSMTLGLVKGYPFPTVTVNSGSLSSGVHTFFPAVLQS 179
DB 1 SAKTTPSVPLAPGSAOATNSMTLGLVKGYPFPTVTVNSGSLSSGVHTFFPAVLQS 60
QY 180 DLYTLSSVTPSTWSPSTVTCNVAHPASSTKVDKKI-----VPRDS 222
DB 61 GLYSLTSMWTPS-----SOKATCNVAHPASSTKVDXTEPIRTZPBPCCTCKPAPPENL 116
QY 223 GGPSEKSEBINEKDLKSELQGTALGNLQVYVNSKAITSSSEKSAQDFTLTLFLKGF 282
DB 117 GGPS-----VFIPPKP-----128
QY 283 FTGHPWYNDLLVLGTAATSEYEGSSVDLYGAYGYQAGGTPNKTAQMGVTLHDNN 342
DB 129 -----KDTLMISL-----TPRVT-CVVVDVS-----148
QY 343 RLTEKKVPINLWDGK-----QTTVPIDKVKTSKEVTVOELDQARHVLHGKGLYNS 397
DB 149 --QDEPEVQTFWVDNKPVGNAETKRVEQYNTFFRVESV--LPIQHQLWLRGK-----198
QY 398 DSFGGKQVGRGLVIFHSSEGSTVSYDLFDAQGYPTDRLIYRDNNTTISLSLSLYLT 457
DB 199 -----198
QY 458 TSIVMTQTPSLVLSAGDRVTITCKASQSVNSDVANVYQKPGSPKLLISYSSRYAGVP 517
DB 199 -----EFCKV-----YNKALPAP---TEKTSKTKGAP 224
QY 518 DRFSGSGYGTDFLTITSSVQAEAAVYFCQDYNSPPTFGGGTKLEIKRAADAAPTYSIFP 577
DB 225 -----RMPDYVTLTP 233
QY 578 PSSEQLTSGASVVCFLNNYPKDINVKW---KIDGSEKONGVNLNWTODSDKSTYSMS 634
DB 234 PSRDELKSKSVTCLLIINFPPADIIHVEWASNRVPVSEK--YKNTFPPIEDA-DGSYFLY 290
QY 635 STLTLTKDEYRHNSYCEATHKTSTSPIV-KSFNRN 670
DB 291 SKLTVDSKAWDQGGIVYTCVSNVHEALHNHVTQKAIRS 327

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RESULT 36
KV4B HUMAN
ID KV4B HUMAN STANDARD; PRT; 133 AA.
AC P06313; 1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-JAN-1988 (Rel. 06, Last annotation update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DB Ig kappa chain V-IV region JI precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
MEDLINE=86041853; PubMed=2997712;
RA Klobeck H.G., Bornkamm G.W., Combriato R., Pohlenz H.D.,
Zachau H.G.
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
single germline gene.";
RL Nucleic Acids Res. 13:6515-6529(1985).
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CC -----
CC EMBL; Z00022; CAA77317.1; -.
CC PIR; A01904; K4HJL.
CC HSSP; P80362; 1WTL.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 133 IG KAPPA CHAIN V-IV REGION JI.
FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 61 75 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 83 114 COMPLEMENTARITY-DETERMINING-4.
FT DOMAIN 115 122 BY SIMILARITY.
FT DISULFID 43 114
FT NON TER 133 133
SQ SEQUENCE 133 AA; 14632 MW; 5FB3953066744AF4 CRC64;

Query Match 11.5%; Score 406.5; DB 1; Length 133;
Best Local Similarity 63.9%; Pred. No. 9.5e-19;
Matches 85; Conservative 16; Mismatches 21; Indels 11; Gaps 3;

QY 444 ISSSTLSLSLYLT-----SIVMTQTPSLVLSAGDRVTITCKASQSV-----SNDVAV 493
DB 2 VLQVTFISLLWISLGAYGDIVMTQSPDSLAVSLGERATINCKSSQSVLSSNNKNVLA 61
QY 494 YQKPGSPKLLISYSSRYAGVPDRFSGSGYGTDFLTITSSVQAEAAVYFCQDYNSP 553
DB 62 YQKPGSPKLLISYSSRYAGVPDRFSGSGYGTDFLTITSSVQAEAAVYFCQDYNSP 553
QY 554 PTFGGTKLEIKR 566
DB 121 PTFGGTKVKEIKR 133

RESULT 37

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KV4C_HUMAN          STANDARD;          PRT;   134 AA.
ID   KV4C_HUMAN
AC   P06314;
DT   01-JAN-1988 (Rel. 06, Created)
DI   01-APR-1988 (Rel. 07, Last sequence update)
DE   15-JUL-1999 (Rel. 38, Last annotation update)
DR   IG kappa chain V-IV region B17 precursor.
DS   Homo sapiens (Human).
OS   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RS   SEQUENCE FROM N.A.
RX   MEDLINE=86041854; PubMed=2997713;
RA   Marsh P., Mills F., Gould H.;
RT   "Detection of a unique human V kappa IV germline gene by a cloned
RL   cDNA probe.";
RL   Nucleic Acids Res. 13:6531-6544(1985).
RN   [2]
RS   REVISION TO 76.
RA   Marsh P.;
RL   Submitted (OCT-1986) to the EMBL/GenBank/DBJ databases.
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@sib-sib.ch).
CC   -----
DR   EMBL; X02990; CAA26733.1; -.
DR   HSSP; P80362; IWL.
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0003823; F:antigen binding; NAS.
DR   GO; GO:0006955; P:immune response; NAS.
DR   InterPro; IPR007110; Ig-like.
DR   InterPro; IPR003596; Ig_v.
DR   Pfam; PF00047; Ig; 1.
DR   SMART; SM00406; IGV; 1.
DR   PROSITE; PS50835; IG_LIKE; 1.
DR   Immunoglobulin V region; Signal.
KW   SIGNAL
FT   CHAIN          1      20
FT   SIGNAL         20
FT   CHAIN         21     134
FT   DOMAIN         21     43
FT   DOMAIN         44     60
FT   DOMAIN         61     75
FT   DOMAIN         76     82
FT   DOMAIN         83     114
FT   DOMAIN         115    121
FT   DOMAIN         122    133
FT   DISULFID       43     114
FT   NON_TER       134     134
FT   SEQUENCE      134 AA; 14966 MW; 6413A22FDD0738832 CRC64;
SQ
Query Match          11.5%; Score 406; DB 1; Length 134;
Best Local Similarity 63.2%; Pred. No. 1e-18;
Matches 84; Conservative 15; Mismatches 24; Indels 10; Gaps 2;

QY  444  ISSTLSISLIYLT-----SYVMTQPTSLVSGDRVITCKASQSV-----SNDVAV 493
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   2  VLQTVFISLLWISGAYGIVNTQSPDSLAVSLGERATINCKSSQILSYSDNKNYLAW 61
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY  494  YQKPKQSPKLLISYTSRRVAGVDFRFSGGYGTDFTLTISVQAEDAAYVFCQDYNSP 553
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   62  YQKPKQPPKLLIYWASTRESGVDFRFSGGSGTDFTLTISLQAEADVAVYCCQYINLP 121
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY  554  PTFGGGTKEIKR 566
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db   122  WTFGGGTKEIKR 134
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

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HV05 MOUSE
ID -HV05 MOUSE STANDARD; PRT; 117 AA.
AC P01739;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
IG heavy chain V region 3 precursor.
GN IGH-V0558.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=C57BL/6;
RX MEDLINE=81234548; PubMed=6788376;
RA Bothwell A.L.M., Paskind M., Reth M., Imanishi-Kari T., Rajewsky K.,
RA Baltimore D.;
RT "Heavy chain variable region contribution to the NPb family of
RT antibodies: somatic mutation evident in a gamma 2a variable region.";
RL Cell 24:625-637(1981).
CC -1- MISCELLANEOUS: THIS GERMLINE GENE BELONGS TO A SET OF CLOSELY
CC RELATED GENES THAT COULD ENCODE V REGIONS OF NPB ANTIBODIES.
-----
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CC or send an email to license@isb-sib.ch)
-----
EMBL: J00536; AAA38605.1; --
PIR: A02031; HYMS3.
DR HSP; P01810; 2FBU.
DR MGD; MGI:96486; IGH-V0558.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin v region; Signal.
FT SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION 3.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 427C861C53975EDC CRC64;
Query Match 11.5%; Score 404; DB 1; Length 117;
Best Local Similarity 76.5%; Pred. No. 1,1e-18;
Matches 75; Conservative 12; Mismatches 11; Indels 0; Gaps 0;
QY 1 EYVQLQSGDPLVKPGASVKISCKASGYSTGYTHMEHWKSPGKGLEWIGRIINPNNVTLV 60
Db 20 QVQLQPGAEIVPGSSVKLSCKASYTFTSYMDVWKVQPGQGLEWIGNIYPSDSETH 79
QY 61 NQKFKDKALITVDKSSITAYMELRLTSDSAYVYCAR 98
Db 80 NQKFKDKALITVDKSSITAYMQLSLTSDSAYVYCAR 117
RESULT 39
GC3 MOUSE
ID -GC3 MOUSE STANDARD; PRT; 329 AA.
AC F22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

```

DE Ig gamma-3 chain C region, secreted form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RT "Structural analysis of the murine IgG3 constant region gene";
RL EMBO J. 3:2041-2046(1984).
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CC -----
CC EMBL; J00451; -; NOT_ANNOTATED_CDS.
CC PIR; B02156; G3MSM.
CC HSSP; P01857; 1FC1.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; Ig cl.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00047; Ig; 3.
CC SMART; SM00407; Igc1; 2.
CC PROSITE; PS00835; IG_LIKE; 3.
CC PROSITE; PS00290; IG_MHC; 1.
CC Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
CC Transmembrane; Alternative splicing.
CC NON_TER 1 1
CC DOMAIN 1 97 CHI.
CC DOMAIN 98 113 HINGE.
CC DOMAIN 114 223 CH2.
CC DOMAIN 224 327 CH3.
CC SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;
Query Match 11.4%; Score 401; DB 1; Length 329;
Best Local Similarity 24.6%; Pred. No. 7.2e-18;
Matches 135; Conservative 51; Mismatches 111; Indels 252; Gaps 15;
QY 123 TTPSVYPLAPGSAAGTNSMTVGLKVGFPPEVTVTWNSGLSGSVHTFPAVLQSDILY 182
DB 2 TTPSVYPLVPGSDTSGSVTLGCLVKGFPPEVTVKNGYALSGSVHTVSSVLQSGFY 61
QY 183 TLSSSVTPSTWPSSTVTCNVAHPASSTKVDKIVPRDSGGPSEKSEINEKDLRKKE 242
DB 62 SLSSLVTPSSTWPSQTVCNVAHPASKTELKRIEPR-----IPKPS 105
QY 243 LQGTAL--GNLKIYYNSKAITSEKSDQFLTNLLFKGFTGHPWYNDLLVDLGSTA 300
DB 106 PGSSCCPGNI-----LG--- 118
QY 301 ATSEYEGSSVDLYGAYGYOCAGGTNKTACMYGVTLHNNRLTBKVPINLWIDGQ 360
DB 119 -----GPSVFIF-----DPK-----PKDALMISLTPKV 141
QY 361 TTPIDKVKTSKEVTVQELDLQARVHLHGKFGLYNSDSFGKVGQGLIVFHSSEGSTVS 420
DB 142 TCVVVD-----VSEDD----- 152
QY 421 YDLFDAQQVPTLLRLRYRNTTISSTLSISLYLTTSIVMTQTPTSLVSAGDRVIT 480
DB 153 -----PDVHVSFWFNKEVHT----- 168
QY 481 CKASQSVNDVAVYQKPGGPKLLISYSSRYAGVDPDRFGSGGYCTDP-TLTISVQAE 539
DB 169 -----AWTQPREAQ-----YNSTFRVVSALPIQHQ 193
QY 540 D---AAVYFCQDYSPTFGGGTKLEIKRAAAPTVISPPSSEQLTSGGASVVCFLNN 596
Db 194 DWMRGFEKCKVNNKALPAPIERTISKPKGKRAQTPQVYTIPTPPREQMCKKVKSLTCLVIN 253
QY 597 FYPKIDNVKWKIDGSRQVGLNSWTDQDSK-----DSTYSMSSTLTLTDEVERHN 648
Db 254 FFEAISVEVE-----ENGEL-----EQDYKNTPPILDSDGTFLYSLKLTVDTSWLOGE 303
QY 649 SYTCEATHK 657
Db 304 IFTCSVVHE 312
RESULT 40
GC3M_MOUSE STANDARD; PRT; 398 AA.
ID GC3M_MOUSE
AC P03987;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig gamma-3 chain C region, membrane-bound form.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85027161; PubMed=6092053;
RA Wells J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene";
RL EMBO J. 3:2041-2046(1984).
[2]
RP SEQUENCE OF 328-398 FROM N.A.
RX MEDLINE=84041483; PubMed=6314258;
RA Konarsky M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA Wall R.;
RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
segment";
RL Nucleic Acids Res. 11:6775-6785(1983).
CC
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CC
CC -----
CC EMBL; J00451; AAB59655.1; -;
CC EMBL; V01526; CAA24767.1; ALT_SEQ.
CC PIR; A02156; G3MSM.
CC HSSP; P01857; 1FC1.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; Ig cl.
CC InterPro; IPR003006; Ig_MHC.
CC Pfam; PF00047; Ig; 3.
CC SMART; SM00407; Igc1; 2.
CC PROSITE; PS00835; IG_LIKE; 3.
CC PROSITE; PS00290; IG_MHC; 1.
CC Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
CC Transmembrane; Alternative splicing.
CC NON_TER 1 1
CC DOMAIN 1 97 CHI.
CC DOMAIN 98 113 HINGE.
CC DOMAIN 114 223 CH2.
CC DOMAIN 224 327 CH3.
CC TRANSMEM 346 362 POTENTIAL.
CC DOMAIN 363 398 CYTOPLASMIC (POTENTIAL).
CC CONFLICT 333 333 E -> G (IN REF. 2).
CC CONFLICT 342 342 E -> Q (IN REF. 2).
CC CONFLICT 388 388 P -> F (IN REF. 2).
CC SEQUENCE 398 AA; 43929 MW; CF7F264B50A41B95 CRC64;

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Query Match      11.4%; Score 401; DB 1; Length 398;
Best Local Similarity 24.6%; Pred. No. 9.4e-18;
Matches 135; Conservative 51; Mismatches 111; Indels 252; Gaps 15;

QY 123 TTPSPVYPLAPGSAQAQTSTWTLGCLVKGYPPEPTVTWNSGLSSGVTTPAVLQSDLY 182
DB 2 TTPSPVYPLAPGSAQAQTSTWTLGCLVKGYPPEPTVTWNSGLSSGVTTPAVLQSDLY 61

QY 183 TLSSSVTPSSWPSETVTCNVAHPASSTKVDKIIVPRDSDGSPSKSEINEKOLRKKSE 242
DB 62 SLSSLVTPSSWPSETVTCNVAHPASSTKVDKIIVPRDSDGSPSKSEINEKOLRKKSE 105

QY 243 LOGTAL--GNLQKIYYNSKAITSEKSAQDLTNLLFKGFTGHPWYNLLVDLGSTA 300
DB 106 PGSSCPPGNI-----VSDD-----LG--- 118

QY 301 ATSEYEGSSVDLYGAYGYQCAGGTENKTACWYGGVTLHDNNRLTEKKVPIINLWIDGK 360
DB 119 -----GPSVFIF-----PPK-----PKDALMISLTPKV 141

QY 361 TVVPIDKVKTSKEVTVVQELDLQARHYLHGKFLYNSDSFGKQVORGLIVFHSSEGSTVS 420
DB 142 TCWVVD-----VSDD----- 152

QY 421 YDLFDAQGYQPTLLRIYRDNTTISSTLSISLYLVTTSIVMTQPTPTLLVSAGDRVIT 480
DB 153 -----PQVHSVFWVDNKEVT----- 168

QY 481 CKASQSVNDVAYQYQKPGQSPKLLISYTSRYAGVDPFGSGYGTDF-TLTSSVQAE 539
DB 169 -----AWTQPREAQ-----YNSTFRVVSALPIQHQ 193

QY 540 D---AAVFCQDYNSTPTFGGKLEIKRADAAPTIVSIFPPSSBOLTSGASVVCPLNN 596
DB 194 DMRGKFKCKNNKALPAPIERTSKPKGRAQTPQVITPPPRQMSKKVSLTCLVTN 253

QY 597 FYPKIDINKWKIDGSRQNGVNSWTDQDSK-----DSTYSMSLTITLKDEYERHN 648
DB 254 PFSEALSVEWE-----RNGEL-----EODYKNTPPILSDGTGYFLYSLKLTVDTSWLQGE 303

QY 649 SYTCEATHK 657
DB 304 IFTCSVWHE 312

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RESULT 41
ID_GCL_HUMAN STANDARD; PRT; 330 AA.
AC P01857;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-MAR-2004 (Rel. 43, Last annotation update)
DE IG gamma-1 chain C region.
GN IGHG1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_SEQUENCE FROM N.A.
RP MEDLINE=82274238; PubMed=6287432;
RX Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [2]
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [3]

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RP SEQUENCE OF 136-329 (EU).
RX MEDLINE=71064025; PubMed=5530842;
RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
RA Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
RL Biochemistry 9:3171-3181(1970).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN NIE).
RX MEDLINE=77070269; PubMed=826475;
RA Ponstingl H., Hilschmann N.;
RT "The rule of antibody structure. The primary structure of a
RT monoclonal IgG1 immunoglobulin (myeloma protein NIE). III. The
RT chymotryptic peptides of the H-chain, alignment of the tryptic
RT peptides and discussion of the complete structure.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
RN [5]
RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
RX MEDLINE=83289131; PubMed=6884994;
RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
RT "Three-dimensional structure determination of antibodies. Primary
RT structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE=71064027; PubMed=4923144;
RA Gall W.E., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. X.
RT Intrachain disulfide bonds.";
RL Biochemistry 9:3188-3196(1970).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE=77070267; PubMed=1002129;
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein NIE). I: Purification and
RT characterization of the protein, the L- and H-chains, the
RT cyanogen bromide cleavage products, and the disulfide bridges.";
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RN [8]
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RX MEDLINE=81208100; PubMed=7236608;
RA Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A resolution.";
RL Biochemistry 20:2361-2370(1981).
RN [9]
RP MISCELLANEOUS: NIE has the G1M(17) allotypic marker, 97-K, and the
CC G1M(1) markers, 239-D and 241-L. KOL and EU sequences have the
CC G1M(3) marker and the G1M (non-1) markers.
CC -I- MISCELLANEOUS: NIE also differs in the amidation states of
CC 35, 116, 198, 269 and 272.
CC -I- MISCELLANEOUS: EU also differs in the amidation states of residues
CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues
CC 268-272.
CC -I- MISCELLANEOUS: KOL also differs in the amidation states of
CC residues 198, 267 and 272.
RN [10]
RP SEQUENCE FROM N.A.
RX MEDLINE=82274238; PubMed=6287432;
RX Ellison J.W., Berson B.J., Hood L.E.;
RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
RL Nucleic Acids Res. 10:4071-4079(1982).
RN [11]
RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
RX MEDLINE=71064024; PubMed=5489771;
RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
RA Waxdal M.J., Edelman G.M.;
RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
RT acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
RL Biochemistry 9:3161-3170(1970).
RN [12]

```

DR PDB; 1D6V; 04-OCT-00.
 DR PDB; 1DN2; 17-MAY-00.
 DR PDB; 1E4K; 06-JUN-01.
 DR PDB; 1FCC; 20-JUL-95.
 DR PDB; 1H2H; 12-JUN-02.
 DR PDB; 1I7Z; 08-AUG-01.
 DR PDB; 1IIS; 16-MAY-01.
 DR PDB; 1IIX; 16-MAY-01.
 DR PDB; 1L6X; 10-APR-02.
 DR PDB; 2RCS; 12-NOV-97.
 DR Genew; HGNC:5525; IGHG1.
 DR MIM; 147100; .
 DR GO; GO:0005624; C:membrane fraction; NAS.
 DR GO; GO:0003823; F:antigen binding; TAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig-cl.
 DR InterPro; IPR003006; Ig_MHC.
 DR Pfam; PF00047; Ig; 3.
 DR SMART; SM00407; IGcl; 2.
 DR PROSITE; PS00835; IG_LIKE; 3.
 DR PROSITE; PS00290; IG_MHC; 2.
 DR immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW 3D-structure. 1 1
 KW NON_TER 1 98
 FT DOMAIN 1 98 CH1.
 FT DOMAIN 99 110 HINGE.
 FT DOMAIN 111 223 CH2.
 FT DOMAIN 224 330 CH3.
 FT DISULFID 27 83
 FT DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).
 FT DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT CARBOHYD 180 180
 FT MOD_RES 330 330
 FT VARIANT 97 97
 FT VARIANT 239 239
 FT VARIANT 241 241
 FT STRAND 122 126
 FT HELIX 130 134
 FT TURN 136 137
 FT STRAND 141 147
 FT STRAND 157 162
 FT TURN 163 164
 FT STRAND 165 166
 FT TURN 168 171
 FT STRAND 176 179
 FT TURN 180 181
 FT STRAND 182 190
 FT HELIX 193 197
 FT TURN 198 199
 FT STRAND 202 207
 FT TURN 209 210
 FT STRAND 215 219
 FT STRAND 227 227
 FT STRAND 230 234
 FT HELIX 238 242
 FT STRAND 245 256
 FT STRAND 260 265
 FT STRAND 270 270
 FT STRAND 274 276
 FT STRAND 280 281
 FT TURN 283 284
 FT STRAND 287 296
 FT HELIX 297 301
 FT TURN 302 303
 FT STRAND 305 312
 FT TURN 313 314

FT TURN 316 317
 FT STRAND 320 325
 SQ SEQUENCE 330 AA; 36106 MW; 3770EE106C2FA33D CRC64;
 Query Match 11.3%; Score 397; DB 1; Length 330;
 Best Local Similarity 24.9%; Pred.No.1.3e-17;
 Matches 135; Conservative 46; Mismatches 126; Indels 236; Gaps 16;
 QY 121 AKTTPSPVPLAGSAAQTNSMTLGLCLVKGYPPEPVYTNWSSGSLSSGSGVHTTFAVLQSD 180
 DB 1 ASTKGPSVFLAPSSKSTSGTAAALGCLVXDYFPEPVTVSWNSGALTGVHTTFAVLQSS 60
 QY 181 -LYTLSSSVTPSPSTWPTVTCNVAHPASSTKVDKXIVPRDSGGSPSEKSENEKDLRK 239
 DB 61 GLYSLSSVTPSPSSSLGTQYICNVNHPKPTKVDKKEPKSC----- 103
 QY 240 KSELQGTALGNLKOIYYNSKAITSSSEKSDAQELTNTLLFKGFTHGHPWYNDLLVDLGST 299
 DB 104 -----DKTHTCPPCPAPPELLGGPSVF--LPPPKP--KDTLM----- 135
 QY 300 AATSEYEGSSVDLYGAYGYQCAGGTENKTAQMYGGVTLHDNNRLTEKKVPINLMIDGK 359
 DB 136 -----ISRTPETV-CVVVDVS-----HEDPEVKENWYVDG- 164
 QY 360 QTVPIDKVTSKKEVTVQELDLQARHYLHGKFLGYNLSDSFGKGVQRLIVPHSSSEGSTV 419
 DB 165 ---VEVHNKTKPREQ-----YNSY---RVSVLTVLHQMNLNGK 200
 QY 420 SYDLFDAQGVDPDLLRIYRDNTTISSTLSLSLYLTTSIVMTQTPTSLLSAGDRVTI 479
 DB 201 EY----- 202
 QY 480 TKKASQSVNDVAWYQKQPKLISYTSRYAGVDPDRFSGSGYGTDTLTLISSVQAE 539
 DB 203 KCKVS-----NKALPAP---IEKTSIRAKGP----- 226
 QY 540 DAAYFCQDYNPPTTGGGKLEIKADAAPTVISIPPSSSEQLTSGASVWCFLANNFYP 599
 DB 227 -----REPQYTLPPSRDELTKNOVSLTCLVKGFP 257
 QY 600 KDINVKWKIDGSEFQN-----GVLSNWTQDSKDSYMSSTLTLTDEYERNHSYTCFA 654
 DB 258 SDIAVEWESNGQPNYKTTTPPVLD-----DGSFLYKLTVDKSRWQQGNVFCSV 310
 QY 655 THK 657
 DB 311 MHE 313

RESULT 42

HV01_MOUSE
 ID HV01_MOUSE STANDARD; PRT; 121 AA.
 AC P01745;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ig heavy chain V region MPC 11.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=81053741; PubMed=6253904;
 RA Zakut R., Cohen J., Givol D.;
 RT "Cloning and sequence of the cDNA corresponding to the variable
 region of immunoglobulin heavy chain MPC11.";
 RL Nucleic Acids Res. 8:3591-3601(1980).
 RN [2]
 RP REVISIONS.
 RA Zakut R., Cohen J., Givol D.;
 RL Nucleic Acids Res. 8:4839-4840(1980).
 CC -!- MISCELLANEOUS: THIS SEQUENCE WAS TRANSLATED FROM AN MRNA ISOLATED

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CC FROM A MYELOMA THAT SECRETES IGG2B.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR PIR; A93708; GMS11.
DR HSSP; P01810; 2FBJ.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 112 IG-LIKE.
FT NON TER 121 121
SQ SEQUENCE 121 AA; 13135 MW; 227AEF3EC56ED0BF CRC64;

Query Match 11.3%; Score 396.5; DB 1; Length 121;
Best Local Similarity 62.8%; Pred. No. 3.4e-18;
Matches 76; Conservative 16; Mismatches 28; Indels 1; Gaps 1;

QY 1 EYQLQQSPDLVKPGASVKISKAGSYFTGYMHWKSPKGLGWIGRINPNNGVTLY 60
DQ 1 EAQLQQSAGELVRPTSVKISKAGSYFTGYMHWKSPKGLGWIGRINPNNGVTLY 60
QY 61 NQKFKDKATLVVDKSGSTAYMELSLTSEDVAIYCARSTMI-TNYVMDYWGQSTVTVS 119
DQ 61 NDNLKGRATLTADTSSTAYIQLSLTSEDVAIYCARSTMI-TNYVMDYWGQSTVTVS 120
QY 120 S 120
DQ 121 S 121

RESULT 43
GC4_HUMAN STANDARD; PRT; 327 AA.
AC P01861.
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig gamma-4 chain C region.
GN IGHG4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83157104; PubMed=6299662;
RA Ellison J.W., Buxbaum J.N., Hood L.E.;
RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
RL DNA 1:11-18(1981).
RP [2]
RX SEQUENCE OF 1-30 AND 81-326.
RX MEDLINE=70207560; PubMed=4192699;
RA Pink J.R.L., Buttery S.H., de Vries G.W., Milstein C.;
RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
RL constant region of a gamma 4 chain.";
RL Biochem. J. 117:33-47(1970).
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; K01316; AAB59394.1; ALT_INIT.
DR PIR; A90933; G4HU.
DR PDB; IADQ; 16-SEP-98.
DR Genew; HGNC:5528; IGHG4.
DR MIM; 147130; -.
DR GO; GO:0005624; C:membrane fraction; NAS.
DR GO; GO:0003823; F:antigen binding; TAS.
```

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DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_3.
DR SMART; SM00407; IGC1; 2.
DR PROSITE; PS00835; IG_LIKE; 3.
DR PROSITE; PS00290; IG_MHC; 2.
KW Immunoglobulin domain; Immunoglobulin C region; 3D-structure.
FT DOMAIN 1 98 CHI.
FT DOMAIN 99 110 HINGE.
FT DOMAIN 111 220 CH2.
FT DOMAIN 221 327 CH3.
FT DISULFID 14 14 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 83 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 141 201
FT DISULFID 247 305
SQ SEQUENCE 327 AA; 35940 MW; 3EDBD811EF208E7A CRC64;

Query Match 11.3%; Score 396.5; DB 1; Length 327;
Best Local Similarity 23.3%; Pred. No. 1.4e-17;
Matches 131; Conservative 52; Mismatches 102; Indels 277; Gaps 16;

QY 121 AKTTPSVVPLAPCSAAQTNSVTLGCLVKGYPPEPVTVTNWSGLSSGVHTFPAVLQSD 180
DQ 1 ASTKGPSVPLAPCSRSTSESTAALGCLVKDYFPEPVTVSNWNGALTSGVHTFPAVLQSS 60
QY 181 -LYTLSSVTVPSSTWPSSTVTCNVAHPASSTKVDKKI-----VPRDSGGPSE 227
DQ 61 GLYSLSVVTVFSSSLGTYTCNVDDHKPSNKNVDKRVESKYGPCPCPAPEFLGGPS- 119
QY 228 KSEEINEKOLRKSELOQTALGNLKOIYYNKAITSSEKSAQDFLTNLLPKGFTHP 287
DQ 120 -----VLFPPPKP-----KDTLMI----- 133
QY 288 WYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLTEE 347
DQ 134 -----SRTPEVT-CVVVDVS-----QED 150
QY 348 KKVPINLWIDGKQTVPIDKVTSKKEV-----TVQELDLQARHYLHGKFLYNSDSF 400
DQ 151 PEVOFNWYVDG---VEVHNAXTKPREQFNSTYRVSVTLVLHQDWLNGK----- 197
QY 401 GKKVQRLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTIISTSLISLYLTTSI 460
DQ 198 -----EY----- 199
QY 461 VMTQTPTSLVAGDRVTITCKASQSVNDVAVYQKQSPKLLISYTSRYAGVPDRF 520
DQ 200 -----CKKVSNK-----GLP--- 209
QY 521 SSGGYGTDFTLISSVQAEADAAYFQQQDYNBPPTFGGQTKLEIKRADAAPTVSIPTSPS 580
DQ 210 -----SSIEK-----TISKAKGQPREPQVYTLPPSQ 235
QY 581 EQLTSGGASVGVCLNNFYPKDINVKWKIDGSEKQ-----GYLNSWTDQDSKDYSMSS 635
DQ 236 EEMTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTPVDS-----DGSFFLYS 288
QY 636 TLTLTKDEYERHNSVTCEATHK 657
DQ 289 RLTVDSKRWQEGNVFSCVMHE 310

RESULT 44
KV4A_HUMAN STANDARD; PRT; 114 AA.
ID KV4A_HUMAN
AC P01625;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
```

DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-IV region Len.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=76004342; PubMed=50995;
RA Schneider M., Hilschmann N.;
RT "The primary structure of a monoclonal immunoglobulin-L-chain of
RL subgroup IV of the kappa type (Bence-Jones protein Len).";
RN Hoppe-Seyler's Z. Physiol. Chem. 356:507-557(1975).
(2)
RP REVISION TO 9.
RA Salomon A.;
RL Submitted (AUG-1996) to Swiss-Prot.
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PDB; 1ERQ; 01-FEB-01.
DR PDB; 1ERQ; 03-FEB-01.
DR PDB; 1ERQ; 09-FEB-01.
DR PDB; 1EK3; 06-MAR-01.
DR PDB; 1LVE; 21-JAN-98.
DR PDB; 3LVE; 18-MAY-99.
DR PDB; 5LVE; 28-MAR-01.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 40 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 41 55 FRAMEWORK-2.
FT DOMAIN 56 62 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 63 94 FRAMEWORK-3.
FT DOMAIN 95 101 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 102 113 FRAMEWORK-4.
FT DISULFID 123 94 BY SIMILARITY.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12640 MW; 0647F1D17F236485 CRC64;
Query Match 11.2%; Score 395; DB 1; Length 114;
Best Local Similarity 69.9%; Pred. No. 3.9e-18;
Matches 79; Conservative 12; Mismatches 16; Indels 6; Gaps 1;
QY 460 IVMTQFTSLVAGDRVTITCKASGV-----SNDVAVYQKPKQSPKLLISTSSRY 513
Db 2 IVMTQSPDSLAVSLGERATINCKSSQSVLYSSNKNYLAWYQKPKQPKLLIYWASTRE 61
QY 514 AGVDPDRFSGSGYGTDFTLTISVQAEADAAVYFCQDYNSSPTFGGKLEIKR 566
Db 62 SGVDPDRFSGSGYGTDFTLTISVQAEADAAVYFCQDYNSSPTFGGKLEIKR 114
RESULT 45
KV5B_MOUSE
ID KV5B_MOUSE STANDARD; PRT; 136 AA.
AC P01634; 1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig kappa chain V-V region MOPC 21 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.

RX MEDLINE=82059477; PubMed=6170937;
RA Hamlyn P.H., Gait M.J., Milstein C.;
RT "Complete sequence of an immunoglobulin mRNA using specific priming
RT and the dideoxynucleotide method of RNA sequencing.";
RN Nucleic Acids Res. 9:4485-4494(1981).
(2)
RP SEQUENCE OF 30-136.
RX MEDLINE=73053310; PubMed=4638343;
RA Svasti J., Milstein C.;
RT "The complete amino acid sequence of a mouse kappa light chain.";
RL Biochem. J. 128:427-444(1972).
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; V00810; CAA24192.1; ALT_TERM.
DR PIR; A93736; KVM521.
DR PDB; 1IGC; 03-JUN-95.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
DR Immunoglobulin V region; Signal; 3D-structure.
KW SIGNAL 1 29
FT CHAIN 30 136 IG KAPPA CHAIN V-V REGION MOPC 21.
FT DOMAIN 30 52 FRAMEWORK-1.
FT DOMAIN 53 63 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 64 78 FRAMEWORK-2.
FT DOMAIN 79 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DOMAIN 118 126 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 127 136 FRAMEWORK-4.
FT NON_TER 136 136
SQ SEQUENCE 136 AA; 14902 MW; 8CDD85113996D1C2 CRC64;
Query Match 11.2%; Score 395; DB 1; Length 136;
Best Local Similarity 60.9%; Pred. No. 5e-18;
Matches 81; Conservative 18; Mismatches 34; Indels 0; Gaps 0;
QY 433 TLLRIYRDNVTISSTLSISLYITTSIVMTQFTSLVAGDRVTITCKASQSVNDVA 492
Db 4 TSMGIKMSHTLVFISILLCYLGADGNIVMTQSPKMSMSVGERVTLTCKASENVTVYS 63
QY 493 WYQKPKQSPKLLISTSSRYAGVDPDRFSGSGYGTDFTLTISVQAEADAAVYFCQDYN 552
Db 64 WYQKPKQSPKLLIYGASNYTGVDPDRFTGSGATDFTLTISVQAEADLADYHCGQYSY 123
QY 553 PPTFGGKLEIKR 565
Db 124 PYTFGGGKLEIKR 136
RESULT 46
HV52_MOUSE
ID HV52_MOUSE STANDARD; PRT; 117 AA.
AC P06327;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig heavy chain V region VH558 A1/A4 precursor.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85099340; PubMed=2578321;

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RA Yancopoulos G.D., Alt F.W.;
RT "Developmentally controlled and tissue-specific expression of
RT unarranged VH gene segments.";
RL Cell 40:271-281(1985).
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CC -----
CC EMBL; M13787; AAA38499.1; -.
CC PIR; A02029; HVMGAL.
CC HSSP; P01810; 2FBJ.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IGV; 1.
CC PROSITE; PS00835; IG LIKE; 1.
CC Immunoglobulin V region; Signal.
KW SIGNAL 1 19
FT CHAIN 20 117 IG HEAVY CHAIN V REGION VH558 A1/A4.
FT DOMAIN 20 49 FRAMEWORK-1.
FT DOMAIN 50 54 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 55 68 FRAMEWORK-2.
FT DOMAIN 69 85 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 86 117 FRAMEWORK-3.
FT DISULFID 41 115 BY SIMILARITY.
FT NON_TER 117 117
SQ SEQUENCE 117 AA; 12971 MW; 8B0BC138856DFC9D CRC64;

Query Match 11.1%; Score 392; DB 1; Length 117;
Best Local Similarity 75.5%; Pred. No. 6.3e-18;
Matches 74; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

QY 1 EVQLQSGPDLVKPGASVKISKASGYSTGYMHVQSPCKGLEWIGRINPNNGVTLY 60
DB 20 QVQLQSGPELVKPGALVKISKASGYTFTSDYNVQRPGQGLEWIGVYDGGSTKY 79
QY 61 NQKFKDKATLTVDKSTTAYMELRLTSDSAVYYCAR 98
DB 80 NEKFKGKATLTADKSSSTAYMQLSLTSENSAVYFCAR 117

RESULT 47
ID_HVIC_HUMAN STANDARD; PRT; 147 AA.
AC P01744;
DT 21-JUL-1986 (Rel. 01, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region ND precursor (Fragments).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=83065234; PubMed=6815656;
RA Kenten J.H., Molgaard H.V., Houghton M., Derbyshire R.B., Viney J.,
RA Bell L.O., Gould H.J.;
RT "Cloning and sequence determination of the gene for the human
RT immunoglobulin epsilon chain expressed in a myeloma cell line.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:6661-6665(1982).
RN [2]
RP SEQUENCE OF 20-147.
RA Bennich H.H., Johansson S.G.O., von Bahr-Lindstrom H.;
RL (In) Bach M.K. (eds.);
RL Immediate hypersensitivity: modern concepts and developments, pp.1-36,
RL Marcel Dekker, New York (1978).
CC -!- MISCELLANEOUS: THIS EPSILON CHAIN WAS ISOLATED FROM A MYELOMA

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CC -----
CC PROTEIN.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
DR HSSP; P01789; IMCP.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 1.
KW Immunoglobulin V region; Signal; Pyrrolidone carboxylic acid.
FT SIGNAL 1 19
FT CHAIN 20 147 IG HEAVY CHAIN V-I REGION ND.
FT DOMAIN 20 131 IG-LIKE.
FT MOD_RES 20 20 PYRROLIDONE CARBOXYLIC ACID.
FT DISULFID 41 115
FT CONFLICT 21 21 T -> V (IN REF. 2).
FT CONFLICT 53 54 IH -> HI (IN REF. 2).
FT CONFLICT 67 68 VG -> GV (IN REF. 2).
FT CONFLICT 125 125 MISSING (IN REF. 2).
FT NON_TER 147 147
SQ SEQUENCE 147 AA; 9489F72A5366C20 CRC64;

Query Match 10.9%; Score 385; DB 1; Length 147;
Best Local Similarity 55.5%; Pred. No. 2.3e-17;
Matches 71; Conservative 24; Mismatches 25; Indels 8; Gaps 1;

QY 1 EVQLQSGPDLVKPGASVKISKASGYSTGYMHVQSPCKGLEWIGRINPNNGVTLY 60
DB 20 QVQLVSGAEVRKPGASRVSCASGYTFTDSVIHWIRQAPGKLEWIGVNSGVTNY 79
QY 61 NQKFKDKATLTVDKSTTAYMELRLTSDSAVYYCARs-----TWITVYMDYWGQ 112
DB 80 APRFQGRVTMTDASFTSTAYMDLRLSRDSDSAVFYCAKSDPFWSDYNTFDYSYTLVDWGQ 139
QY 113 GTSVTYSS 120
DB 140 GTTIVTVSS 147

RESULT 48
ID_GC2_HUMAN STANDARD; PRT; 326 AA.
AC P01859;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig gamma-2 chain C region.
GN IGHG2...
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE OF 2-326 FROM N.A.
RX MEDLINE=82197621; PubMed=6804948;
RA Ellison J.W., Hood L.E.;
RT "Linkage and sequence homology of two human immunoglobulin gamma
RT heavy chain constant region genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).
RN [2]
RP SEQUENCE OF 88-115 FROM N.A.
RX TISSUE=Fetal liver;
RX MEDLINE=83001943; PubMed=6811139;
RA Takahashi N., Ueda S., Obata M., Nikaide T., Nakai S., Honjo T.;
RT "Structure of human immunoglobulin gamma genes: implications for
RT evolution of a gene family.";
RL Cell 29:671-679(1982).
RN [3]
RP SEQUENCE OF 99-177 AND 310-326 FROM N.A.
RX TISSUE=Fetal liver;
RX MEDLINE=84235992; PubMed=6329676;
RA Krawinkel U., Rabbitts T.H.;

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RT "Comparison of the hinge-coding segments in human immunoglobulin gamma
RT heavy chain genes and the linkage of the gamma 2 and gamma 4 subclass
RT genes.";
RL EMBO J. 1:403-407(1982).
RN [4]

RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).
RX MEDLINE=81007873; PubMed=6774012;
RA Wang A.-C., Tung E., Fudenberg H.H.;

RT "The primary structure of a human IgG2 heavy chain: genetic,
RT evolutionary, and functional implications.";
RL J. Immunol. 125:1048-1054(1980).
RN [5]

RP SEQUENCE OF 1-95 AND 132-325 (MYELOMA PROTEIN ZIE).
RX MEDLINE=80001357; PubMed=111060;
RA Connell G.E., Parr D.M., Hofmann T.;

RT "The amino acid sequences of the three heavy chain constant region
RT domains of a human IgG2 myeloma protein.";
RL Can. J. Biochem. 57:758-767(1979).
RN [6]

RP SEQUENCE OF 238-275 (ZIE).
RX MEDLINE=80114419; PubMed=118920;
RA Hofmann T., Parr D.M.;

RT "A note of the amino acid sequence of residues 381-391 of human
RT immunoglobulins gamma chains.";
RL Mol. Immunol. 16:923-925(1979).
RN [7]

RP REVISIONS TO 25; 59; 60 AND 264-268 (ZIE).
RA Hofmann T., Parr D.M.;

RT Submitted (MAR-1980) to the PIR data bank.
RL [8]

RP SEQUENCE OF 1-121 (DOT).
RX MEDLINE=95255298; PubMed=7737190;
RA Stoppini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;

RT "Characterization of the two unique human anti-flavin monoclonal
RT immunoglobulins.";
RL Eur. J. Biochem. 228:886-893(1995).
RN [9]

RP DISULFIDE BONDS.
RX MEDLINE=72033500; PubMed=4940472;
RA Milstein C., Frangione B.;

RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
RL Biochem. J. 121:217-225(1971).
RN [10]

RP DISULFIDE BONDS.
RX MEDLINE=69064124; PubMed=5782707;
RA Frangione B., Milstein C., Pink J.R.L.;

RT "Structural studies of immunoglobulin G.";
RL Nature 221:145-148(1969).
RN [11]

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DR EMBL; J00230; AAB59393.1; -.

DR PIR; A93906; G2HU.

DR HGSP; P01857; IFC1.

DR Genew; HGNC:5526; IGHG2.

DR MIM; 147110; -.

DR GO; GO:0005624; C:membrane fraction; NAS.

DR GO; GO:0003623; F:antigen binding; TAS.

DR GO; GO:0006955; P:immune response; NAS.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003597; Ig ci.

DR InterPro; IPR003006; Ig_YMC.

DR Pfam; PF00047; Ig; 3.

DR SMART; SM00407; IGH1; 2.

DR PROSITE; PS00835; IG_LIKE; 3.

DR PROSITE; PS00290; IG_YMC; 2.

KW Immunoglobulin domain; Immunoglobulin C region.

FT NON TER	1	1	CHI.
FT DOMAIN	99	110	HINGE.
FT DOMAIN	111	219	CH2.
FT DOMAIN	220	326	CH3.
FT DISULFID	14	14	INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID	27	83	
FT DISULFID	102	102	INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID	103	103	INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID	106	106	INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID	109	109	INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID	140	200	
FT DISULFID	246	304	
FT SITE	156	156	AT OR NEAR THE COMPLEMENT-BINDING SITE.
FT MOR_RES	326	326	REMOVED POST-TRANSLATIONALLY (PROBABLE).
FT VARIANT	60	60	S -> A (IN MYELOMA PROTEINS TIL & ZIE).
FT CONFLICT	109	109	/FTid=VAR_003889.
FT SEQUENCE	326 AA;	35884 MW;	C -> S (IN REF. 3).
			8310878C6878CF9C CRC64;

Query Match 10.78; Score 378; DB 1; Length 326;

Best Local Similarity 22.2%; Pred. No. 1.9e-16;

Matches 123; Conservative 56; Mismatches 113; Indels 262; Gaps 14;

QY	121	AKTTPPSVYPLAPGSAQTNSMVTLCGLVKGYPEPVTVTWNSGSLSSGVHTTTPAVLQSD	180
DB	1	ASTKGPSVFPLAPCSRSTSESTAALGCLVKDYFPEPVTVSWNSGALTSGVHTTTPAVLQSS	60

QY	181	LYTLSSVTVFSPSTWPESETVTCNVAHPASSTKVDKIVPR	228
DB	61	GLYSLSSVTVFSPSNFGTQTYTCNVDPKNTKVDKTVERRKCCVECPAPPVAVGES	118

QY	229	SEINEKDLRKSELOQTALGNLQKIIYYNSKAITSEKSAQDLTNTLTFKGFTHPW	288
DB	119	-----VLFPPKP-----KDTLMI-----	132

QY	289	YNDLLVLGSTATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNLTTEK	348
DB	133	-----SRTPVT-CVVVDVS-----HEDP	150

QY	349	KVPINLMDGQTTVPIDIKVTKSKETVQELDLQARHLHGKFLYNSDSFGKVGQRL	408
DB	151	EVQFNWIVDG-----VEVNAKTPRE-----	172

QY	409	IVFHSSEGSTVSYDLFDAQQGYPTLLRIYRDNTTISTSLISLYLYTTSIVNTQPTS	468
DB	173	-----EQFNSTFRVSVLTVVHQD-----	191

QY	469	LLVSAGDRVTITCKASQSVNDVAWYQKQKQSPKLLISYTSRYAGVPDRFSGSGYGD	528
DB	192	-----WLNKEYKC-----KVSNGKGLPAP	210

QY	529	FTLTISSVQARDAAVFCQDYNPPTFGGKTKLEIKRADAAPTIVSIFPPSSEQLTSGGA	588
DB	211	TEKTSITKQG-----PREPQVYTLPPSREMTKNQV	242

QY	589	SVVCFNLNFFPKDINVKWKIDGSRQN-----GVLSNWTQDSDKSTYSMSSTLTITKDE	643
DB	243	SLTCLVKGFYPSDIAVEWESNGQPENNYKTPPMLDS-----DGSFFLYSKLTVDKSR	295

QY	644	YERHNSYTCEATHK	657
DB	296	WQQGNVFCSCVWHE	309

RESULT 49

KWIM HUMAN

ID KWIM HUMAN STANDARD; PRT; 108 AA.

AC P01605;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 15-JUL-1999 (Rel. 38, Last annotation update)

DE Ig kappa chain V-I region Lay.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=77038198; PubMed=824717;
 RA Capra J.D., Klapper D.G.;
 RT "Complete amino acid sequence of the variable domains of two human
 IT IGM anti-gamma globulins (Lay/Pom) with shared idiotypic
 RL specificities".
 RL Scand. J. Immunol. 5:677-684(1976).
 CC -!- MISCELLANEOUS: THE SECOND AND THIRD HYPERVARIABLE REGIONS OF THIS
 CC CHAIN ARE IDENTICAL WITH THOSE OF THE HUMAN POM V-III KAPPA CHAIN,
 CC WITH WHICH IT SHARES CERTAIN IDIOTYPIC DETERMINANTS.
 CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
 CC GLOBULIN ACTIVITY.
 DR PIR: A01871; KIHULY.
 DR HSSP: P01607; IREI.
 DR GO: G0:0005576; C:extracellular; NAS.
 DR GO: G0:0003823; F:antigen binding; NAS.
 DR GO: G0:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 KW Immunoglobulin V region.
 FT DOMAIN 1 23
 FT DOMAIN 24 34
 FT DOMAIN 35 49
 FT DOMAIN 50 56
 FT DOMAIN 57 88
 FT DOMAIN 89 97
 FT DOMAIN 98 107
 FT DISULFID 23 88
 FT NON TER 108 108
 SQ SEQUENCE 108 AA; 11834 MW; 739993A95431434A CRC64;
 Query Match 10.6%; Score 375; DB 1; Length 108;
 Best Local Similarity 69.2%; Pred. No. 6.3e-17;
 Matches 74; Conservative 12; Mismatches 21; Indels 0; Gaps 0;
 QY 460 IVMTCTPTSLVSGDRVTITCKASQSVNDVAVYQKQSPKLLISYTSRYAGVPDR 519
 Db 2 IQMTSPSLSVSGDRVTITCKASQSVNDVAVYQKQSPKLLISYTSRYAGVPDR 519
 QY 520 FSGSGYGTDTLTISVQAEADAAVYFCQDYNPPFTFGGKLEIKR 566
 Db 62 FSGSGYGTDTLTISVQAEADAAVYFCQDYNPPFTFGGKLEIKR 108
 RESULT 50.
 ID KV3H HUMAN STANDARD; PRT; 129 AA.
 AC P04207;
 DT 20-MAR-1987 (Rel. 04; Created)
 DT 01-NOV-1990 (Rel. 16; Last sequence update)
 DT 15-JUL-1999 (Rel. 38; Last annotation update)
 DE Ig kappa chain V-III region CLL precursor (Rheumatoid factor).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8617570; PubMed=3083417;
 RA Jirik P.R., Sorge J., Fong S., Heitzmann J.G., Curd J.G., Chen P.P.,
 RA Goldfien R., Carson D.A.;
 RT "Cloning and sequence determination of a human rheumatoid factor
 RT light-chain gene".
 RL Proc. Natl. Acad. Sci. U.S.A. 83:2195-2199(1986).
 CC

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 CC -----
 DR EMBL: M12740; AAA58992.1; -.
 DR HSSP: P80362; 1WTL.
 DR GO: G0:0005576; C:extracellular; NAS.
 DR GO: G0:0003823; F:antigen binding; NAS.
 DR GO: G0:0006955; P:immune response; NAS.
 DR InterPro: IPR007110; Ig-like.
 DR InterPro: IPR003596; Ig_v.
 DR Pfam: PF00047; Ig_1.
 DR SMART: SM00406; IGV; 1.
 DR PROSITE: PS50835; IG LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION CLL.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 54 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 55 69 FRAMEWORK-2.
 FT DOMAIN 70 76 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 77 108 FRAMEWORK-3.
 FT DOMAIN 109 118 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 119 129 JK1 SEGMENT.
 FT DISULFID 43 108 BY SIMILARITY.
 FT NON TER 129 129
 SQ SEQUENCE 129 AA; 14275 MW; 5C13B411BB60CC14 CRC64;
 Query Match 10.6%; Score 372.5; DB 1; Length 129;
 Best Local Similarity 65.8%; Pred. No. 1.2e-16;
 Matches 73; Conservative 17; Mismatches 20; Indels 1; Gaps 1;
 QY 457 TTSIVMTQPTSLVSGDRVTITCKASQSVNDVAVYQKQSPKLLISYTSRYAGV 516
 Db 19 TGEIVMTQSPATLSVSPGERATLSCASQSVNNLAWYQKQPPRLIYGASTRATGI 78
 QY 517 PDRFSGSGYGTDTLTISVQAEADAAVYFCQDYNPPFTFGGKLEIKR 566
 Db 79 PARFSGSGSGTEFTLTISRLQSEDAVYICQYNNWPPWTFGGGTRVEIKR 129
 RESULT 51
 ID HV1G HUMAN STANDARD; PRT; 117 AA.
 AC P23083;
 DT 01-NOV-1991 (Rel. 20; Created)
 DT 01-NOV-1991 (Rel. 20; Last sequence update)
 DT 10-OCT-2003 (Rel. 42; Last annotation update)
 DE Ig heavy chain V-I region V35 precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88296408; PubMed=2841108;
 RA Matsuda F., Lee K.H., Nakai S., Sato T., Kodaira M., Zeng S.Q.,
 RA Ohno H., Fukuhara S., Honjo T.;
 RT "Dispersed localization of D segments in the human immunoglobulin
 RT heavy-chain locus".
 RL EMBO J. 7:1047-1051(1988).
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
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CC EMBL; X07448; -; NOT_ANNOTATED_CDS.
 DR PIR; S00476; HVH035.
 DR HSP; P01772; 2FB4.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 117 IG HEAVY CHAIN V-I REGION V35.
 FT DOMAIN 20 >117 IG-LIKE.
 FT NON TER 117 117
 FT SEQUENCE 117 AA; 13009 MW; BE61CE63F8CE97BD CRC64;
 SQ
 Query Match 10.5%; Score 370; DB 1; Length 117;
 Best Local Similarity 68.4%; Pred. No. 1.4e-16;
 Matches 67; Conservative 15; Mismatches 16; Indels 0; Gaps 0;
 QY 1 EVLOQSGPLVPGASVKISCKASGYSTGYMHVWVKSPGKGLGWIGRIINPNNGVTLY 60
 Db 20 QVQLVQSGAEVKKPGASVKVCKASGYTFGYMHVWRQPGQGLEWGRINPNSGGTNY 79
 QY 61 NQKFKDKATITVDKSTTAYMELRLSTSDSAVYYCAR 98
 Db 80 AQKFGQVITSTRTSISTAYMELRLSRSDTVYYCAR 117

RESULT 52
 KV1W HUMAN
 ID KV1W HUMAN STANDARD; PRT; 108 AA.
 AC P01600;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Hau.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=71032830; PubMed=4097974;
 RA Watanabe S., Hilschmann N.;
 RT "The primary structure of a monoclonal kappa-type immunoglobulin L-chain of subgroup I (Bence-Jones Protein Hau): subdivision within subgroups."
 RL Hoppe-Seyler's Z. Physiol. Chem. 351:1291-1295 (1970).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A01868; KIHUHU.
 DR HSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 FRAMEWORK-1. DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.
 FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 98 107 FRAMEWORK-4.

FT DISULFID 23 88 BY SIMILARITY.
 FT NON TER 108
 SQ SEQUENCE 108 AA; 11671 MW; 08D3A6160D8D0618 CRC64;
 Query Match 10.5%; Score 369; DB 1; Length 108;
 Best Local Similarity 65.4%; Pred. No. 1.5e-16;
 Matches 70; Conservative 19; Mismatches 18; Indels 0; Gaps 0;
 QY 460 IVMTQTPTSLVSGADRVTTTCASQSVNDVAVYQKQPGQSKLLISYTSRYAGVDP 519
 Db 2 IQMTQSPSSLSASVGDRTVITTCASQSVNSISSYLSWYQKPGKAPQVLIYAASSLPSGVPSR 61
 QY 520 FSGSGYGTDTLTITSSVQAEAAVYFCQDYNPPTFGGQTKLEIKR 566
 Db 62 FSGSGGTDTLTITSLQPEDFAVYCCQNYITPTSFQGITRVEIKR 108
 RESULT 53
 KV3D HUMAN
 ID KV3D HUMAN STANDARD; PRT; 109 AA.
 AC P01622;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region Ti.
 OS Homo sapiens (Human)
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=72188439; PubMed=5027703;
 RA Suter L., Barnikol H.U., Watanabe S., Hilschmann N.;
 RT "Rule of antibody structure. The primary structure of a monoclonal immunoglobulin L-chain of kappa-type, subgroup 3 (Bence-Jones protein Ti). IV. The complete amino acid sequence and its significance for the mechanism of antibody production."
 RL Hoppe-Seyler's Z. Physiol. Chem. 353:189-208 (1972).
 CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A01895; K3HUTI.
 DR HSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; F:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DISULFID 23 89 BY SIMILARITY.
 FT NON TER 109
 SQ SEQUENCE 109 AA; 11788 MW; 8C35058CDC7749BC CRC64;
 Query Match 10.5%; Score 368.5; DB 1; Length 109;
 Best Local Similarity 65.7%; Pred. No. 1.6e-16;
 Matches 71; Conservative 18; Mismatches 18; Indels 1; Gaps 1;
 QY 460 IVMTQTPTSLVSGADRVTTTCASQSVNDVAVYQKQPGQSKLLISYTSRYAGVDP 518
 Db 2 IVLTSQPTLSLSPGERATISCRASQSVNSFLAWYQKPGQAPRLLIYVASSRATGIPD 61
 QY 519 RFGSGYGTDTLTITSSVQAEAAVYFCQDYNPPTFGGQTKLEIKR 566
 Db 62 RFGSGGTDTLTITSLQPEDFAVYCCQYGVSSPSTFGQITKVELKR 109

RESULT 54
 KV1W HUMAN
 ID KV1W HUMAN STANDARD; PRT; 129 AA.
 AC P04431;
 DT 13-AUG-1987 (Rel. 05, Created)

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DN 13-AUG-1987 (Rel. 05, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-I region Walker precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85014148; PubMed=6091049;
RA Kloebeck H.G., Combriato G., Zachau H.G.;
RT "Immunoglobulin genes of the kappa light chain type from two human lymphoid cell lines are closely related.";
RL Nucleic Acids Res. 12:6995-7006(1984).
CC -----
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CC -----
DR EMBL; X00965; CA25477.1; ALT_TERM.
DR PIR; A01883; K1HUK.
DR HSSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 22
FT CHAIN 23 129 IG KAPPA CHAIN V-I REGION WALKER.
FT DOMAIN 23 45 FRAMEWORK-1.
FT DOMAIN 46 56 FRAMEWORK-2.
FT DOMAIN 57 71 FRAMEWORK-3.
FT DOMAIN 72 78 FRAMEWORK-4.
FT DOMAIN 79 110 FRAMEWORK-5.
FT DOMAIN 111 119 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 120 129 FRAMEWORK-6.
FT DISULFID 45 110 BY SIMILARITY.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14069 MW; F941FA07D4AFC2F9 CRC64;

Query Match 10.4%; Score 368; DB 1; Length 129;
Best Local Similarity 67.9%; Pred. No. 2,2e-16;
Matches 72; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVSAGDRVTITCKASQSVNDVAVYQKPGSPKLLISYTSRYAGVDPDR 519
Db 24 IQMTQSPSLVSAGDRVTITCKASQSVNDVAVYQKPGSPKLLISYTSRYAGVDPDR 83
QY 520 FSGSGYGDFTLTISVQAEADAAVYFCQDYNPSPTFGGKLEIK 565
Db 84 FSGSGSGDFTLTISVQAEADAAVYFCQDYNPSPTFGGKLEIK 129

RESULT 55
KV3F HUMAN
ID KV3F HUMAN STANDARD; PRT; 109 AA.
AC P01624;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ig kappa chain V-III region POW.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

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RN SEQUENCE.
RP MEDLINE=76276460; PubMed=60899;
RX Klapper D.G., Capra J.D.;
RT "The amino acid sequence of the variable regions of the light chains from two idiotypically cross reactive IGM anti-gamma globulins.";
RL Ann. Immunol. (Paris) 127C:261-271(1976).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA GLOBULIN ACTIVITY.
CC PIR; A01897; K3HUPM.
DR HSSP; P80362; IWTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DISULFID 23 89 BY SIMILARITY.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11922 MW; 62821DDC6A8ABA86 CRC64;

Query Match 10.3%; Score 364.5; DB 1; Length 109;
Best Local Similarity 65.7%; Pred. No. 2,9e-16;
Matches 71; Conservative 17; Mismatches 19; Indels 1; Gaps 1;

QY 460 IVMTQPTSLVSAGDRVTITCKASQSVNDVAVYQKPGSPKLLISYTSRYAGVDP 518
Db 2 IVMTQPTSLVSAGDRVTITCKASQSVNDVAVYQKPGSPKLLISYTSRYAGVDP 61
QY 519 RFSGSGYGDFTLTISVQAEADAAVYFCQDYNPSPTFGGKLEIKR 566
Db 62 RFSGSGSGTEFTLTISVQAEADAAVYFCQDYNPSPTFGGKLEIKR 109

RESULT 56
KV3L HUMAN
ID KV3L HUMAN STANDARD; PRT; 129 AA.
AC P18135;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region HAH precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88171307; PubMed=3127527;
RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
RT "Autoantibody-associated kappa light chain variable region gene expressed in chronic lymphocytic leukemia with little or no somatic mutation. Implications for etiology and immunotherapy.";
RL J. Exp. Med. 167:840-852(1988).
CC -1- DISEASE: The protein is one of the surface immunoglobulin M autoantibodies expressed in patients with chronic lymphocytic leukemia.
CC PIR; P00022; K3HJHA.
DR HSSP; P80362; IWTL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HAH.

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FT DOMAIN 21 43 FRAMEWORK-1.
FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 56 70 FRAMEWORK-2.
FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 78 109 FRAMEWORK-3.
FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 119 129 JK1 SEGMENT.
FT DISULFID 43 109 BY SIMILARITY.
FT NON TER 129 129
SQ SEQUENCE 129 AA; 14073 MW; D3C55292772774D0 CRC64;

Query Match 10.3%; Score 364.5; DB 1; Length 129;
Best Local Similarity 64.9%; Pred. No. 3.6e-16;
Matches 72; Conservative 17; Mismatches 21; Indels 1; Gaps 1;

Qy 457 TTSIVMTQPTSLVLSAGDRVTITCKASQSVND-VAVYQKPGQSPKLLISYTSRYAG 515
Db 19 TGEIVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIYGASSRATG 78

Qy 516 VPRFSGSGVGTDFTLTISVQAEADAAVFCQDYNPSPTFGGTYKLEIKR 566
Db 79 IPDRFSGSGVGTDFTLTISRLEPEDFAVYQCOQYGTSPRTFGGTYKLEIKR 129

RESULT 57
KV1B_HUMAN STANDARD; PRT; 117 AA.
ID KV1B_HUMAN
AC P01743;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig heavy chain V-I region HG3 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=63144028; PubMed=6298778;
RX Rechavi G., Ram D., Glazer L., Zakut R., Givol D.;
RT "Evolutionary aspects of immunoglobulin heavy chain variable region
RT (VH) gene subgroups."
RL Proc. Natl. Acad. Sci. U.S.A. 80:855-859(1983).
CC -1- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC -----
CC EMBL; J00240; AAA52988.1; -.
CC PIR; A02024; HVHUG.
CC HSP; P01772; 2FB4.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC SMART; SM00406; IG; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
CC Immunoglobulin V region; Signal.
KW SIGNAL
FT CHAIN 1 19 IG HEAVY CHAIN V-I REGION HG3.
FT DOMAIN 20 117 IG-LIKE.
FT NON TER 117 117
SQ SEQUENCE 117 AA; 12946 MW; 2D3F92FC60CD1FE7 CRC64;

Query Match 10.3%; Score 362; DB 1; Length 117;
Best Local Similarity 66.3%; Pred. No. 4.5e-16;

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Matches 65; Conservative 16; Mismatches 17; Indels 0; Gaps 0;

Qy 1 EVQLQQSGDPLVRPGASVKISKASGYSTFGYGMHWVKSPGKLEWIGRIINPNNVTLY 60
Db 20 QVQLVQSGAEVKKFGASVKVSKASGYTFNFSYTHHWVRQAPGQGLEWMGIINPSSGGS 79
Qy 61 NQKFKDKATITVDKSTTAYWELRSLTSEDSAVVYCAR 98
Db 80 AQKFGQRTVMTTRDTSTSTVYNELSLRSEDATVYCAR 117

RESULT 58
KV3B_HUMAN STANDARD; PRT; 109 AA.
ID KV3B_HUMAN
AC P01620;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region SIE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RA MEDLINE=82046598; PubMed=6794615;
RX Andrews D.W., Capra J.D.;
RT "Amino acid sequence of the variable regions of light chains from two
RT idiotypically cross-reactive human IgM anti-gamma-globulins of the Wa
RT group."
RL Biochemistry 20:5816-5822(1981).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGM WITH ANTI-GAMMA
CC GLOBULIN ACTIVITY.
CC PIR; A01892; K3HUSI.
CC HSP; P80362; 1WTL.
CC GO; GO:0005576; C:extracellular; NAS.
CC GO; GO:0003823; F:antigen binding; NAS.
CC GO; GO:0006955; P:immune response; NAS.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003596; Ig_v.
CC Pfam; PF00047; Ig; 1.
CC SMART; SM00406; IG; 1.
CC PROSITE; PS00835; IG_LIKE; 1.
CC Immunoglobulin V region.
KW DISULFID 23 89 BY SIMILARITY.
FT NON TER 109 109
SQ SEQUENCE 109 AA; 11775 MW; 7689C3ECD646FFB4 CRC64;

Query Match 10.3%; Score 361.5; DB 1; Length 109;
Best Local Similarity 64.8%; Pred. No. 4.4e-16;
Matches 70; Conservative 19; Mismatches 18; Indels 1; Gaps 1;

Qy 460 IVMTQTPTSLVLSAGDRVTITCKASQSVND-VAVYQKPGQSPKLLISYTSRYAGVDP 518
Db 2 IVLTQSPGTLSPGERATLSCRASQSVSSYLAWYQKPGQAPRLIYGASSRATGIPD 61

Qy 519 RFSGSGVGTDFTLTISVQAEADAAVFCQDYNPSPTFGGTYKLEIKR 566
Db 62 RFSGSGSGVGTDFTLTISRLEPEDFAVYQCOQYGTSPRTFGGTYKLEIKR 109

RESULT 59
KV2G_MOUSE STANDARD; PRT; 113 AA.
ID KV2G_MOUSE
AC P01631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-II region 26-10.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

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RN RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=83178921; PubMed=6404298;
RA Novotny J., Margolies W.N.;
RT "Amino acid sequence of the light chain variable region from a mouse
anti-digoxin hybridoma antibody.";
RL Biochemistry 22:1153-1158(1983).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM AN IGG2A HYBRIDOMA
PROTEIN THAT BINDS DIGOXIN.
DR PIR; A01914; KVMG26.
DR HSP; P80362; IWL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Monoclonal antibody; Hybridoma.
FT DOMAIN 1 23
FT DOMAIN 24 39
FT DOMAIN 40 54
FT DOMAIN 55 61
FT DOMAIN 62 93
FT DOMAIN 94 102
FT DOMAIN 103 112
FT DISULFID 23 93
FT NON TER 113 113
SQ SEQUENCE 113 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match 10.3%; Score 361.5; DB 1; Length 113;
Best Local Similarity 65.2%; Pred. No. 4.6e-16;
Matches 73; Conservative 14; Mismatches 20; Indels 5; Gaps 2;

QY 460 IVMTQPTSLVSGAGDRVTITCKASQSV--SND---VAVYQCKPGQSPKLLISVTSRYA 514
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
2 VVMTQPTSLVSGAGDRVTITCKASQSV--SND---VAVYQCKPGQSPKLLISVTSRYA 514
QY 515 GVPDRFSGSGGTDTFTLTISVQAEAAVYFCQDYNSSPTFGGTTKLEIKR 566
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
62 GVPDRFSGSGGTDTFTLTISVQAEADLGIYFCSTHTVPPFFGGTTKLEIKR 113

RESULT 60
KV4D HUMAN STANDARD; PRT; 109 AA.
ID KV4D HUMAN STANDARD; PRT; 109 AA.
AC P83593.
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Ig kappa chain V-IV region STH (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX TISSUE=Abdominal adipose tissue;
MEDLINE=98249779; PubMed=9588180;
RA Olsen K.E., Sletten K., Westmark P.;
RT "Extended analysis of AL-amyloid protein from abdominal wall
subcutaneous fat biopsy: kappa IV immunoglobulin light chain.";
RL Biochem. Biophys. Res. Commun. 245:713-716(1998).
CC -!- FUNCTION: May play an important role in fibrillogenesis.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; IG.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 40
SQ SEQUENCE 24 AA; 12273 MW; F9F39CE949A84C2A CRC64;

Query Match 10.2%; Score 360; DB 1; Length 108;
Best Local Similarity 65.4%; Pred. No. 5.3e-16;
Matches 70; Conservative 14; Mismatches 23; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVSGAGDRVTITCKASQSVNDVAVYQCKPGQSPKLLISVTSRYAGVDR 519
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
2 IQWTQSTSLASLGDRTITCKASQSDISNLYNWYQKPDGTGTVKLLIYTSRLHSGVFSR 61
QY 520 FSGSGYGTDTFTLTISVQAEAAVYFCQDYNSSPTFGGTTKLEIKR 566

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FT DOMAIN 41 55
FT DOMAIN 56 62
FT DOMAIN 63 94
FT DOMAIN 95 101
FT DOMAIN 102 109
FT DISULFID 23 94
FT UNSURE 23 23
FT UNSURE 94 94
FT NON TER 109 109
SQ SEQUENCE 109 AA; 12060 MW; 0C4F31EA11E12A0B CRC64;

Query Match 10.2%; Score 361; DB 1; Length 109;
Best Local Similarity 65.7%; Pred. No. 4.7e-16;
Matches 71; Conservative 12; Mismatches 19; Indels 6; Gaps 1;

QY 460 IVMTQPTSLVSGAGDRVTITCKASQV-----SNDVAVYQCKPGQSPKLLISVTSRY 513
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
2 IVMTQPTSLVSGAGDRVTITCKASQSVNDVAVYQCKPGQSPKLLISVTSRY 513
QY 514 AGVPDRFSGSGGTDTFTLTISVQAEAAVYFCQDYNSSPTFGGTTK 561
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
62 SGVPDRFSGSGGTDTFTLTIPGLQAEADVAVYCCQVYRIPYTFGGCAK 109

RESULT 61
KVSX_MOUSE STANDARD; PRT; 108 AA.
ID KVSX_MOUSE STANDARD; PRT; 108 AA.
AC P01646;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Ig kappa chain V-V region HP 123E6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
from five monoclonal anti-p-azophenylarsenate antibodies differing
with respect to a crossreactive idiotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSP; P01607; IREI.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11989 MW; 4C98599C08EBA09A CRC64;

Query Match 10.2%; Score 360; DB 1; Length 108;
Best Local Similarity 65.4%; Pred. No. 5.3e-16;
Matches 70; Conservative 14; Mismatches 23; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVSGAGDRVTITCKASQSVNDVAVYQCKPGQSPKLLISVTSRYAGVDR 519
Db :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
2 IQWTQSTSLASLGDRTITCKASQSDISNLYNWYQKPDGTGTVKLLIYTSRLHSGVFSR 61
QY 520 FSGSGYGTDTFTLTISVQAEAAVYFCQDYNSSPTFGGTTKLEIKR 566

```

Db 62 PFGSGGTDYSLTISNLEQEDATFCQGYMLPTFGGKLEIKR 108
RESULT 62
KV3K_HUMAN STANDARD; PRT; 128 AA.
AC P06311;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-III region IARC/BL41 precursor.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041852; PubMed=2997711;
RA Klobbeck H.G., Meindl A., Combratio G., Solomon A., Zachau H.G.;
RT "Human immunoglobulin kappa light chain genes of subgroups II and III";
RL Nucleic Acids Res. 13:6499-6513 (1985).
CC -----
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CC -----
CC EMBL; Z00021; CAA77316.1; -
DR PIR; A01899; K3HU41.
DR HSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
KW Immunoglobulin V region; Signal.
FT SIGNAL 1 20
FT CHAIN 21 128 IG KAPPA CHAIN V-III REGION IARC/BL41.
FT FRAMEWORK-1.
FT DOMAIN 21 43
FT DOMAIN 21 44
FT DOMAIN 44 54
FT DOMAIN 55 69
FT DOMAIN 70 76
FT DOMAIN 77 108
FT DOMAIN 109 117
FT DOMAIN 118 128
FT DISULFID 43 108
FT NON TER 128 128
SQ SEQUENCE 128 AA; 14070 MW; CC8957P0FE3B9012 CRC64;
Query Match 10.2%; Score 360; DB 1; Length 128;
Best Local Similarity 64.5%; Pred. No. 6.8e-16;
Matches 71; Conservative 16; Mismatches 23; Indels 0; Gaps 0;
QY 457 TTSTVMTQPTSLVSGADRVTTICKASQSVNDVAVYFCQDYNPPTFGGKLEIKR 516
Db 19 TGEIVLTQSGTSLSPGESATLSCRASQSVSNLAWYQKRGQSPRLIRDAASSFRANGI 78
QY 517 PDRFSGGSGTDFLTITSSVQAEADAVYFCQDYNPPTFGGKLEIKR 566
Db 79 PDRFSGGSGTDFLTITSLRLEPDAFVYCCQYTSPTSTPTFGGKLEIKR 128
RESULT 63
KV5K_MOUSE STANDARD; PRT; 108 AA.
ID KV5K_MOUSE

AC P01644;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-V region HP R16.7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE
RX STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idiotype";
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683 (1981).
CC -!- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR PIR; A01927; KVSAR.
DR HSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG-LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON TER 108 108
SQ SEQUENCE 108 AA; 11910 MW; A554642C63BFF597 CRC64;
Query Match 10.2%; Score 358; DB 1; Length 108;
Best Local Similarity 65.4%; Pred. No. 7.1e-16;
Matches 70; Conservative 14; Mismatches 23; Indels 0; Gaps 0;
QY 460 IVMTQPTSLVSGADRVTTICKASQSVNDVAVYFCQDYNPPTFGGKLEIKR 519
Db 2 IQMTQTTSSLASLGDVTTICRASQDISNLYNWYQKPGDTVKLLIYVTSRLHSGVPSR 61
QY 520 PFGSGGTDYSLTISNLEQEDATFCQGYMLPTFGGKLEIKR 566
Db 62 PFGSGGTDYSLTISNLEQEDATFCQGYMLPTFGGKLEIKR 108
RESULT 64
KV40_HUMAN STANDARD; PRT; 121 AA.
ID KV40_HUMAN
AC P06312;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-IV region precursor (Fragment).
GN IGKV4-I.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041853; PubMed=2997712;
RA Klobbeck H.G., Bornkamm G.W., Combratio G., Mocikat R., Pohlentz H.D.,
RA Zachau H.G.;
RT "Subgroup IV of human immunoglobulin K light chains is encoded by a
RT single germline gene";
RL Nucleic Acids Res. 13:6515-6529 (1985).
CC -!- MISCELLANEOUS: THERE IS ONLY ONE IG KAPPA V-IV GENE.

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DR EMBL; Z00023; CAA77318.1; -;
 DR PIR; A01902; K4HU.
 DR HSSP; P80362; 1WTL.
 DR Genew; HGNC:5834; IGKV4-1.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 >121 IG KAPPA CHAIN V-IV REGION.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 60 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 61 75 FRAMEWORK-2.
 FT DOMAIN 76 82 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 83 114 FRAMEWORK-3.
 FT DOMAIN 115 121 COMPLEMENTARITY-DETERMINING-3.
 FT DISULFID 43 114 BY SIMILARITY.
 FT NON TER 121 121
 SQ SEQUENCE 121 AA; 13380 MW; 9586AD4188D33974 CRC64;

Query Match 10.2%; Score 358; DB 1; Length 121;
 Best Local Similarity 61.7%; Pred. No. 8.3e-16;
 Matches 74; Conservative 15; Mismatches 21; Indels 10; Gaps 2;
 QY 444 ISSISLSISLYLT-----SIWMTQTPTSLVSGDRVTITCKASQSV-----SNDVAV 493
 Db 2 VLQGVFSLLLWISGAGDIVMTQSPDSLAVSGERATINCKSQSVLYSSNNKNYLA 61
 QY 494 YQKPGQSPKLLISYTSRYAGVDPFSGSGYGTDFLTITSSVQAEAAVYFCQDYN 553
 Db 62 YQKPGQSPKLLIYWASTRESGVDPFSGSGYGTDFLTITSSVQAEAAVYFCQY 121

RESULT 65
 KV3M_HUMAN
 ID KV3M_HUMAN STANDARD; PRT; 129 AA.
 AC P18136;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-III region HIC precursor.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=8171307; PubMed=3127527;
 RA Kipps T.J., Tomhave E., Chen P.P., Carson D.A.;
 RT "Autoantibody-associated kappa light chain variable region gene
 RT expressed in chronic lymphocytic leukemia with little or no somatic
 RT mutation. Implications for etiology and immunotherapy.";
 RT J. Exp. Med. 167:840-852(1988).
 CC -!- DISEASE: The protein is one of the surface immunoglobulin M
 CC autoantibodies expressed in patients with chronic lymphocytic
 CC leukemia.
 DR PIR; P00021; K3HUHI.
 DR HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.

DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Signal.
 FT SIGNAL 1 20
 FT CHAIN 21 129 IG KAPPA CHAIN V-III REGION HIC.
 FT DOMAIN 21 43 FRAMEWORK-1.
 FT DOMAIN 44 55 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 56 70 FRAMEWORK-2.
 FT DOMAIN 71 77 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 78 109 FRAMEWORK-3.
 FT DOMAIN 110 118 COMPLEMENTARITY-DETERMINING-3.
 FT DOMAIN 119 129 JK1 SEGMENT.
 FT DISULFID 43 109 BY SIMILARITY.
 FT NON TER 129 129
 SQ SEQUENCE 129 AA; 14070 MW; 7395528EA2B74D6 CRC64;

Query Match 10.2%; Score 357.5; DB 1; Length 129;
 Best Local Similarity 64.0%; Pred. No. 9.8e-16;
 Matches 71; Conservative 18; Mismatches 21; Indels 1; Gaps 1;
 QY 457 TTSIVMTQTPTSLVSGDRVTITCKASQSVND-VAVYQKPGQSPKLLISYTSRYAG 515
 Db 19 TGEIVLTQSPGTLSPGERATLSCASQSVSSSYLAWYQKPGQAPRLIYGASRATG 78
 QY 516 VDPFSGSGYGTDFLTITSSVQAEAAVYFCQDYNPPTFGGKLEIKR 566
 Db 79 IPRFSGSGYGTDFLTITSRLEPDPFVAVYCCQYGGSPWTFGGKVEIKR 129

RESULT 66
 KV1S_HUMAN
 ID KV1S_HUMAN STANDARD; PRT; 108 AA.
 AC P01611;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Ig kappa chain V-I region Wes.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=81092279; PubMed=6778806;
 RA Kratzin H., Yang C., Krusche J.U., Hilschmann N.;
 RT "Preparative separation of the tryptic hydrolysate of a protein by
 RT high-pressure liquid chromatography. The primary structure of a
 RT monoclonal L-chain of k-type, subgroup I (Bence-Jones Protein
 RT Wes).";
 RL Hoppe-Seyler's Z. Physiol. Chem. 361:1591-1598(1980).
 CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
 CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
 DR PIR; A01877; K1HUWS.
 DR HSSP; P80362; 1WTL.
 DR GO; GO:0005576; C:extracellular; NAS.
 DR GO; GO:0003823; P:antigen binding; NAS.
 DR GO; GO:0006955; P:immune response; NAS.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PF00047; Ig; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 KW Immunoglobulin V region; Bence-Jones protein.
 FT DOMAIN 1 23 FRAMEWORK-1.
 FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
 FT DOMAIN 35 49 FRAMEWORK-2.
 FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
 FT DOMAIN 57 88 FRAMEWORK-3.

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FT DOMAIN      89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN      98 107 FRAMEWORK-4.
FT DISULFID    23 88 BY SIMILARITY.
FT NON TER     108 108
SQ SEQUENCE    108 AA; 11608 MW; 782B14A649A60E45 CRC64;

Query Match
Best Local Similarity 65.4%; Pred. No. 8.2e-16; Length 108;
Matches 70; Conservative 15; Mismatches 22; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVAGDRVTITCKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDPDR 519
Db 2 IQMTQSPSSVSASVGRVITTCRASQDISHLAWYQKSGKAPKLLIYSASLENGVPSR 61

QY 520 FSGSGVGTDTFTLTISVQAEADAAVFCQDYNPPTFGGTTKLEIKR 566
Db 62 FSGSGSGTDTFTLTISVQAEADAAVFCQDYNPPTFGGTTVDIKR 108

RESULT 67
KVSP MOUSE
ID_KVSP_MOUSE STANDARD; PRT; 108 AA.
AC P01649;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-V regions (Anti-arsonate antibodies).
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=77250895; PubMed=70482;
RA Capra J.D., Tung A.S., Nisonoff A.;
RT "Structural studies on induced antibodies with defined idiotypic
RT specificities. V. The complete amino acid sequence of the light chain
RT variable regions of anti-p-azophenylarsonate antibodies from A/J mice
RT bearing a cross-reactive idiotype."
RL J. Immunol. 119:993-999 (1977).
CC -1- MISCELLANEOUS: THE MIXTURE SEQUENCED CONTAINED AT LEAST TWO OR
CC THREE DIFFERENT LIGHT CHAINS. PEPTIDES CONTAINING THE FOLLOWING
CC SUBSTITUTIONS WERE ALSO ISOLATED: 3-VAL, 10-ILE, AND 12-LEU;
CC 22-LEU; 36-PHE, 41-GLU, AND 43-ALA; 63-THR AND 68-ARG; 76-SER,
CC 77-SER, 78-VAL, 80-ALA, AND 85-ASP; AND 100-GLN AND 107-ARG.
DR PIR; A01928; KMSAA.
DR HSP; P80362; IWL.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23 FRAMEWORK-1.
FT DOMAIN 24 34 COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 35 49 FRAMEWORK-2.
FT DOMAIN 50 56 COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 57 88 FRAMEWORK-3.
FT DOMAIN 89 97 COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 98 108 FRAMEWORK-4.
FT DISULFID 23 88 BY SIMILARITY.
FT NON TER 108 108
SQ SEQUENCE 108 AA; 12056 MW; AE2861E8AAC09DD2 CRC64;

Query Match
Best Local Similarity 66.4%; Pred. No. 9.5e-16; Length 108;
Matches 71; Conservative 9; Mismatches 27; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVAGDRVTITCKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDPDR 519
Db 2 IQMTQSPSSLSAGLGRVSIKCRASQDLSQLFWYQKPGQPPKLLIYRVSLRTNGVDPDR 61

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QY 520 FSGSGVGTDTFTLTISVQAEADAAVFCQDYNPPTFGGTTKLEIKR 566
Db 62 FSGSGSGTDTFTLTIDPNEEDDTATYFCQSRLLIPRTFGGTTKLEIKR 108

RESULT 68
GC RABBIT
ID_GC_RABBIT STANDARD; PRT; 323 AA.
AC P01870;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Ig gamma chain C region.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84030930; PubMed=6313520;
RA Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IGG heavy chain from the recombinant
RT F-I haplotype."
RL Immunogenetics 18:387-397 (1983).
RN [2]
RP SEQUENCE OF 1-128.
RX MEDLINE=76135469; PubMed=1243651;
RA Pratt D.M., Mole L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit
RT immunoglobulin G of different allotype."
RL Biochem. J. 151:337-349 (1975).
RN [3]
RP SEQUENCE OF 88-266 FROM N.A.
RX MEDLINE=8329917; PubMed=6193512;
RA Martens C.L., Moore K.W., Steinmetz M., Hood L., Knight K.L.;
RT "Heavy chain genes of rabbit IGG: isolation of a cDNA encoding gamma
RT heavy chain and identification of two genomic C gamma genes."
RN Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022 (1982).
RN [4]
RP SEQUENCE OF 132-161.
RX MEDLINE=70110015; PubMed=5461106;
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT "Sequence studies of the Fd section of the heavy chain of rabbit
RT immunoglobulin G."
RL Biochem. J. 116:249-259 (1970).
RN [5]
RP SEQUENCE OF 129-131 AND 155-322.
RA Hill R.L., Lebowitz H.E., Fellows R.E. Jr., Delaney R.;
RL (In) Killander J. (eds.);
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
RL Stockholm (1967).
CC -1- MISCELLANEOUS: Ref.1 sequence has the D12 allotypic marker,
CC 104-Thr, and the E14 marker, 185-Thr. Ref.3 has the D11 and E15
CC markers and Ref.5 the E15 marker.
CC -1- SIMILARITY: Contains 3 immunoglobulin-like domains.
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CC or send an email to license@sb-sib.ch).
CC -----
CC EMBL; M16426; AAA31289.1; -.
CC PIR; A91749; GHRB.
CC HSP; P01857; 1FC1.
CC InterPro; IPR007110; Ig-like.
CC InterPro; IPR003597; IG cl.
CC InterPro; IPR003006; IG_VHC.
CC Pfam; PF00047; Ig; 3.
CC SMART; SM00407; IGC1; 2.
CC PROSITE; PS50835; IG_LIKE; 3.

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DR PROSITE; PS00290; IG MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Repeat.
FT NON_TER 1
FT DOMAIN 6
FT DOMAIN 114
FT DOMAIN 222
FT DOMAIN 318
FT VARIANT 104
FT VARIANT 185
FT VARIANT 185
FT CONFLICT 48
FT CONFLICT 71
FT CONFLICT 144
FT CONFLICT 173
FT CONFLICT 187
FT CONFLICT 201
FT CONFLICT 218
FT CONFLICT 233
FT CONFLICT 246
FT CONFLICT 256
FT CONFLICT 260
FT CONFLICT 266
FT CONFLICT 280
FT CONFLICT 284
FT CONFLICT 284
SQ SEQUENCE 323 AA; 35404 MW; 69B8AA118D579A8B CRC64;

Query Match
Best Local Similarity 10.1%; Score 356; DB 1; Length 323;
Matches 134; Conservative 57; Mismatches 111; Indels 256; Gaps 19;

QY 126 PSVYLPARGSAQAQNSMTVGLGVKGYPEPVTVTWNSGSLSSGVHTFPVAVLQSD-LYTL 184
DQ 6 PSVYLPARGSAQAQNSMTVGLGVKGYPEPVTVTWNSGSLSSGVHTFPVAVLQSD-LYTL 184
QY 185 SSVVTPSTPSEVTVTCNVAHPASTKVDKIVPRDGGSGPSEKSEINEKDLKKSELQ 244
DQ 66 SSVVTPSTPSEVTVTCNVAHPASTKVDKIVPRDGGSGPSEKSEINEKDLKKSELQ 244
QY 245 GTALGNLQIYYNSKAITSEKSDAQLTNTLLFKGFTTGHPTWNTDLLVLDLSTAATSE 304
DQ 113 GPSV-----FIFPPKPTLM----- 128
QY 305 YEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPIINLWIDGKQTV 364
DQ 129 -----ISRTPEVT-CVVVDVS-----QDDPEVQFTWINEQ--- 159
QY 365 LDKVTSKKEVTQELDLQARHLYHGKGLNSDFGKVGKVGRLIVHSSSGSVSDLF 424
DQ 160 ---VATAPPPUREQF----- 172
QY 425 DAQGYPTLLRIYRDNTTISSTLSLSISLYTTSIVMTQPTSLVLSAGDRV---TITC 481
DQ 173 -----NSTIRWS-----TLPTHQDMLRGKFKC 197
QY 482 KASQSVNDVAVYQKQSPKLLISYTSRYAGVDPDFSGSGYGTDTLTISVQAE 541
DQ 198 KV-----HNKALPAP---IEKTSKARGQP----- 219
QY 542 AVYFQQDYNPPTFGGKGLKRAADAPVTSIPPSSEQLTSGGASVVCFLNAYPKD 601
DQ 220 -----LE-----PKVYTMGPPELSRSVSLTCNMGFTPSD 252
QY 602 INVKKIDGSEKQN-----GVNSWTDQSDKSTYSMSSTLTITKDEYRHNSVTC--- 652
DQ 253 ISVEWKNKGAEDNYKTPPAVLDS-----DGSVFLYNKLSVPTSEWQGRDVTCSVMH 305
QY 653 EATHKTSPIVKSFRN 670
DQ 306 EALHNHYTQ---KSISRS 320

RESULT 69
KVLP HUMAN
ID KVLP HUMAN STANDARD; PRT; 108 AA.
AC P01608;

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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Ig kappa chain V-1 region Roy.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
RN [1]
RP SEQUENCE
RX MEDLINE=68362076; PubMed=5595110;
RA Hilschmann N.;
RT "Chemical structure of 2 kappa-type Bence Jones proteins (Roy and
RT Cum.).";
RL Hoppe-Seyler's Z. Physiol. Chem. 348:1077-1080(1967).
[2]
RP REVISIONS TO 39 AND 41.
RA Hilschmann N., Barnikol H.U., Hess M., Langer B., Ponstingl H.,
RA Steinmetz-Kayne M., Suter L., Watanabe S.;
RL (in) Franek F., Shugar D. (eds.);
RL Gamma globulins: structure and function, pp.57-74, Academic Press,
RL New York (1969).
CC -1- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (1,2)
CC MARKER.
CC -1- MISCELLANEOUS: This is a Bence-Jones protein.
DR PIR; A91638; KIHURY.
DR HSP; P80362; IWL.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; P:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 1.
DR SMART; SMC0406; IGV; 1.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11782 MW; F5ACEB5A313DF3A CRC64;

Query Match
Best Local Similarity 10.1%; Score 355; DB 1; Length 108;
Matches 70; Conservative 12; Mismatches 25; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVLSAGDRVITCKASQSVNDVAVYQKQSPKLLISYTSRYAGVDP 519
DQ 2 IQMTQSPSLASVSGDRVITTCQASQDISIFLNWYQKQSPKLLISYTSRYAGVDP 519
QY 520 FSGSGYGTDTLTISVQAEAAVYFCQDYNPPTFGGKGLKIKR 566
DQ 62 FSGTSGTDTLTISLQPDIAITYCQDFDLPLTFGGGKTVDFR 108

RESULT 70
KV5L MOUSE
ID KV5L MOUSE STANDARD; PRT; 108 AA.
AC P01645;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-V region HP 93G7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]

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SEQUENCE.
RC STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idiotype."
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSP: P01607; IREI.
DR InterPro: IPR007110; Ig-like.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS0835; IG LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT CONFLICT 30 31
FT STRAND 4 7
FT STRAND 10 13
FT STRAND 15 16
FT TURN 19 25
FT TURN 30 31
FT TURN 33 38
FT TURN 40 41
FT TURN 45 49
FT TURN 50 52
FT TURN 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT STRAND 80 82
FT STRAND 84 90
FT STRAND 98 99
FT STRAND 102 106
FT NON_TER 108
SQ SEQUENCE 108 AA; 11954 MW; 22F4642C63EFFF58E CRC64;

Query Match 10.1%; Score 355; DB 1; Length 108;
Best Local Similarity 65.4%; Pred. No. 1.1e-15;
Matches 70; Conservative 13; Mismatches 24; Indels 0; Gaps 0;

QY 460 IVMTQTPTSLVSAGDRVTITCKASQSVNDVAWYQKPKLLISYTSRYAGVDPDR 519
DB 2 IQMTQSPSSLSASVGDRTVTITCRASQDITNVVWFQQRPGQAPKVIYASILETGVPDR 61

QY 520 FSGSGYGTDTFTLTSSVQAEADAAVYFCQDYNSPPTFGGKLEIKR 566
DB 62 FSGSGGTDFTLTSSLSQEDIAITYCQQGNMLPTFGGKLEIKR 108

RESULT 71
KV1Y HUMAN STANDARD; PRT; 108 AA.
AC P80362;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-I region WAT.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE, AND X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95086080; PubMed=7939311;
RA Huang D.-B., Chang C.-H., Ainsworth C., Bruenger A.T., Eulitz M.,
RA Solomon A., Stevens F.J., Schiffer M.;
RT "Comparison of crystal structures of two homologous proteins:
RT structural origin of altered domain interactions in immunoglobulin
RT light-chain dimers."
RL Biochemistry 33:14848-14857(1994).
RN [2]
RP SEQUENCE OF 1-35.
RX MEDLINE=81267384; PubMed=6167731;
RA Stevens F.J., Westholm F.A., Panagiotopoulos N., Schiffer M.,
RA Popp R.A., Solomon A.;
RT "Characterization and preliminary crystallographic data on the V-
RT related fragment of the human kappa Bence Jones protein wat."
RL J. Mol. Biol. 147:185-193(1991).
CC -!- MISCELLANEOUS: This is a Bence-Jones protein.
DR PDB: 1WTU; 01-NOV-94.
DR GO: GO:0005576; C:extracellular; NAS.
DR GO: GO:0003823; F:antigen binding; NAS.

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GO: GO:0006955; P:immune response; NAS.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003596; Ig_v.
DR Pfam: PF00047; Ig_1.
DR SMART: SM00406; IG; 1.
DR PROSITE: PS0835; IG LIKE; 1.
KW Immunoglobulin V region; Bence-Jones protein; 3D-structure.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT CONFLICT 30 31
FT STRAND 4 7
FT STRAND 10 13
FT STRAND 15 16
FT TURN 19 25
FT TURN 30 31
FT TURN 33 38
FT TURN 40 41
FT TURN 45 49
FT TURN 50 52
FT TURN 53 54
FT TURN 56 57
FT TURN 60 61
FT STRAND 62 67
FT TURN 68 69
FT STRAND 70 75
FT STRAND 80 82
FT STRAND 84 90
FT STRAND 98 99
FT STRAND 102 106
FT NON_TER 108
SQ SEQUENCE 108 AA; 11737 MW; D9D941B3F0FAE697 CRC64;

Query Match 10.1%; Score 354; DB 1; Length 108;
Best Local Similarity 64.5%; Pred. No. 1.3e-15;
Matches 69; Conservative 13; Mismatches 25; Indels 0; Gaps 0;

QY 460 IVMTQTPTSLVSAGDRVTITCKASQSVNDVAWYQKPKLLISYTSRYAGVDPDR 519
DB 2 IQMTQSPSSLSASVGDRTVTITCRASQDITNVVWFQQRPGQAPKVIYASILETGVPDR 61

QY 520 FSGSGYGTDTFTLTSSVQAEADAAVYFCQDYNSPPTFGGKLEIKR 566
DB 62 FSGSGGTDFTLTSSLSQEDIAITYCQQYDTLPLTFGGTKVDIKR 108

RESULT 72
KV5N MOUSE STANDARD; PRT; 108 AA.
AC P01647;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Ig kappa chain V-V region HP 124B1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX STRAIN=A/J;
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
RT from five monoclonal anti-p-azophenylarsenate antibodies differing
RT with respect to a crossreactive idiotype."
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: Anti-arsenate hybridoma protein.

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DR HSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11965 MW; 39971BC653EFEP2A2 CRC64;

Query Match
Best Local Similarity 10.1%; Score 354; DB 1; Length 108;
Matches 69; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVSGDRVTITCKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVPDR 519
Db 2 IQMTZSPSSLSASVGBRVTITCRASZTISYLBWYZKPGKAPBLLIYAASBLHSGVPSR 61
QY 520 FSGSGYGTDFLTITSSVQAEADAAVYFCQDYNSPPTFGGQTKLEIKR 566
Db 62 FSGSGSGTDFLTITSSLSLZPZBFAFYCYCZSYSSPTTFGZGTRLZIKR 108

RESULT 73
KVIN_HUMAN STANDARD; PRT; 108 AA.
AC P01606;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG kappa chain V-I region OU.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=70201507; PubMed=5447531;
RA Kohler H., Shimizu A., Paul C., Putnam F.W.;
RT "Macroglobulin structure: variable sequence of light and heavy
chains."
RL Science 169:56-59(1970).
CC -!- MISCELLANEOUS: THE C REGION OF THIS CHAIN HAS THE INV (3) MARKER.
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A WALDENSTROM'S
MACROGLOBULIN.
DR PIR; A01872; KIHUOV.
DR HSP; P01607; IREI.
DR GO; GO:0005576; C:extracellular; NAS.
DR GO; GO:0003823; F:antigen binding; NAS.
DR GO; GO:0006955; P:immune response; NAS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 107
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11965 MW; 39971BC653EFEP2A2 CRC64;

Query Match
Best Local Similarity 10.1%; Score 354; DB 1; Length 108;
Matches 69; Conservative 14; Mismatches 24; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVSGDRVTITCKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVPDR 519
Db 2 IQMTZSPSSLSASVGBRVTITCRASZTISYLBWYZKPGKAPBLLIYAASBLHSGVPSR 61
QY 520 FSGSGYGTDFLTITSSVQAEADAAVYFCQDYNSPPTFGGQTKLEIKR 566
Db 62 FSGSGSGTDFLTITSSLSLZPZBFAFYCYCZSYSSPTTFGZGTRLZIKR 108

RESULT 74
KV5Q_MOUSE STANDARD; PRT; 108 AA.
AC P01648;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE IG kappa chain V-V region HP 91A3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE.
RX MEDLINE=82150934; PubMed=6801658;
RA Siegelman M., Capra J.D.;
RT "Complete amino acid sequence of light chain variable regions derived
from five monoclonal anti-p-azophenylarsonate antibodies differing
with respect to a crossreactive idiotype."
RL Proc. Natl. Acad. Sci. U.S.A. 78:7679-7683(1981).
CC -!- MISCELLANEOUS: Anti-arsenate hybridoma protein.
DR HSP; P01607; IREI.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
KW Immunoglobulin V region.
FT DOMAIN 1 23
FT DOMAIN 24 34
FT DOMAIN 35 49
FT DOMAIN 50 56
FT DOMAIN 57 88
FT DOMAIN 89 97
FT DOMAIN 98 108
FT DISULFID 23 88
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11961 MW; D52EDA5E9A45291C CRC64;

Query Match
Best Local Similarity 10.0%; Score 353; DB 1; Length 108;
Matches 68; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVSGDRVTITCKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVPDR 519
Db 2 IQMTZSPSSLSASVGBRVTITCRASZTISYLBWYZKPGKAPBLLIYAASBLHSGVPSR 61
QY 520 FSGSGYGTDFLTITSSVQAEADAAVYFCQDYNSPPTFGGQTKLEIKR 566
Db 62 FSGSGSGTDFLTITSSLSLZPZBFAFYCYCZSYSSPTTFGZGTRLZIKR 108

RESULT 75
KV5J_MOUSE STANDARD; PRT; 108 AA.
AC P01643;
DT 21-JUL-1986 (Rel. 01, Created)

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21-JUL-1986 (Rel. 01, last sequence update)
15-JUL-1999 (Rel. 38, last annotation update)
IG kappa chain V-V region MOPC 173.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RX [1]
RN SEQUENCE.
RP MEDLINE=76091934; PubMed=812696;
RX Schiff C., Fougereau M.;
RA "Determination of the primary structure of a mouse IgG2a
RT immunoglobulin. Amino-acid sequence of the light chain.";
RL Eur. J. Biochem. 59:525-537(1975).
CC -!- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM A MYELOMA PROTEIN.
DR PIR; A01926; KWS673.
DR HSSP; P01607; IREI.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
DR Immunoglobulin V region.
FT DOMAIN 1 23
FT FRAMEWORK-1.
FT COMPLEMENTARITY-DETERMINING-1.
FT DOMAIN 24 34
FT FRAMEWORK-2.
FT DOMAIN 35 49
FT COMPLEMENTARITY-DETERMINING-2.
FT DOMAIN 50 56
FT FRAMEWORK-3.
FT DOMAIN 57 88
FT COMPLEMENTARITY-DETERMINING-3.
FT DOMAIN 89 97
FT FRAMEWORK-4.
FT DOMAIN 98 108
FT BY SIMILARITY.
FT NON_TER 108 108
SQ SEQUENCE 108 AA; 11819 MW; 2AD29D92A72AA0A3 CRC64;

Query Match
Best Local Similarity 63.6%; Score 352; DB 1; Length 108;
Matches 68; Conservative 14; Mismatches 25; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVASGDRVTITCKASQSVNDVAWYQKQPGSKLLISYTSRRYAGVPDR 519
DB 2 IQMTQTTSSLASLGDRVTITCSASQSIGNYLWYQKPDGTVKLLIYTTSSLHSGVPSR 61

QY 520 FSGSGYGDTFTLTSSVQAEADAAVFCQDDYNSPPTFGGQTKLEIKR 566
DB 62 FSGSGGSDYSLTTSBLZPBIATYICOOXSKLPRFFGGGQTKLEIKR 108

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OM protein - protein search, using sw model

Run on: August 12, 2004, 13:23:20 ; Search time 58.4605 Seconds
(without alignments)
3626.866 Million cell updates/sec

Title: US-09-900-766-1

Perfect score: 3522
Sequence: 1 EVQLQQSGPDLVKPGASVKI.....EATHKTSPIVKSFNRNES 672

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

- Database : SPREMBL 25:*
- 1: sp_archaea:*
 - 2: sp_bacteria:*
 - 3: sp_fungi:*
 - 4: sp_human:*
 - 5: sp_invertebrate:*
 - 6: sp_mammal:*
 - 7: sp_mhc:*
 - 8: sp_organelle:*
 - 9: sp_phage:*
 - 10: sp_plant:*
 - 11: sp_rodent:*
 - 12: sp_virus:*
 - 13: sp_vertebrate:*
 - 14: sp_unclassified:*
 - 15: sp_rvirus:*
 - 16: sp_bacteriap:*
 - 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	1010	28.7	463	11 Q99LC4	Q99LC4 mus musculus
2	948	26.9	260	16 Q91M4	Q91M4 staphylococ
3	929.5	26.4	238	11 Q8VC16	Q8VC16 mus musculus
4	924.5	26.2	473	11 Q98BL4	Q98BL4 mus musculus
5	918	26.1	260	16 Q99SU3	Q99SU3 staphylococ
6	917.5	26.1	473	11 Q99L25	Q99L25 mus musculus
7	910	25.8	239	11 Q8VC55	Q8VC55 mus musculus
8	909.5	25.8	238	11 Q99M37	Q99M37 mus musculus
9	908	25.8	234	11 Q91WF8	Q91WF8 mus musculus
10	902	25.6	468	11 Q99L31	Q99L31 mus musculus
11	900	25.6	233	11 Q91WS9	Q91WS9 mus musculus
12	899.5	25.5	470	11 Q7TMK1	Q7TMK1 mus musculus
13	897	25.5	236	11 Q7TMK3	Q7TMK3 mus musculus
14	896	25.4	234	11 Q8R062	Q8R062 mus musculus
15	893	25.4	278	11 Q921K1	Q921K1 mus musculus
16	890.5	25.3	235	11 Q7TMK0	Q7TMK0 mus musculus

17	889	25.2	459	11 Q8R3V9	Q8R3V9 mus musculus
18	888.5	25.2	474	11 Q8R3H6	Q8R3H6 mus musculus
19	886	25.2	236	11 Q7TS98	Q7TS98 mus musculus
20	881.5	25.0	235	11 Q91W12	Q91W12 mus musculus
21	880.5	25.0	239	11 Q8K0F8	Q8K0F8 mus musculus
22	870.5	24.7	234	11 Q8R028	Q8R028 mus musculus
23	870	24.7	214	11 Q9R1A5	Q9R1A5 mus musculus
24	862	24.5	437	11 Q9R1A4	Q9R1A4 mus musculus
25	850	24.1	234	11 Q8VC20	Q8VC20 mus musculus
26	803	22.8	473	11 Q91Z05	Q91Z05 mus musculus
27	768	21.8	268	2 Q85217	Q85217 staphylococ
28	750	21.3	469	4 Q7Z7P5	Q7Z7P5 homo sapien
29	691	19.6	234	4 Q7Z473	Q7Z473 homo sapien
30	689	19.5	236	4 Q7Z3V4	Q7Z3V4 homo sapien
31	686.5	19.5	482	4 Q7Z351	Q7Z351 homo sapien
32	669.5	19.0	239	4 Q8NEK0	Q8NEK0 homo sapien
33	666.5	18.9	470	4 Q7Z5W1	Q7Z5W1 homo sapien
34	662.5	18.8	473	4 Q8TC63	Q8TC63 homo sapien
35	654.5	18.6	239	4 Q8TCD0	Q8TCD0 homo sapien
36	648	18.4	614	11 Q7TMT6	Q7TMT6 mus musculus
37	641	18.2	521	4 Q8N4Y9	Q8N4Y9 homo sapien
38	619.5	17.6	488	11 Q8K0F2	Q8K0F2 mus musculus
39	618.5	17.6	482	11 Q8K172	Q8K172 mus musculus
40	618.5	17.6	613	11 Q8VCX7	Q8VCX7 mus musculus
41	606	17.2	243	11 Q7TQM2	Q7TQM2 mus musculus
42	603	17.1	614	4 Q96GA6	Q96GA6 homo sapien
43	602.5	17.1	488	11 Q91WR1	Q91WR1 mus musculus
44	583	16.6	481	11 Q91WT1	Q91WT1 mus musculus
45	573	16.3	481	11 Q8VCV5	Q8VCV5 mus musculus
46	566.5	16.1	480	11 Q8K0Z4	Q8K0Z4 mus musculus
47	565	16.0	489	11 Q8VCX4	Q8VCX4 mus musculus
48	561	15.9	597	4 Q96BB9	Q96BB9 homo sapien
49	548	15.6	237	13 Q7S236	Q7S236 xenopus lae
50	545	15.5	597	4 Q8BQ38	Q8BQ38 homo sapien
51	540	15.3	588	4 Q8WUX4	Q8WUX4 homo sapien
52	540	15.3	597	4 Q9BU10	Q9BU10 homo sapien
53	540	15.3	618	4 Q96AA6	Q96AA6 homo sapien
54	537.5	15.3	613	4 Q8WUX1	Q8WUX1 homo sapien
55	535	15.2	145	11 Q924Q9	Q924Q9 mus musculus
56	535	15.2	481	11 Q91WT3	Q91WT3 mus musculus
57	534	15.2	145	11 Q924Q6	Q924Q6 mus musculus
58	533	15.1	136	11 Q7TPE3	Q7TPE3 mus musculus
59	527.5	15.0	484	11 Q99LA6	Q99LA6 mus musculus
60	527	15.0	145	11 Q924R4	Q924R4 mus musculus
61	525.5	14.9	613	4 Q96EY0	Q96EY0 homo sapien
62	523.5	14.9	500	4 Q9BRV0	Q9BRV0 homo sapien
63	519	14.7	145	11 Q924R1	Q924R1 mus musculus
64	518.5	14.7	146	11 Q924Q3	Q924Q3 mus musculus
65	515	14.6	145	11 Q924F7	Q924F7 mus musculus
66	514	14.6	143	11 Q924R0	Q924R0 mus musculus
67	514	14.6	573	4 Q8WU38	Q8WU38 homo sapien
68	508.5	14.4	117	11 Q9QXE9	Q9QXE9 mus musculus
69	507.5	14.4	142	11 Q924Q1	Q924Q1 mus musculus
70	507	14.4	143	11 Q924P6	Q924P6 mus musculus
71	506.5	14.4	140	11 Q924R2	Q924R2 mus musculus
72	506	14.4	497	4 Q8W124	Q8W124 homo sapien
73	505.5	14.4	146	11 Q924R8	Q924R8 mus musculus
74	504.5	14.3	496	4 Q96DK0	Q96DK0 homo sapien
75	503.5	14.3	298	11 Q9QVF0	Q9QVF0 mus musculus
76	502.5	14.3	168	11 Q8VDC9	Q8VDC9 mus musculus
77	500	14.2	145	11 Q924R3	Q924R3 mus musculus
78	500	14.2	145	11 Q924Q7	Q924Q7 mus musculus
79	498.5	14.2	117	11 Q9QXF0	Q9QXF0 mus musculus
80	498.5	14.2	146	11 Q924Q8	Q924Q8 mus musculus
81	496	14.1	137	11 Q924R6	Q924R6 mus musculus
82	493	14.0	241	11 Q921A6	Q921A6 mus musculus
83	492	14.0	141	11 Q924Q4	Q924Q4 mus musculus
84	492	14.0	587	13 Q7T0F1	Q7T0F1 xenopus lae
85	491.5	14.0	140	11 Q924P8	Q924P8 mus musculus
86	488	13.9	143	11 Q924R7	Q924R7 mus musculus
87	484	13.7	493	4 Q8NCL6	Q8NCL6 mus musculus
88	483	13.7	143	11 Q91VA2	Q91VA2 mus musculus
89	483	13.7	143	11 Q924Q5	Q924Q5 mus musculus

90 481.5 13.7 144 11 Q924P5
 91 474 13.5 139 11 Q924R5
 92 468 13.3 499 4 Q924K4
 93 467.5 13.3 494 4 Q924K6
 94 465.5 13.2 123 11 Q924J1
 95 465 13.2 143 11 Q924P9
 96 462 13.1 143 11 Q91V67
 97 461 13.1 143 11 Q924Q0
 98 460.5 13.1 142 11 Q924Q2
 99 458.5 13.0 482 11 Q91X92
 100 458 13.0 99 11 Q9JL74
 Q924P5 mus musculus
 Q924R5 mus musculus
 Q924K4 homo sapien
 Q924K6 homo sapien
 Q924J1 mus musculus
 Q924P9 mus musculus
 Q91V67 mus musculus
 Q924Q0 mus musculus
 Q924Q2 mus musculus
 Q91X92 mus musculus
 Q9JL74 mus musculus

ALIGNMENTS

RESULT 1

Q99LC4
 ID Q99LC4 PRELIMINARY; PRT; 463 AA.
 AC Q99LC4;
 DT 01-JUN-2001 (TREMELrel. 17, Created)
 DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Similar to RIKEN CDNA 1810060009 gene.
 GN IGH-4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC003435; AA03435.1; -
 DR PIR; B45837; B45837.
 DR HSP; P01842; 7FAB.
 DR MGD; MGI:96446; Igh-4.
 DR InterPro; IPR007110; Igh-like.
 DR InterPro; IPR003006; Igh.MHC.
 DR InterPro; IPR003596; Igh_v.
 DR Pfam; PF00047; Igh_3.
 DR SMART; SM00406; Igh; 1.
 DR PROSITE; PS00835; IGH LIKE; 4.
 DR PROSITE; PS00290; IGH.MHC; 1.
 SQ SEQUENCE 463 AA; 51007 MW; EAA674C6BBC30783 CRC64;

Query Match 28.7%; Score 1010; DB 11; Length 463;
 Best Local Similarity 36.0%; Pred. No. 1.7e-55;
 Matches 240; Conservative 64; Mismatches 114; Indels 248; Gaps 13;
 QY 1 EVOIQSGPDLVKPGASVKISCKASGYFTGYHHWVKQSPGKLEWIRNPNNGVTLY 60
 DB 20 QVQLQQSGAELARPGASVRLSKASGYFTFGYGVSWYKRTGQGLEWVGSIYFGSGNTYY 79
 QY 61 NQKFKDKATLVDSKSTAYNELASLTSEDSAVYICARSTMITNYVDYNGQGTSTVSS 120
 DB 80 SEKFKGRATLTDKSSSTAYNHLSSLTSEDSAVYFCARSSYSYDLFPAYGQGLTVTVA 139
 QY 121 AKTTPSPYPLAPGSAQTSNMTLGLGVKGYFPEPVTVTWNGSSLSGGVHTTFAVLQSD 180
 DB 140 AKTTPSPYPLAPGSAQTSNMTLGLGVKGYFPEPVTVTWNGSSLSGGVHTTFAVLQSD 199
 QY 181 LYTLLSSVTPSSWPSETVTCNVAHPASSTKVDKIKVPSDSDGSPSEINEKDLRKX 240
 DB 200 LYTLLSSVTPSSWPSETVTCNVAHPASSTKVDKIKVPSDSDGSPSEINEKDLRKX 242
 QY 241 SELOQTALGNLKOIYYNKAITSSEKSAQDLFTNTLLFKGFTGHFWYNDLLVDLGSTA 300
 DB 243 CKPCICITVPESSVFIPPK-----PKDLVTITL----- 271
 QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPTNKACMYGGVTLHDNNRLTEKKYPINLWDGKQ 360
 DB 272 -----TP-KVTCVVVDIS-----KDDPEQVQFSNFDV--- 296

QY 361 TTVPTDKVTSKEV-----TVQELDQARHYLHGK-FGL-YNSDSFGKGVQGLIVF 411
 DB 297 -DVEVHTAQTPREBQFNSTFRSVSELPFMHDLWLNKGKFKCRVNSAAPPAPIEK----- 350
 QY 412 HSSEGSTVSYDLFDAQGQYDPTLLRIYRDNTTISSTLSISLSLYTTSIVMTQTPTSLIV 471
 DB 351 -----TISKT----- 355
 QY 472 SAGDRVTITCKASQSVSNDVAWYQKPGQPKLLISYTSRYAGVDPDRFSGSGYGTDTTL 531
 DB 356 ----- 355
 QY 532 TISSVQAEADAAYVFCQDYNSPPTFGGKTKLEIKRADAAPTVISIPPSSEQLTSGASVW 591
 DB 356 -----KGRKAPQVYTIPTPKQWAKDKVSLT 382
 QY 592 CFLNPNPKDINVKWKIDGSEKQNGVLNSWTDQDSKSTYSMSSTLTITKQIEYEHNSYT 651
 DB 383 CMITDFFPDITVEQWNGQPAEN-YKNTQPIMDT-DGSYFIYKLVKSNWAGNTFT 440
 QY 652 CEATHK 657
 DB 441 CSVLHE 446

RESULT 2

Q931M4
 ID Q931M4 PRELIMINARY; PRT; 260 AA.
 AC Q931M4;
 DT 01-DEC-2001 (TREMELrel. 19, Created)
 DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
 DE Enterotoxin P.
 GN SEP OR SAV1948.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcaceae.
 OX NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiratsuku K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus".
 RT Lancet. 357:1225-1240(2001).
 RL EMBL; AF003364; BAB8110.1; -
 DR GO; GO:0005576; Extracellular; IEA.
 DR GO; GO:0015070; P:toxin activity; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bact_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox OB.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_tox C; 1.
 DR PRINTS; PR00279; BACTRLTXIN-
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 260 AA; 30016 MW; 15C2D36270FA8241 CRC64;
 Query Match 26.9%; Score 948; DB 16; Length 260;
 Best Local Similarity 76.4%; Pred. No. 6.2e-52;
 Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
 QY 226 SEKSEINEKDLRKXSELOQTALGNLKOIYYNKAITSSEKSAQDLFTNTLLFKGFTG 285

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Db 28 SESEINEKDLKKSELOQTALGNLKIYYNEKAKTENKSHQFOHQLTLFKGFFTD 87
Qy 286 HPWYNLLVDLSTAAATSEYSSVDLYGAYYGQCAGTGNKTKACMYGGVTLHDNNRLT 345
Db 88 HSWYNLLVDLSDKOIVDKYKGGKVDLYGAYYGQCAGTGNKTKACMYGGVTLHDNNRLT 147
Qy 346 EEKVPINLWIDGKQRTVVIDKTKSKVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 148 EEKVPINLWIDGKQRTVVIDKTKSKVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 207
Qy 406 RGLIVPHSSEGSTSVSYDLFDAQOQYPTLLRIYRDNTTTSSTSLSTSLYLYTT 458
Db 208 RGLIVPHSTEPSVNYDLFCAQOQYNTLLRIYRDNTTSENHMDIYLYTS 260

RESULT 3
Q8VC16 PRELIMINARY; PRT; 238 AA.
AC Q8VC16;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC Tissue=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019760; AAH19760.1; -
DR PIR; A27887; A27887.
DR PIR; A32448; A32448.
DR PIR; A33933; A33933.
DR PIR; B27887; B27887.
DR PIR; B30577; B30577.
DR PIR; B31485; B31485.
DR PIR; B32248; B32248.
DR PIR; B41940; B41940.
DR PIR; C27887; C27887.
DR PIR; C32248; C32248.
DR PIR; C34904; C34904.
DR PIR; D27887; D27887.
DR PIR; D29380; D29380.
DR PIR; E28833; E28833.
DR PIR; F32530; F32530.
DR PIR; H31485; H31485.
DR PIR; PH0106; PH0106.
DR PIR; PH1030; PH1030.
DR PIR; PH1031; PH1031.
DR PIR; PH1034; PH1034.
DR PIR; PL0257; PL0257.
DR PIR; PT0359; PT0359.
DR PIR; S07455; S07455.
DR PIR; S16112; S16112.
DR PIR; S26334; S26334.
DR PIR; S53750; S53750.
DR PIR; S60066; S60066.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 238 AA; 26224 MW; 35EC08E3DE5414AD CRC64;
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Query Match 26.4%; Score 929.5; DB 11; Length 238;
Best Local Similarity 81.8%; Pred. No. 8e-51;

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Matches 180; Conservative 15; Mismatches 20; Indels 5; Gaps 2;
Qy 457 TTSIVMTQTPTSLVSGADRVITICKASQV--SND---VAMVQKQFGQPKLLIYSTSS 511
Db 18 SSDVMTQTPTSLVSLGDDQASISCRSSQSLVHSGNTYLHWYLOKQSPKLLIYKVS 77
Qy 512 RYAGVPRFSSGGSGTDTTLTISSVQAEDAAYVFCQDYNSSPTFGGTGLEIKRADAAP 571
Db 78 RFGVUPRFGSGSGTDTTLKISRVEADLGVFCQSOSTHVPPFTFGGTGLEIKRADAAP 137
Qy 572 TVSIFFPSSEQLTSGGASVVCFLNNFYPKQINVKWKIDGSRQNGVLNSMTDQDSKDY 631
Db 138 TVSIFFPSSEQLTSGGASVVCFLNNFYPKQINVKWKIDGSRQNGVLNSMTDQDSKDY 197
Qy 632 SMSSTLTLLTKDEYERHNSYTCEATHKTSTSPVKSFNENE 671
Db 198 SMSSTLTLLTKDEYERHNSYTCEATHKTSTSPVKSFNENE 237

RESULT 4
Q9D8L4 PRELIMINARY; PRT; 473 AA.
ID Q9D8L4;
AC Q9D8L4;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 181006O009Rik protein.
GN IGH-1 OR 181006O009RIK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Pancreas;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikolaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staebli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bona M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 403:685-690(2001).
DR EMBL; AK007918; BAB25349.1; -
DR PIR; S26746; S26746.
DR HSP; P01842; 7FAB.
DR MGD; MGI:96443; Igh-1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
SQ SEQUENCE 473 AA; 51699 MW; 9DED57A514475FBB CRC64;
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Query Match 26.2%; Score 924.5; DB 11; Length 473;
Best Local Similarity 33.8%; Pred. No. 4.2e-50;
Matches 239; Conservative 53; Mismatches 123; Indels 293; Gaps 15;

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QY 1 EVQLOOSGPDVLKPGASVKISKASGYSTFTGYMHVWKQSPGKGLWIGRINPNNGVTLY 60
D 20 QVQLKQSGAELVKGPGASVKISKASGYSTFTDYINWVKQRPQGLEWIGKIPGSGSTYY 79
QY 61 NOKPKDKATLTVDSSTTAYNELASLTSEDSAVYICARSTMITNYVMD---YWGQGSFT 117
D 80 NEKFKGKATLADKSSSTAYVQLSLSLTSEDSAVYFCARS---CYDYDFAYWCGGLT 135
QY 118 VSSAKTTPSPVPLAPGSAATNMTVLCGLVKGYPPEPVTVTNWNSGLSSGVTHTPPAVL 177
D 136 VSAKTTAPSVPLAPVCGGTGSSVTLGCVLVKGYPPEPVTLTNWNSGLSSGVTHTPPALL 195
QY 178 QSLDVLTSSTVPSSTWPSSTVTCNVAPHPASSTKVDKIVPRDSGGPSEKSEINEKDL 237
D 196 QSLGTLTSSTVTSNTWPSSTVTCNVAPHPASSTKVDKIEPR----- 238
QY 238 RKKSELQGTALGNLQKIYYNSKAITSEKSAQDQFLNTLLFKGFTTGHFWYNDLLVDLG 297
D 239 ----- 238
QY 298 STAATSEYEGSDVLYGAYGYCAGGTPNKTACMGYGVTLHDNNRLTEKKYPIINLWID 357
D 239 -----VPI----- 241
QY 358 GKQTTVPIDKVKTSKKEVTVOELDQARHLYLHKGFLYNSDSFGKVGQRLVIFHSSEGS 417
D 242 ---IQNCPCLKECPCAA-----PDLGGP----- 264
QY 418 TVSYDLPDAQGYPDTLIRIVRDNNTTSSTLSLSLYLYTSIVMTQPTSLVLSVAGDRV 477
D 265 ---SVTFIPPKIKDVL-----ISLSPWVTCVV----- 290
QY 478 TITCKASQSVNDVAWYQKQKPGKPKLLISYTSRYAGVDPDRFSGSGVGTDTLTISVQ 537
D 291 -----DVSED-----DPDVQISW-----FYNNVE 309
QY 538 AEDAAVYFCQDYNSSPPFFGGTKLEIKRAD----- 568
D 310 VHTAQOTQTHREDYNS--TLRVVSALPIQHQDMSGKEFKCKVNNRALPSPIEKTISKPRG 367
QY 569 --AAPTQSIIPPSSQSLTSGGASVVCFLNFPYKIDINVKWKIDGSRQNGVLSWTDQDS 626
D 368 PVRAQVTVLPFPAPAEEMTKFEKFTCMITGFLPAEIAVDWTSNRTSQN-YKNTATVLD 426
QY 627 KDSYVMSSTLTNRDEYRHNSTCEATHK-----TSTSPVKSFN 669
D 427 -DGSYFMYSKLRVQKSTWERSLFPACSVVHGLNHLTTKTISSLGK 473
RESULT 5
Q99SU3 PRELIMINARY; PRT; 260 AA.
AC Q99SU3;
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Enterotoxin P.
GN SEP OR SA1761.
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.I., Nagai Y., Iino T., Kanamori M.,
RA Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
RA Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
RA Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,
RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
RA Ogasawara N., Hayashi H., Hirayama K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus aureus.";
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RL Lancet 357:1225-1240 (2001).
DR EMBL; AP003135; BAB43036.1; -.
DR F1R; C89984; C89984.
DR HSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_cox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox C; 1.
DR PRINTS; PR00279; BACTRLOXIN_1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 260 AA; 29708 MW; 087C5B4EC028CFDB CRC64;

Query Match 26.1%; Score 918; DB 16; Length 260;
Best Local Similarity 73.0%; Pred. No. 4.8e-50;
Matches 170; Conservative 21; Mismatches 42; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELQGTALGNLQKIYYNSKAITSEKSAQDQFLNTLLFKGFTT 285
D 28 SEKSEINEKDLRKSELQGTALGNLQKIYYNSKAITSEKSAQDQFLNTLLFKGFTT 87
QY 286 HPWYNDLLVGLSTAAATSEYEGSDVLYGAYGYCAGGTPNKTACMGYGVTLHDNNRLT 345
D 88 HPWYNDLLVGLSTAAATSEYEGSDVLYGAYGYCAGGTPNKTACMGYGVTLHDNNRLT 147
QY 346 EKKYPIINLWIDKQTVPIIDKVKTSKKEVTVOELDQARHLYLHKGFLYNSDSFGSKVQ 405
D 148 EKKYPIINLWIDKQTVPIIDKVKTSKKEVTVOELDQARHLYLHKGFLYNSDSFGSKVQ 207
QY 406 RGLIVFHSSEGTSTVYDLFDAQGYPDTLIRIVRDNNTTSSTLSLSLYLYTT 458
D 208 RGLIVFHSSEGTSTVYDLFDAQGYPDTLIRIVRDNNTTSSTLSLSLYLYTT 260

RESULT 6
Q99L25 PRELIMINARY; PRT; 473 AA.
AC Q99L25;
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Similar to RIKEN CDNA 181060C009 gene.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
NCBI_TaxID=10090;
RX NCBI_TaxID=10090;
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC003888; AAH03888.1; -.
DR HSP; P01842; 7FAB.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; igf_3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; 1.
SQ SEQUENCE 473 AA; 52449 MW; BE9898B7986DA155 CRC64;

Query Match 26.1%; Score 917.5; DB 11; Length 473;
Best Local Similarity 33.8%; Pred. No. 1.2e-49;
Matches 232; Conservative 59; Mismatches 141; Indels 255; Gaps 12;

QY 1 EVQLQQSGDPLVKGASVKISKASGYSTFTGYMHVWKQSPGKGLWIGRINPNNGVTLY 60
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Db 20 QVQLQQSDELVRFGASVKLSCKVGYTFDTHIHWKQRPQGLEWIGYIYPRDGS TKY 79
QY 61 NQFKKATLTVDKSTAYWELRSITSESAVYICARSTMINN-----YMDYWGOGTSV 116
Db 80 NERFKKATLTADKSSSTATWQNSITSESAVCFCSGSGSIYGYGLYFDYWGOGTTI 139
QY 117 TVSSAKTTPPSVYPLAPGSAATQNSMVTGLCLVKGYFPEPPFVTVTNWNSGLSSGVHFFPAV 176
Db 140 TVSSAKTTPPSVYPLAPGSDTTGSSVTLGLCLVKGYFPEPPFVTVTNWNSGLSSGVHFFPAV 199
QY 177 LQSDLYLTSSSVTPSTPSEVTVTCNVAHPASTKVDKLIYPRDGGSGSEKSEINEKD 236
Db 200 LQSDLYLTSSSVTVTSSPQSITCNVAHPASTKVDKKBEP-----GPIKPCP----- 251
QY 237 LRKKSBLQGTALGNLKIYVYNSKAITSEKSAQDELNTLLFKGFTGHPWYNLDLVDL 296
Db 252 ----- 251
QY 297 GSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLTEKKVPINLMI 356
Db 252 -----PCKCPAPN-----LLGGPSPF----- 267
QY 357 DGKQTTVPIDKVKTSKEVTQVQLDQARHYLHGKFGLYNSDFGKGVQGLIVFHSSEG 416
Db 268 -----IPPKIKDVLMI-----SLUS 282
QY 417 STVSYDLFDAGQYPTLLRIYRDNTTISSTLSISLYITTSIVMTQPTSLIVSAGDR 476
Db 283 PMVTCVVDVSEDDP-----VQISWFWNNVEVLTAQT----- 317
QY 477 VTITCKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVPDRFSGSGYGTFTLTISV 536
Db 318 -----HREDYNSTLRVY 329
QY 537 QA-----EDAAVYFCQDYNPPTFGGTTKLEIKRADAAPTVSIFPPPSSEQLTSGGA 588
Db 330 SALPIQHODWNSKEFKCKVNNKALPAPIERTISKPGSVRAPQVYVLPPEEMTKQV 389
QY 589 SVVCFNLNFPKIDINVKWIDGSERON-----GVLSNWTDDQSKDSTYMSNSTLTITKDE 643
Db 390 TLTCTMTDFPEDIYVETWNNGTSLNKNTEPVLDS-----DGSYFWYSKLRVEKN 442
QY 644 YERHNSVTEATHK-TSTSPVKSFNK 669
Db 443 WVERNSYSCSVVHEGLNHHHTKXFSR 469

RESULT 7
Q8VC55 PRELIMINARY; PRT; 239 AA.
AC Q8VC55;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC021781; AH21781.1; -
DR PIR; A33933; A33933.
DR PDB; 1KCS; 24-JUL-02.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR004214; Conotoxin.
DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF02950; Conotoxin; 1.
DR Pfam; PF00047; Ig; 2.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 239 AA; 26303 MW; C16119CACA25C337 CRC64;
Query Match 25.8%; Score 910; DB 11; Length 239;
Best Local Similarity 76.0%; Pred. No. 1.4e-49;
Matches 177; Conservative 21; Mismatches 25; Indels 10; Gaps 2;
QY 449 LSISLYLT-----TSIVMTQPTSLIVSAGDRVTITCKASQSVSND-----VAVYQKPG 498
Db 6 LLVLLFTSPASSDVLVLTQPLSLPWNIGDQASISCKSTKSLNSDGFYLDWYLQKP 65
QY 499 QGSPKLLISYTSRYAGVPDRFSGSGYGTFTLTISVQAEADAAYFCQDYNPPTFGG 558
Db 66 QGSPQLLIYLVNRFSGVPDRFSGSGGTDTFTLKISRVEAEDLGVYYCFQSNHLPYTFGG 125
QY 559 GTKLEIKRADAAPTVSIFPPPSSEQLTSGGASVWCFLNNFYPKDINVKWIDGSRQNGVL 618
Db 126 GTKLEIKRADAAPTVSIFPPPSSEQLTSGGASVWCFLNNFYPKDINVKWIDGSRQNGVL 185
QY 619 NSWTDDQSKDSTYMSNSTLTITKDEYERHNSYTCETHTKTSTSPVKSFNK 671
Db 186 NSWTDDQSKDSTYMSNSTLTITKDEYERHNSYTCETHTKTSTSPVKSFNK 238

RESULT 8
Q99M37 PRELIMINARY; PRT; 238 AA.
AC Q99M37;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL; BC002035; AAHQ2035.1; -
DR PIR; A31807; A31807.
DR PIR; A32248; A32248.
DR PIR; B32248; B32248.
DR PIR; C32248; C32248.
DR PIR; F32530; F32530.
DR PIR; PH1042; PH1042.
DR PIR; PH1043; PH1043.
DR PIR; PH1044; PH1044.
DR PIR; S07455; S07455.
DR PIR; S16112; S16112.
DR PIR; S24500; S24500.
DR PIR; S24501; S24501.
DR PIR; S24503; S24503.
DR PIR; S24504; S24504.
DR PIR; S24529; S24529.
DR PIR; S24532; S24532.
DR PIR; S24533; S24533.
DR PIR; S24535; S24535.
DR PIR; S24536; S24536.
DR PIR; S24538; S24538.
DR PDB; 1I91; 25-DEC-02.
DR PDB; 1LO2; 31-JUL-02.
DR PDB; 1LO4; 31-JUL-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; IG_MHC.


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Db 294 -----PDVHVSFVDNKEVHT----- 309
QY 478 TITCKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDRPFGSGYGDF-TLTISSV 536
Db 310 -----AWTQPREAQ-----YNSFPRWSALPI 331
QY 537 QAED---AAVFCQDYNSPPTFGGKLEIKRADAAPTYSIPPSSEQLTSGASVWCF 593
Db 332 QHQDWMRGKFKCKVNNKALPAPERTISKPKGRAQTPQVTTIPPPREQMKSXKVSUTCL 391
QY 594 LNNFYPKDINVKKIDGSRQGVLSNWTQDQSK-----DSTXSMSTLTLTLDXEYE 645
Db 392 VTNFSEAISEWE-----RNGEL-----EQDYKNTPIILSDSGTYFLYSLKLIWTDLSL 441
QY 646 RHNSYTCETHK 657
Db 442 QGEIFTCVWHE 453

RESULT 13
Q7TMK3 PRELIMINARY; PRT; 236 AA.
AC Q7TMK3;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZSCH II; TISSUE=Breast tumor;
RX MEDLINE=22386257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.B., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC055906; RAH55906.1; --
KW Hypothetical protein.
SQ SEQUENCE 236 AA; 26299 MW; 0DB03488AAA6396F CRC64;

Query Match 25.5%; Score 897; DB 11; Length 236;
Best Local Similarity 80.2%; Pred. No. 8, 48-49;
Matches 170; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 460 IYWTQPTSLVSAGDRVTITCKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDR 519
Db 24 IKMTQSPSMYASLGERVTITCKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDR 83

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QY 520 FSGSGYGTDTLTITSSVQAEADAAYVFCQDYNSPPTFGGKLEIKRADAAPTYSIPPS 579
Db 84 FSGSGGQDYSITLTISSLESDDTATYICLQHGESPTFGSGTKLEIKRADAAPTYSIPPS 143
QY 580 SEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQGVLSNWTQDQSKDSTYSMSSTLT 639
Db 144 SEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQGVLSNWTQDQSKDSTYSMSSTLT 203
QY 640 TKDEYERHNSYTCETHKTTSTSPIVKSFNRNE 671
Db 204 TKDEYERHNSYTCETHKTTSTSPIVKSFNRNE 235

RESULT 14
Q8R062 PRELIMINARY; PRT; 234 AA.
AC Q8R062;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC027418; RAH27418.1; --
DR InterPro; IPR007110; IG-LIKE.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25857 MW; 4EB08C81426AEB1 CRC64;

Query Match 25.4%; Score 896; DB 11; Length 234;
Best Local Similarity 81.6%; Pred. No. 1e-48;
Matches 173; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

QY 460 IYWTQPTSLVSAGDRVTITCKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDR 519
Db 22 IQMTQTSLSASLGRVTITCSASQGISNLYLNWYQKPGDGVKLLIYTTSLHSGVFSR 81
QY 520 FSGSGYGTDTLTITSSVQAEADAAYVFCQDYNSPPTFGGKLEIKRADAAPTYSIPPS 579
Db 82 FSGSGGTHYSITINLEPEDATYVCCQYSQFPPTFGSGTKLEIKRADAAPTYSIPPS 141
QY 580 SEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQGVLSNWTQDQSKDSTYSMSSTLT 639
Db 142 SEQLTSGGASVVCFLNNFYPKDINVKKIDGSRQGVLSNWTQDQSKDSTYSMSSTLT 201
QY 640 TKDEYERHNSYTCETHKTTSTSPIVKSFNRNE 671
Db 202 TKDEYERHNSYTCETHKTTSTSPIVKSFNRNE 233

RESULT 15
Q921K1 PRELIMINARY; PRT; 278 AA.
AC Q921K1;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR ENBL: BC012207, AAH12207.1; -.
DR InterPro; IPR007110; Ig-like.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IGV_LIKE; 2.
KW Hypothetical protein_IG_LIKE; 2.
SQ SEQUENCE 278 AA; 29778 MW; F894F955DDCD948A CRC64;

Query Match 25.4%; Score 893; DB 11; Length 278;
Best Local Similarity 76.8%; Pred. No. 2e-48;
Matches 169; Conservative 18; Mismatches 33; Indels 0; Gaps 0;

QY 1 EVCLQSGDPLVKGASVKISCKASGYSTGYMHWKVGSPKGLIEWIRPNNGVTLY 60
Db 20 QVQLQQFQAEVLKPGASVKLSKASGYTFTSYMHWVKRRGGGLEWIGNINPSGGTNY 79
QY 61 NQFKDKATLTVDKSSTTAYMELSLTSDSAVYICARSTMITNYMVDYMGQSTVTYSS 120
Db 80 NQFKDKATLAVDKSSSTYMQLSLTSDSAVYICTRGYDDYFVFWGAGTIVTSS 139
QY 121 AKTTPSVPLAPGSAQAQNSWMTLGLVKGFPEPVTWNSGSLSSGVHTFPVAVLQSD 180
Db 140 AKTTPSVPLAPGSAQAQNSWMTLGLVKGFPEPVTWNSGSLSSGVHTFPVAVLQSD 199
QY 181 LYTLLSSVTVPSSTWPTSETVTCNVAHPASSTKVDKKIVER 220
Db 200 LYTLLSSVTVTNTWFSQITTCNVAHPASSTKVDKKIEPR 239

RESULT 16
Q77MKO
ID Q77MKO PRELIMINARY; PRT; 235 AA.
AC Q77MKO;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CZECH II; TISSUE=Breast tumor;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore T.I., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McWan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalhus D.E., Scherch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
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RC STRAIN=CZECH II; TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR ENBL: BC055911; AAR55911.1; -.
KW Hypothetical protein.
SQ SEQUENCE 235 AA; 25861 MW; 3EBA0312A87613F4 CRC64;

Query Match 25.3%; Score 890.5; DB 11; Length 235;
Best Local Similarity 78.0%; Pred. No. 2.2e-48;
Matches 174; Conservative 18; Mismatches 30; Indels 1; Gaps 1;

QY 449 LSIISLYLTTSIVMTQTPTSLVAGDRVTITCKASQSVNDVAVYQKQSPKLLISY 508
Db 13 LSIISVMSRGSVLTQSPAIMASLIGKVTMSCRASSRV-NYMYWYQKSGASPKLIYY 71
QY 509 TSSRYAGVPEDRFSGSGYGTDFTLTISSVQAEADAAYVFCQDDYNSPPTFGGTTKLEIK 568
Db 72 TSNLAPGVPARFSGSGGTSYSLTISVVEAEADAATYYCQQLSTSPWTFGGGSKLEIKRAD 131
QY 569 AAPTIVSIFPPSSEQLTSGGASVWCFLNNFYPKDNVWKIDGSRQNGVLNSWTDQDSKD 628
Db 132 AAPTIVSIFPPSSEQLTSGGASVWCFLNNFYPKDNVWKIDGSRQNGVLNSWTDQDSKD 191
QY 629 STYSMSSTLTITKDEYERHNSYTCEATHKSTSTSPVKSFNRE 671
Db 192 STYSMSSTLTITKDEYERHNSYTCEATHKSTSTSPVKSFNRE 234

RESULT 17
Q8R3V9
ID Q8R3V9 PRELIMINARY; PRT; 469 AA.
AC Q8R3V9;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR ENBL: BC024405; AAR24405.1; -.
DR PIR; B45837; B45837.
DR MGD; MGI:96446; IGH-4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IGV_LIKE; 4.
DR PROSITE; PS00290; IGV_MHC; 1.
KW Hypothetical protein_IGH-4.
SQ SEQUENCE 469 AA; 51976 MW; 534793F155D05457 CRC64;

Query Match 25.2%; Score 889; DB 11; Length 469;
Best Local Similarity 32.9%; Pred. No. 7.2e-48;
Matches 221; Conservative 68; Mismatches 129; Indels 254; Gaps 16;

QY 1 EVQLQQSGDPLVKGASVKISCKASGYSTGYMHWKVGSPKGLIEWIGFI-NPNNGVTIL 59
Db 20 EVNLVESGGGLVQPGGSLRLSCAASGFTFDYTNMWRQPPGKALEWLFIRKANGYTT 79
QY 60 -YNQKFKDKATLTVDKSSTTAYMELSLTSDSAVYICARSTMITNYV----MDYWGQGT 114
Db 80 EYSASVKGRTISKDNSSQSLYLQMNALRAEDSATYICARDRSSYYISGTSFAYWGQGT 139
QY 115 SVTVSSAKITPPSPVYPLAPGSAQAQNSWMTLGLVKGFPEPVTWNSGSLSSGVHTFP 174
Db 140 LVTVSAAKITPPSPVYPLAPGSAQAQNSWMTLGLVKGFPEPVTWNSGSLSSGVHTFP 199
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175 AVLOSGLYTLSSSVTPSSVTPSETVTCNVAHPASSKVDKTIKIPRDSGSPSEKSEINE 234
 200 AVLOSGLYTLSSSVTPSSVTPSGTTCNVAHPASSKVDKTIKIPRDCG----- 248
 235 KDLAKKSELOGTALGNLQIYYNNSKAITSSSEKSAOFLNTLLFKGFFTGHPWYNDLLV 294
 249 -----CKPCICTVPEVSSVFIFPK-----PKDVLITL----- 277
 295 DLGSTAATSEVSSVDLYGAYYQACAGTGNKTCMVGVTLLHNNRLTEBKKVPINL 354
 278 -----TP-KVTCVVVDIS-----KDDPEVQFSW 299
 355 WIDGKQTTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKQVQ 405
 300 FVD-----DVEHTACTPREBQNFSTFVSSELPIMHQDWLNGKFKRVSNSAFAPIE 355
 406 RGLVIFHSSEGSTVSVDLFDAGQGYPTDLRIYRDNNTTISSTLSISLYLYTT-SIVMTQT 465
 356 K-----TISK----- 361
 466 PTSLLSAGDRVTITCKASQSVNDVAVYQKQKQSPKLLISYTSRYAGVDPDRFGSGY 525
 362 ----- 361
 526 GTDFTLTSSVOAEDAAVYFCQDYNPPTFGGKTKLEIKRADAPTSTVIFPSSBQLTS 585
 362 -----KGRKAPQVYTIPTPKQMAK 382
 586 GGASVVCFLNFPKIDINVKIKIDGSRONGVLSWTDQDSKSTYSMSSTLTLTIDEYE 645
 383 DKVSLTCTMITDFPEDITVQWNGQPAEN-YKNTQPIMDT-DGSFYFYSKLVNQSKE 440
 646 RHNSYTCBATHK 657
 441 AGNTFTCSVLHE 452

RESULT 18
 Q8R3H6 PRELIMINARY; PRT; 474 AA.
 AC Q8R3H6;
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Hypothetical protein.
 GN AU044919.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC025447; AAH25447.1; --
 DR MGD; MGI:2144567; AU044919.
 DR GO; GO:0005488; P:electron transporter activity; IEA.
 DR GO; GO:0006118; P:electron transport; IEA.
 DR InterPro; IPR000345; CytC_heme_BS.
 DR InterPro; IPR007110; IG-like.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_v.
 DR Pfam; PF00047; ig; 3.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS00190; CYTOCHROME_C; 1.
 DR PROSITE; PS00835; IG-LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; 1.
 DR KW Hypothetical protein.
 SQ SEQUENCE 474 AA; 51748 MW; 8608B57C6CD2874A CRC64;

Query Match 25.2%; Score 888.5; DB 11; Length 474;
 Best Local Similarity 35.0%; Pred. No. 7.8e-48;

Matches 234; Conservative 69; Mismatches 124; Indels 241; Gaps 18;
 QY 1 EVLQSQGPDILVPCASVKISCKASGYFTGYMHWKQSPGKLEWIGRINPNNGVTLY 60
 DB 20 QVQLLQSGPELVPCGASVKISCRASGVAFSKSMWNVKRRPGKLEWIGRIFPGDGDTHY 79
 QY 61 NQPKDKATLTVDKSSTAYMELSLTSEDSAVYCARSTMITNVMVDYQOGQSVTVSS 120
 DB 80 SGKFGKAKLTADKSSVTAFLQLTSLTSEDSAVYFCARDSYGY-FDDWQGAFTVSS 138
 QY 121 AKTTPPSVYPLAPGSAQAOTNSMVTGLCVKGYFPPEVTVTNWNSGSLSSGVHTFPFVAVLQSD 180
 DB 139 AKTTPPSVYPLAPGCGDTTSGSVTLGCLVKGYPFESVTVTNWNSGSLSSGVHTFPFVAVLQSG 198
 QY 181 LYTSSSVTVSSVTPSETVTCNVAHPASSKVDKTIKIPRDSGSPSEKSEINE-----KD 236
 DB 199 LYTSSSVTVSSVTPSETVTCNVAHPASSKVDKTIKIPRDSGSPSEKSEINE-----SGP-----ISTINPCPCKE 252
 QY 237 LRK--KSELOGTALGNLQIYYNNSKAITSSSEKSAOFLNTLLFKGFFTGHPWYNDLLV 294
 DB 253 CHKCAPNLEG---GPSVFIIPPNIKDV-----LMI 280
 QY 295 DLGSTAATSEVSSVDLYGAYYQACAGTGNKTCMVGVTLLHNNRLTEBKKVPINL 354
 DB 281 SL-----TP----- 284
 QY 355 WIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQVQGLIVFHSS 414
 DB 285 -----KVTCVVVD-----VSEDDPQVQISWVNN-----VEVHTA 314
 QY 415 EGSTVSYDLFDAGQGYPTDLRIYRDNNTTISSTLSISLYLYTT-SIVMTQPTSLLYSAG 474
 DB 315 QNTTHREDY-----NGTIR-----VWSA- 332
 QY 475 DRVTITCKASQSVNDVAVYQKQKQSPKLLISYTSRYAGVDPDRFGSGYGTDTLTIS 534
 DB 333 -----LPQHQDWMGSKFEKCKVN 351
 QY 535 SVOAEDAAVYFCQDYNPPTFGGKTKLEIKRADAPTSTVIFPSSBQLTSGGASVVCFL 594
 DB 352 N-----KDLPSPIE---RTISKIKGLVEAPQVWILPPPAEQLSRKDVSLTCLV 396
 QY 595 NNFPKIDINVKIKIDGSRON-----GVLSWTDQDSKSTYSMSSTLTITKDEVERHNS 649
 DB 397 VGFNPGDISVWTSNGHTEENYKDTAPVLDS-----DGSFYIYKLDITKTSKWEKTD 449
 QY 650 YTCBATHK 657
 DB 450 FSCNVRHE 457

RESULT 19
 Q7TS98 PRELIMINARY; PRT; 236 AA.
 AC Q7TS98;
 DT 01-OCT-2003 (Tremblrel. 25, Created)
 DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
 DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
 DE Anti-colorectal carcinoma light chain.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-93383497; PubMed=8372513;
 RA Tonge D.W., Hennam J.P., Greene A.R., Lee I.D., Edge M.D.;
 RT "Cloning and characterization of 116NS19.9 heavy and light chain
 RT cDNAs and expression of antibody fragments in Escherichia coli.";
 RL Year Immunol. 7:56-62(1993).
 DR EMBL; S65921; AAB28160.1; --
 SQ SEQUENCE 236 AA; 26454 MW; 2C586EBF5EA10F4C CRC64;

```
Query Match      25.2%; Score 886; DB 11; Length 236;
Best Local Similarity 79.2%; Pred. No. 4.3e-48;
Matches 168; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVAGDRVTITCKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVPR 519
Db 24 IKMTQSPSSMYASLGERVTITCKASQDINSYLSWFQKPGKSPKLLYRANRLVDGPR 83
QY 520 FSGSGVGTDTLLTSSVQAEADAAVYFCQDYNPPFTFGGKLEIKRAAAPTYSIFPPS 579
Db 84 FSGSGGQDYSLLTSSLEVEDMGIYCLQYDEPRTFGGKLEIKRAAAPTYSIFPPS 143
QY 580 SEGLTSGGASVGCFLNNFYPKDINVKWKIDGSRQNGVLSWTDQSKDSTYSMSSTLTL 639
Db 144 SEGLTSGGASVGCFLNNFYPKDINVKWKIDGSRQNGVLSWTDQSKDSTYSMSSTLTL 203
QY 640 TKDEYERHNSYTCEATHKTSTSPVKSFNNE 671
Db 204 TKDEYERHNSYTCEATHKTSTSPVKSFNNE 235

RESULT 20
Q91W12
ID Q91W12 PRELIMINARY; PRT; 235 AA.
AC Q91W12;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006643; AAH06643.1; -.
DR PDB; 1AX1; 30-JAN-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR Hypothetical protein.
KW SEQUENCE FROM N.A.
SQ SEQUENCE 235 AA; 5FC73BDEB5E8FEF CRC64;

Query Match      25.0%; Score 881.5; DB 11; Length 235;
Best Local Similarity 76.7%; Pred. No. 8.3e-48;
Matches 171; Conservative 19; Mismatches 32; Indels 1; Gaps 1;

QY 449 LSISLYTTSIVMTQPTSLVAGDRVTITCKASQSVNDVAVYQKPGQSPKLLISY 508
Db 13 ISASVTSRQIVLTQSPAIMSASGERVTITCKASQSVSH-MHWYQKSGTSPKRWIYD 71
QY 509 TSSRVAGVDPDRSGSGYGTDTLLTSSVQAEADAAVYFCQDYNPPFTFGGKLEIKRAD 568
Db 72 TPKLTSVGVDPDRSGSGSGTSYSLTISNMEADVATYICQWGRNPPTFGVTKLEKRAD 131
QY 569 AAPTYSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLSWTDQSKD 628
Db 132 AAPTYSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLSWTDQSKD 191
QY 629 STYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPVKSFNNE 671
Db 192 STYSMSSTLTLTKDEYERHNSYTCEATHKTSTSPVKSFNNE 234

Query Match      25.0%; Score 880.5; DB 11; Length 239;
Best Local Similarity 76.3%; Pred. No. 9.8e-48;
Matches 174; Conservative 17; Mismatches 32; Indels 5; Gaps 2;

QY 449 LSISLYTTSIVMTQPTSLVAGDRVTITCKASQSV--SND---VAVYQKPGQSPK 503
Db 11 LVLSIQEINGDVVMTQTPTLTSVTIGQPASISCKSSQSLFVTKGKYLWLLQRPQSPK 70
QY 504 LLISVTSRVAGVDPDRSGSGYGTDTLLTSSVQAEADAAVYFCQDYNPPFTFGGKLE 563
Db 71 RLISLVSKLDSGVDPDRSGSGGTDFTLKISRVEADLGVYICLQSTHFFPTFGGKLE 130
QY 564 IKRAAAPTYSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLSWTD 623
Db 131 IKRAAAPTYSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLSWTD 190
QY 624 QDSKDYMSSTLTLTKDEYERHNSYTCEATHKTSTSPVKSFNNE 671
Db 191 QDSKDYMSSTLTLTKDEYERHNSYTCEATHKTSTSPVKSFNNE 238

RESULT 22
Q9R028
ID Q9R028 PRELIMINARY; PRT; 234 AA.
AC Q9R028;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]_
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RA Strausberg R.;
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RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028540; AAR28540.1; -.
DR PIR; H33932; H33932.
DR PIR; PH1074; PH1074.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR Hypothetical protein.
KW Hypothetical protein.
SQ
  SEQUENCE 234 AA; 25702 MW; 1483779C1CD0AEE CRC64;

Query Match 24.7%; Score 870.5; DB 11; Length 234;
Best Local Similarity 74.3%; Pred. No. 4e-47;
Matches 168; Conservative 16; Mismatches 37; Indels 5; Gaps 1;

QY 451 ISLYLYTTS-----IVMTQPTSLVSGADRVITCKASQSVNDVAVYQKPGQSPKLL 505
DB 8 LSLLLLCVSDSRAETTVTQSPASLSVATGKVTIRCITSTDIIDDMWYQKFGPEPKLL 67

QY 506 ISYTSRYAGVDPDFSGSGCHDTFLISSVQAEAAVYFCQDYNSPPTFGGKTKLEIK 565
DB 68 ISEGNLRPGVPSPFSSGGYGTDFVFTIENTLSEVDADYICLQSDNNMPLTFGAGTKLELK 127

QY 566 RADAAPTYSIIPPSSQELTSGASVGVCFNNFYPKDINVKWKIDGSRQNGVLNSWTDDQ 625
DB 128 RADAAPTYSIIPPSSQELTSGASVGVCFNNFYPKDINVKWKIDGSRQNGVLNSWTDDQ 187

QY 626 SKDSTYMSSTLTITKDEYERHNSYTCEATHTKSTSPIVKSFNRNE 671
DB 188 SKDSTYMSSTLTITKDEYERHNSYTCEATHTKSTSPIVKSFNRNE 233

RESULT 23
Q9RIA5 PRELIMINARY; PRT; 214 AA.
ID AC Q9RIA5;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Kappa light chain of Mab7 (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G.; Yu X.; Ekrannodoullah A.K.M.; Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scfv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152371; AAD40242.1; -.
DR PDB; 1CIC; 11-MAR-03.
DR PDB; 1E08; 29-NOV-00.
DR PDB; 1K6Q; 18-DEC-02.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
DR NON_TER 1
FT NON TER 214
SQ SEQUENCE 214 AA; 23922 MW; 52BA205FDE995E2A CRC64;

Query Match 24.7%; Score 870; DB 11; Length 214;
Best Local Similarity 77.8%; Pred. No. 3.8e-47;
Matches 165; Conservative 19; Mismatches 28; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVSGADRVITCKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDPDR 519
DB 2 IQLTQSPSSMYASLGERTVITCKASQDINSYLSWFOQKPGKSPKTLIYRANRLVDGVPSR 61

QY 520 PFGSGYGTDFLTITSSVQAEAAVYFCQDYNSPPTFGGKTKLEIKRADAAPTYSIIPPSS 579
DB 62 PFGSGGQDYSLTITSSLEYEDMGIIYCLQYDEFFPTFGSGTKLEIKRADAAPTYSIIPPSS 121

QY 580 SEQLTSGASVGVCFNNFYPKDINVKWKIDGSRQNGVLNSWTDDQSKDSTYMSSTLT 639
DB 122 SEQLTSGASVGVCFNNFYPKDINVKWKIDGSRQNGVLNSWTDDQSKDSTYMSSTLT 181

QY 640 TKDEYERHNSYTCEATHTKSTSPIVKSFNRNE 671
DB 182 TKDEYERHNSYTCEATHTKSTSPIVKSFNRNE 213

RESULT 24
Q9RIA4 PRELIMINARY; PRT; 437 AA.
ID AC Q9RIA4;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Gamma heavy chain of Mab7 (Fragment).
GN IGH-4.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G.; Yu X.; Ekrannodoullah A.K.M.; Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scfv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF152372; AAD40243.1; -.
DR PIR; B45837; B45837.
DR PDB; 1COK; 11-SEP-99.
DR PDB; 1I9I; 25-DEC-02.
DR PDB; 1KCU; 11-MAY-02.
DR MGD; MGI:96446; Igh-4.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Igv; 3.
DR SMART; SM00406; Igv; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
DR NON_TER 1
FT NON TER 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7BB3BE7D697C CRC64;

Query Match 24.5%; Score 862; DB 11; Length 437;
Best Local Similarity 32.3%; Pred. No. 3.3e-46;
Matches 215; Conservative 66; Mismatches 130; Indels 254; Gaps 15;

QY 2 VQLQSGGDLVKPGASVKISCKASGYFTGYVMHWKSPGKGLWIGRINPNNGVTLYN 61
DB 1 VQLQSGGGGLVPGGSLKLSCAASGFTFSYAMSVWRQTPEKLEWVASFS-SGGIIYTT 59

QY 62 QKFKDKATLTVDKSSITAYMELRSLTSEDSAVYYCARSTMTINYYMDYWGQGTSTVTS 121
DB 60 DSVKGRFTIYKDKRNILSLQMSLSRSEDTAMYYCARGDYS-----YMGPGTLTVSAA 114

QY 122 KITPPSVYPLAPGSAQAQNTSMVTLGCLVKGYTPEPVTYTNWNSGSLSSGVHTPAPVLS 181
DB 115 KITPPSVYPLAPGSAQAQNTSMVTLGCLVKGYTPEPVTYTNWNSGSLSSGVHTPAPVLS 174

QY 182 YTLSSSVTPSPSTWPTSETVTCNVAHPASSTKYDKKIVPRDGGPSEKSEINEKOLRK 241
DB 175 YTLSSSVTPSPSTWPTSETVTCNVAHPASSTKYDKKIVPRDCG-----C 217

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QY 242 ELOGTALGNLKIYVNSKAITSEKSDAQFLNTLLFKGFFTGHPWYNDLLVDLGSTAA 301
Db 218 KPCICTVPEVSSVFIRPK-----PKDVLITL----- 245
QY 302 TSEYEGSSVDLYGAYGYQCAGTGNKACMGVTLHNNRLTEKKVPINLWIDGKQT 361
Db 246 -----TP-KVTCVVVDIS-----KDDPEVQFQSFVD----- 270
QY 362 TVPIDKVKTSKKEV-----TVQELDLQARHLYHGK-FGL-YNSDSFGKQVQGLIVFH 412
Db 271 DVEVHTAQTPREQFNFSRSEIPIHQDLWLNKEFKCRVNSAAFAPAEK----- 324
QY 413 SSEGSTVSYDLFDAQGYPTLLRIYRDNTTISSTLSLSLYLTTISVMTQPTPTSLVS 472
Db 325 -----TISKT----- 329
QY 473 AGDRVITCKASQSVNDVAVYQKQKPGQPKLLISYTSRYAGVPRFSGSGYGTDFLT 532
Db 330 ----- 329
QY 533 ISSVQAEDAAVYFCQDYNSPPTFGGKTKLEIKRADAAPTISFPPSSQLTSGGASVVC 592
Db 330 -----KGRPKAPQVVTIPPPKEQMAKDKVSLTC 357
QY 593 FLNNFYPKQINVKWKIDGSRQNGVNSWTDQSDKSTYSMSSTLTTLTKDEYERHNSYTC 652
Db 358 MITDFFPFDITVEWQNGQPAEN-YKNTQFIMDT-DGSYFVYSKLVNQSNNWEAGNTPTC 415
QY 653 EATHK 657
Db 416 SVLHE 420

RESULT 25
Q8VCP0 PRELIMINARY; PRT; 234 AA.
AC Q8VCP0;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC019474; AAH19474.1; -.
DR PIR; B47329; B47329.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG_2.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ
SEQUENCE 234 AA; 25702 MW; 102551C58AC2FA9F CRC64;
Query Match 24.1%; Score 850; DB 11; Length 234;
Best Local Similarity 76.9%; Pred. No. 7.9e-46;
Matches 163; Conservative 17; Mismatches 32; Indels 0; Gaps 0;

QY 460 IVNTQPTSLVAGDRVITCKASQSVNDVAVYQKQKPGQPKLLISYTSRYAGVPR 519
Db 22 IQLTQSPASLSASVGETVTITCRASENIYSLAWYQKQKPGQPKLLVYNAKTLADGVSR 81
QY 520 FSGSGYGTDFLTISVQAEDAAVYFCQDYNSPPTFGGKTKLEIKRADAAPTISFPPSS 579
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Db 82 FSGSRSGTQFSLKINSLOPEDFGSYCQHHSGIPTFGSGTKLEIKRADAAPTISFPPS 141
QY 580 SEQLTSGGASVVCFLNNFYPKQINVKWKIDGSRQNGVNSWTDQSDKSTYSMSSTLT 639
Db 142 SEQLTSGGASVVCFLNNFYPKQINVKWKIDGSRQNGVNSWTDQSDKSTYSMSSTLT 201
QY 640 TKDEYERHNSYTCATHKTSTSPVKSFNRNE 671
Db 202 TKDEYERHNSYTCATHKTSTSPVKSFNRNE 233

RESULT 26
Q91Z05 PRELIMINARY; PRT; 473 AA.
AC Q91Z05;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN AU044919.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC010327; AAH10327.1; -.
DR MGD; MGI:2144967; AU044919.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000345; Cytc_heme_BS.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; IGV; 3.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 1.
KW Hypothetical protein.
SQ
SEQUENCE 473 AA; 51946 MW; CF625F008932AF12 CRC64;
Query Match 22.8%; Score 803; DB 11; Length 473;
Best Local Similarity 32.0%; Pred. No. 1.9e-42;
Matches 214; Conservative 74; Mismatches 138; Indels 242; Gaps 18;

QY 1 EVQLQQSGPDIVKPGASVKISCKASGYFTGYMHVWKQSPGKLEWIGINPNNGVTL 60
Db 20 EVQLVESGGGLVPGGSRKLSCKASGFTSDYGNHWVRQAPKGLWVAVINSGSTTIY 79
QY 61 NQKPKDKATLTVDKSTTAYMELRSLTSEDSAVVYCARSTMITNVMVDYWGQGTSTV 120
Db 80 ADTVKGRFTISRDNKNTLFLQMTSLRASEDTAMVYCARLWLR--IDYWGQGTITV 137
QY 121 AKTTPPSVYPLAPGSAQAQTNMTLGLVKGYPEPVTITWNSGSLSSGVTTPAVLQSD 180
Db 138 AKTTPPSVYPLAPGCGDITGSSVTGLGLVKGYPPESVITVWNSGSLSSSVHTFP 197
QY 181 LYTLSSSVTVPSSTWPSSTVTCNVAPASSTKVDKIVPRDSGPGSEKSEINE---- 236
Db 198 LYTMSSSVTVPSSTWPSSTVTCNVAPASSTVTDKLEP---SGP---ISTINCPCK 251
QY 237 LRK--KSELGQTALGNLKIYVNSKAITSEKSDAQFLNTLLFKGFFTGHPWYND 294
Db 252 CHKCPAPNLEG---GPSVFIFPPENIKDV-----LMI 279
QY 295 DLGSTAATSEYEGSSVDLYGAYGYQCAGTGNKACMGVTLHNNRLTEKKVPINL 354
Db 280 SL-----TP----- 283
QY 355 WIDGKQTVPIDKVKTSKKEVTVQELDLQARHLYHGKFLYNSDSFGKQVQGLIVFH 414
```

[illegible]

DB	87	QYNDLIVQDSKETVNFKGVKQVDLYGYSYGFQSGGKPKTKACMYGCVTLHNNQLYDT	146
QY	348	KQVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQRG	407
DB	147	KKIPINLWIDSRTVVPLDIVKTNKKVTIQELDLQARYYLHKQYINLNPSTFDGKIQKG	206
QY	408	LIVPHESEGSTVSYDLFDAGQGYDTLARIYRDVNTTSSLSLSLYLTTYSVMQTPT	467
DB	207	LIVFHTSKGLVSYDLFNVGIGYDPKLLIKIQDNKILIESENHDIIVLYSLVLSLPL	266
QY	468	SL	469
DB	267	VL	268

RESULT 28

Q727P5 PRELIMINARY; PRT; 469 AA.

AC Q727P5

DT 01-OCT-2003 (TEMBLrel. 25, Created)

DT 01-OCT-2003 (TEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)

DE Hypothetical protein.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_taxID=9606;

XP [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;

EX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T.J., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A., Rubin G.W., Hong L.,

RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshitoki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez A.,

RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzywinski M.I., Skalska U., Smalusz D.E., Schnerch A., Schein J.E.,

RA Jones S.J., Marra M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN [2]

RP SEQUENCE FROM N.A.

RP TISSUE=Spleen;

RA Strausberg R.;

RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC051328; AAHS1328.1; -.

KW Hypothetical protein.

SQ SEQUENCE 469 AA; 51395 MW; C8D5BE12BAAF795C CRC64;

Query Match 21.38; Score 750; DB 4; Length 469;

Best Local Similarity 30.3%; Pred.No. 4e-39;

Matches 201; Conservative 156; Mismatches 156; Indels 236; Gaps 16;

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QY 121 AKITPPSVYPLAPGSAQTNSMVTGLGVKGYPEPVVTVTNSGSLSSGVHTPEAVLQSD 180
D 140 ASIKGPSVFLAPSSKSTSGTAAAGLVYDPEPVTVSWNSGALTGVHTPEAVLQSS 199
QY 181 -LVTSSSVTPSTWPEVTVTVNVAHPASTKVDKXIVPRDGGPSEKSEINEKDLRK 239
D 200 GLYSLSVWVTPSSSLGTQYICNVNHPKNTKVDKXVPEKSC-----242
QY 240 KSELQGTALNLAQIYYVNSKALTSSEKSDAQFLTNTLLPKGFFTGHPWMDLLVDLGS 299
D 243 -----DKHTCTPCPAPELLGGPSVF--LFPKPK--KDTLM-----274
QY 300 AATSEYEGSVLDYAGYGYQCAGGTPNKTCMYGGVTLHDNNRLTEKKVPIINLWDGK 359
D 275 -----ISRTPEVT-CVVWDVS-----HEDPEVKFNWVDG- 303
QY 360 QTTVPIDKVKTSKEVTVQELDLQARHLHGKGLVNSDSFGKVGQGLIVHSSSEGSTV 419
D 304 ---VEVNAKTPREBQ-----YNSTY---RVVSVLTVLHQDWLNGK 339
QY 420 SYDLFDAQGGQYPTLLRIYRDNTTISSTLSISLVLYTTSIVMTQPTSLLSVAGDRVTI 479
D 340 EY-----341
QY 480 TKASQSVNDVAWYQKPGQSKLLISYTSRYAGVDPDRFGSGYGTFTLTISVQAE 539
D 342 KCKVS-----NKALPAP---IEKTIKAKGQP-----365
QY 540 DAAVYFCQDYNSPPTFGGQTKLEIKRAADAPTISFPSPSEOLTSGGASVVCFLNNFYP 599
D 366 -----REPQVYLPFSRDLTKQVSLTCLVKGFGYP 396
QY 600 KDINVKWKIDGSRQ-----GVLSNWTQDQSKDSTYSMSSTLTLPKDEYERHNSYTCBA 654
D 397 SDIAVEWESGQPNKYKTPPVLDS-----DGSFFLYSKLTVDKSRWQCGNVFSCSV 449
QY 655 THK 657
D 450 MHE 452

RESULT 29
Q72473
ID Q72473 PRELIMINARY; PRT; 234 AA.
AC Q72473
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences",
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
```

```
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences",
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RA Strausberg R.;
RA Submitted (AUG-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC056256; AAH56256.1; -.
KW Hypothetical protein.
SQ SEQUENCE 234 AA; 25674 MW; 1A2C259BAB51BC0F CRC64;

Query Match 19.6%; Score 691; DB 4; Length 234;
Best Local Similarity 61.5%; Pred. No. 7.9e-36;
Matches 131; Conservative 32; Mismatches 50; Indels 0; Gaps 0;

QY 459 SIWMTQTPTSLLSVAGDRVTITCKASQSVNDVAWYQKPGQSKLLISYTSRYAGVDP 518
D 21 AIRMTQSPSPFSASTGDRVTITCRASQISGSLAWYQKPGKAPQLLIYAASTLQSGVPS 80
QY 519 RFGSGYGTDTLTLTISVQAEADAAYVFCQDYNSPPTFGGQTKLEIKRAADAPTISVIPP 578
D 81 RFGSASGTDFTLTSLISCLQSEDFATYTCQYTYTPTFGQGTKEIKRTVAAPSVFIFPP 140
QY 579 SSEQLTSGASVVCFLNNFYPKIDINVKWKIDGSRQGVLSNWTQDQSKDSTYSMSSTLT 638
D 141 SDEQLKSGTASVVCLLNNFYPKAVQKVDNALQSGNSQESVTEQDSKSTYSLSLTLT 200
QY 639 LTKDEYERHNSYTCBAHTKSTSPIVKSFNRNE 671
D 201 LSKADYEKHKYACEVTHQGLSSPVTKSFNRGE 233

RESULT 30
Q723Y4
ID Q723Y4 PRELIMINARY; PRT; 236 AA.
AC Q723Y4
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Touchman J.W., Green E.D., Dickinson M.C.,
RA Blakesley R.W., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences",
RL proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
```


Db 82 GVPDRFSGSGGDTFTLKISKVBAEDVIGIYCMQGLQTPQTGGQKVKIKRTVAAPSVF 141
QY 575 IFPPSSSEQLTSGGASVVCFLNFPKIDINVKKIDGSEBQNGVLSNWTDDQSKDSTYSMS 634
Db 142 IFPPSEQLKSGTASVCLLNFPKIDINVKKIDGSEBQNGVLSNWTDDQSKDSTYSMS 201
QY 635 STLTGKDYERHNSVTCATHKTSTSPIVKGFNRNE 671
Db 202 STLTGKADYERHNSVTCATHKTSTSPIVKGFNRNE 671
RESULT 33
Q725W1 PRELIMINARY; PRT; 470 AA.
AC Q725W1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh P.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udwin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC053984; AAH53984.1; -.
KW Hypothetical protein.
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;
Query Match 18.9%; Score 666.5; DB 4; Length 470;
Best Local Similarity 28.6%; Pred. No. 7.2e-34;
Matches 190; Conservative 66; Mismatches 170; Indels 239; Gaps 18;
QY 1 EVOLQSGDPLVKPGASVKISKASGYSTGYMHVWQSPQKGLWIGRINPNNGVTLY 60
Db 20 EVQLVESGGGLVQPGGSLRLSASGFTLNNDYHWRQGIKGLWVSKIG-TAGDRY 78
QY 61 NQKFKDKATLTVDKSTTAYMELRSITSDSAVYVCARST--MITYVMDYWGQGTSTVTV 118
Db 79 AGSVKGRFTISRNKADSLYLQWNSLRVGDAAVYICARGAGWAPLGAFLDINGQGTMTV 138
QY 119 SSAKTPPPSVYPLAPGSAQAQTMVTLGCLVKGYPFPPVTVTWNSGSLSSGVHTPPAVLQ 178
Db 139 SSASTKGPSPVFPAPLSPKSTSGTALGCLVKDYFPPVTVSWNSGALTSGVHTFPAVLQ 198
QY 179 SD-LYTLSSVTVPSSTWPSSEVTCNVAHPASSTKVDKIVPRDSGGPSEKSEINEKDL 237

Db 199 SSGLYSLSSVTVFSSSLGTQTYICNVNHNKESNTKVDKVEPKSC----- 243
QY 238 RKSELOQTALCNLKOIYYNSKAITSEKSAOFLNTLLPKGFFTCGHPWYNDLLVDLG 297
Db 244 -----DKTHTCPPCFAPPELLGGPSVF--LPPPKP--KDTLM-- 275
QY 298 STAATSEYEGSSVDLYGAYGYQCAGGTPNKACMGVGTLDHNNRLTEKKVPINLWID 357
Db 276 -----ISRTPEVT-CVVVDVS-----HEDEPEVKNFYVD 303
QY 358 GKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKGQVORGLIVFHSSEGS 417
Db 304 G-----VEVHNAKTPREEQ-----YNSTY-----RVVSVLTVLHQDWLN 338
QY 418 TVSYDLFDAGQYPTDTLRIYRDNTTISSTLSLSLYTTSIVMTQTPTSLLVSAGDRV 477
Db 339 GKEY----- 342
QY 478 TITCKASQSVSNDAVYQOKPGQSPKLLISYTSRYAGVPDRFSGSGYGTDFTLTISVQ 537
Db 343 --KCKVS-----NKALPAP--IEKTISKAKGQP----- 366
QY 538 AEDAAVFCQDYNSPPTFGGTTKLEIKRADAAPTVSIFFPSSEQLTSGGASVVCFLNPF 597
Db 367 -----RPFQVYTLPPSRDELTKNQVSLTCLVKGF 395
QY 598 YPKDINVKKIDGSEBQNGVLSNWTDDQSKDSTYSMSLTTLTKDEYERHNSYTC 652
Db 396 YPSDIAVEMESGQNGPENNYKTTPVLDL-----DGSFLYSLKLTVDKSRWQGNVFS 448
QY 653 EATHK 657
Db 449 SVMHE 453
RESULT 34
Q8TC63 PRELIMINARY; PRT; 473 AA.
ID Q8TC63
AC Q8TC63;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL, BC025985; AAH25985.1; -.
DR GO; GO:0005507; F:copper ion binding; IEA.
DR GO; GO:0005489; F:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000923; BlueCu_1.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 4.
DR SMART; SMC0406; Ig; 1.
DR PROSITE; PS00196; COPPER_BLUE; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 473 AA; 51986 MW; E29920B09BA369F5 CRC64;
Query Match 18.8%; Score 662.5; DB 4; Length 473;
Best Local Similarity 26.8%; Pred. No. 1.3e-33;
Matches 183; Conservative 78; Mismatches 141; Indels 281; Gaps 19;

Query Match		18.4%; Score 648; DB 11; Length 614;
Best Local Similarity		28.9%; Pred. No. 1.5e-32;
Matches 202; Conservative 91; Mismatches 205; Indels 200; Gaps 28;		
QY	1	EVQLQSGDPLVKGASVKISKASGYSTGYVMHWKQSPKGLGWIRPNNGVTLY 60
DB	20	QVQLQSGDPLVKGASVKISKASGYSTGYVMHWKQSPKGLGWIRPNNGVTLY 79
QY	61	NQKFKDKATLTVDKSTTAYMELRLSTSEDSAVYICARSTMITNYVMDYWGQTSVTSS 120
DB	80	NGKFKDKATLTADKSSSTAYMQLSLTSEDSAVYFCARD-YGSSYFAFWGQTLVTVA 138
QY	121	AKTTPSVPLAP-GSAAQTNMVTLGCLVKGFFPEPVTVW---NSGSLSGVHTFPVAV 176
DB	139	ESQSFNVPFVSCSEPLSKDLVAMGCLARDPLSTISFTWYQNAEVIQIIRTFPTL 198
QY	177	LQSDLYTLSSVTV-PSS-TWPEVTVTCNVAH-----PA---SSTKVDKVI 219
DB	199	RTGKYLATSOVLLSPKSLLEGSEVILVKIHYGKKNKDLHVPPIPAEMNPNVFP 258
QY	220	RDS-GGPFSEKSEINEKDKRKSELOGTALGNLKQIYYNSKAITSEKSAQDLTNTLL 278
DB	259	RDGFGPAP-----RKSKL-----ICEATNTPKPIVTS----- 287
QY	279	FKGFFTGHPYND-LLVDLGSTA--ATSEYEGSSVDLYGAYGYQCAGTGNKTCMYGG 335
DB	288	-----WLKDKLVESGFTDPVTIENKSGTPQTY----- 316
QY	336	VTLHNNRLTEERKVPINLWIDGQTTVPIDVKYKSKVETVQELDLQARHYLHGKFLGY 395
DB	317	-----KVIST---LTISEID----- 330
QY	396	NSDSFGKQVORGLVPHSSEGSTVSDVLDFAQOQYPTLLRIYRDNNTTISLSISLYL 455
DB	331	NLNVYTCRVDRHGLTKLVNSTCA-----ASPTDI----- 362
QY	456	YTTSIWMTQTPTSLLSAGDRVTITCKASQVSND---VAVYQKPGQSPKLLISVTSR 512
DB	363	-----LFTTTPSPADIFLSKANLTCVSNLATYETLNISWASQS-GEPLETKIMESH 417
QY	513	YAGVDRPFGSGVGTDTFTTISGVQAE---AAVYFC---QDYNAPPTFGGTTKLEIKR 566
DB	418	PNGT---PSAKG-----VASVCVEDMNRKEFVCTVTHRDLPSP-----QKFKISK 460
QY	567	ADAA-----TVSIFPPSPSSQLT-SGASVVCFLNFPKDIWVKWKIDGS---ERQNGVLN 619
DB	461	PNEVHXHPFAVILLPPARQLNLRRESATVTCVKGFSPADISVQWLQRLPQEKYVTS 520
QY	620	SWTDQSKDSTYSMSSTLTITKDEYERHNSYTCETHK 657
DB	521	APMPERGAQGFYFTHSILVTEENWSGFTYTCVWSHE 558
RESULT 37		
Q8N4Y9		PRELIMINARY; PRT; 521 AA.
ID	Q8N4Y9	AC Q8N4Y9;
DT	01-OCT-2002	(TREMBlrel. 22, Created)
DT	01-OCT-2002	(TREMBlrel. 22, Last sequence update)
DT	01-OCT-2003	(TREMBlrel. 25, Last annotation update)
DE	Hypothetical protein.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]_TaxID=9606;	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=Primary B-Cells;	
RA	Straussberg R.;	
RL	Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.	
DR	EMBL; BC033178; AAH33178.1; -	
DR	PIR; A60764; A60764.	
DR	InterPro; IPR007110; Ig-like.	

DR	InterPro; IPR003597; IG_c1.	
DR	InterPro; IPR003006; IG_MHC.	
DR	InterPro; IPR003596; IG_V.	
DR	Pfam; PF00047; ig, 4.	
DR	SMART; SM00407; IGC1; 3.	
DR	SMART; SM00406; IGV; 1.	
DR	PROSITE; PS0835; IG LIKE; 4.	
DR	PROSITE; PS00290; IG_MHC; 2.	
KW	Hypothetical protein.	
SQ	SEQUENCE 521 AA; 57156 MW; 2AC7D22E72D6CAA2 CRC64;	
Query Match		18.2%; Score 641; DB 4; Length 521;
Best Local Similarity		27.3%; Pred. No. 3.3e-32;
Matches 181; Conservative 83; Mismatches 215; Indels 184; Gaps 14;		
QY	1	EVQLQSGDPLVKGASVKISKASGYSTGYVMHWKQSPKGLGWIG--RINPNNGVT 58
DB	20	EVQLVDSGGGLVPGGSLRLSCAASGFIVSDHYVWVRQAPGKGPWVGVGCFRKAHKT 79
QY	59	LYNOKFKKATLTVDKSTTAYMELRLSTSEDSAVYICARSTMIT---NYVMDYWGQTS 115
DB	80	EYAAASVYGRFTILRDDSKNSVHLQMNLSLKTDDTAVYICVRDLEGAGKYDWFIDWGRIL 139
QY	116	VTVSSAKTTPPSVYPLAPGSAQTNSMVTGLVKGYPPEPVTVWNSGSLSSGVHTFPA 175
DB	140	VTVSSATKGPSVPLAPCSRSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPA 199
QY	176	VLOSD-LYTLSSVTVPSSTWPEVTVTCNVAPASSTKVDKVIIPRDSGGPSEKSEINE 234
DB	200	VLOSGSLYLSVWTVPPSSSLGTQTYTCNVNHRKSNTRKVDKRV----- 242
QY	235	KDLRKKSLEQGFALGNLQIYYNSKAITSEKSAQDLTNTLLFKGFTGHPWYNDLLV 294
DB	243	-----ELKT 246
QY	295	DLGTAATSEYEGSSVDLYGAYGYQCAGGTGNKTCMYGGVTLHNNRLTEERKVPINL 354
DB	247	PLGDTHTCP-----RC-----PEPKSC---DTPPPCPCEPKSC--- 279
QY	355	WIDGQTTVPIDVKYTSKEVTQELDLQARHYLHGKFLGYNSDSFGKQVORGLVPHSS 414
DB	280	-----DTPPPCPCEPKSCDTPPPCPCAPPELLGGPSVF---LFPKPKDTLMISRT 331
QY	415	EGSTVSYDLFDAQQYPTLLRIYRDNNTTISSTLSISLYLTYSIVMTQTPSLISVAG 474
DB	332	EVTCTV---VVDVSHEDPEVQFKVYDGVVEHNA----- 361
QY	475	DRVTITCKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDPDRPSGSGVGTDTLTIS 534
DB	362	-----KTKPRE-----EQFN-STFRVSVLTVL 383
QY	535	SVQAEAAVFCQDYNAPPTFGGTTKLEIKRADAAPTVIFPPSSQLTSGGASVVCFL 594
DB	384	HQDWLNGKEYKCKVSNKALPAPIEKTISKTKGQPREPQVYTLPSRREMTKNQVSLTCLV 443
QY	595	NNYFVKDINVKWKIDGSRQRNGVLSNWTDDQSKSTYSMSLTITLKDEYERHNSYTC 654
DB	444	KGFYPSDIAVENSSGQPENN--YNTTTPMLDSDGSFFLYSKLTVDKSRWQGGNIFCSV 501
QY	655	THK 657
DB	502	MHE 504
RESULT 38		
Q8K0F2		
ID	Q8K0F2	PRELIMINARY; PRT; 488 AA.
AC	Q8K0F2	
DT	01-OCT-2002	(TREMBlrel. 22, Created)
DT	01-OCT-2002	(TREMBlrel. 22, Last sequence update)
DT	01-OCT-2003	(TREMBlrel. 25, Last annotation update)
DE	Similar to expressed sequence A1893585.	
OS	Mus musculus (Mouse).	

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;

RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC031703; AAH31703.1; -

DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.
DR InterPro; IPR003006; Ig_MHC.

DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00407; IgC1; 3.

DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.

SQ SEQUENCE 488 AA; 53127 MW; 0E3B156E155733F0 CRC64;
Query Match 17.6%; Score 619.5; DB 11; Length 488;
Best Local Similarity 27.9%; Pred. No. 6.8e-31;
Matches 184; Conservative 75; Mismatches 163; Indels 247; Gaps 21;

QY 1 EVQLQSGDPLVKGASVKISKASGYSTGYTHWVKQSPGKLEWIGRINPNNGVTLY 60
DB 20 QVQLQPGDELVKPGASVKLSCKASGYTFTSYWMEHWKQSPGKLEWIGRIDPNSGGTKY 79
QY 61 NOKFKDKATLVVDKSTTAYMELRLSLSSEDSAVYICARSTMTNY-VMDYKQGTSTVTS 116
DB 80 NEKFKSKATLVVDKPSSTAYMQLSLSSEDSAVYICARSTMTNY-VMDYKQGTSTVTS 139
QY 117 TVSSAKTTPPSVYPLAPGSAQTNSMTLGLCLVKGYPPE-PVTVTW-NSGSLSSGVHTFP 174
DB 140 TVSEAPAREPTIPLTFQALSSDPVI-IGCLIHDFPSGTMNTWGSKGDITVNFPP 198
QY 175 AVLQSDLTLLSSVTPSSTWP-SETVTCNVAHPASSTKDKKIVPRDGGPSEKSEIN 233
DB 199 ALASGRYTMSSQLTPAVECEGESVKCSQVH- 240
QY 234 EKDRLKSELOGTALGNLQIYYNSKAITSEKSAQDFLNTLLPKGFTGHPWYNDLL 293
DB 241 V- 273
QY 294 VDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPIN 353
DB 274 --LGSDASIT- 286
QY 354 LWIDGKQTTPIDKVKTSKEVTQELDLQARHYLHGKFLGYNLSDSPFGKVQRLIVFHS 413
DB 287 - 286
QY 414 SEGSTVSVDLEDAQCYQPDTLRIYRDNWTTISLSISLYLTTSTVMTQTPSLVLSVA 473
DB 287 - 302
QY 474 GDRVTITCKASQSVNSDVANVQKPGQSPKLLISVTSRYAGVPDRFSGSGYGTDFTLTI 533
DB 303 KDVA- 341
QY 534 SSVQAEAAVFCQDYNPSPTFGGKTKLEIKRAADAAPTYSIFPPSSEQLTSGG-ASVVC 592
DB 342 THPESDITLGTITAKVTNTFP- 385
QY 593 FLNNFYPKDINVKWKIDSEKQNG- 648
DB 386 LVRAFNPKVELVIRW-LRGNELSPESYLVPFLPEKPEGBGATTVLTVSLVRSABEIKWQGD 444
QY 649 SYTCEATHK 657
DB 445 QYSCMVGHE 453

RESULT 39
Q8K172

ID Q8K172 PRELIMINARY; PRT; 482 AA.

AC Q8K172;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)

DE Similar to expressed sequence A1893585.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RA Strausberg R.;

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC028249; AAH28249.1; -

DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.

DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.

DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003597; Ig_c1.

DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_v.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00407; IgC1; 3.

DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
SQ SEQUENCE 482 AA; 52121 MW; A06FF083E771D084 CRC64;

Query Match 17.6%; Score 618.5; DB 11; Length 482;
Best Local Similarity 27.9%; Pred. No. 7.8e-31;
Matches 186; Conservative 73; Mismatches 160; Indels 247; Gaps 22;

QY 1 EVQLQSGDPLVKGASVKISKASGYSTGYTHWVKQSPGKLEWIGRINPNNGVTLY 60
DB 20 QVQLQPGDELVKPGASVKLSCKASGYTFTSYWMEHWKQSPGKLEWIGRIDPNSGGTKY 79

QY 61 NOKFKDKATLVVDKSTTAYMELRLSLSSEDSAVYICARSTMTNY-VMDYKQGTSTVTS 119
DB 80 NEKFKSKATLVVDKPSSTAYMQLSLSSEDSAVYICARSTMTNY-VMDYKQGTSTVTS 136

QY 120 SAKTTPPSVYPLAPGSAQTNSMTLGLCLVKGYPPE-PVTVTW-NSGSLSSGVHTFP 177
DB 137 SEAPAREPTIPLTFQALSSDPVI-IGCLIHDFPSGTMNTWGSKGDITVNFPPALA 195

QY 178 QSDLYTLSSSVTPSSTWP-SETVTCNVAHPASSTKDKKIVPRDGGPSEKSEIN 236
DB 196 SGGRYTMSSQLTPAVECEGESVKCSQVH- 235

QY 237 LRKSELOGTALGNLQIYYNSKAITSEKSAQDFLNTLLPKGFTGHPWYNDLL 296
DB 236 - 268

QY 297 GSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPIN 356
DB -


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Db 269 GSDASIT-----CTING-----280
QY 357 DGKQTTVPIDKVKTSKEVTQVQELDLQARHYLHGKFGLYNSDSFGKVGQGLIVFHSBEG 416
Db 281 -----280
QY 417 STVSYDLFDAQOYPTLLRIYRDNTTISLSISLYLTTYSIVMTQPTSLLYSAGDR 476
Db 281 -----LRPEG-----AVFTWEP-----TGKDA 299
QY 477 VTTIKASOSVNDVAVYQKQPGSKLLISYTSRYAGVPRFSGSGYGTDTLTISV 536
Db 300 V-----QKAVQNSCCYCS-----VSSVLPGCABRWNS---GASFCKTCTVHP 338
QY 537 QASDAVAVFCQDYNPPTFGGKTKLEIKRADAAPTYSIFPPSSEQLTSGG-ASVVCFLN 595
Db 339 ESTLTGTTAKVTNTP-----PQVHLPPSEELALNELVSLTCLVR 382
QY 596 NFYPKDKINVKWIDGSRQNG-----VLSNWTQDSDSTYSMSSTLTLTCKDYERHNSYT 651
Db 383 AFWPKVLRW-LHGNEELSPESYLVFELPKPEGATTVLTVSLRVSAEIKWQDDQYS 441
QY 652 CEATHK 657
Db 442 CMVGHE 447

RESULT 40
Q8VCX7 PRELIMINARY; PRT; 613 AA.
ID Q8VCX7 AC Q7TCM2 PRELIMINARY; PRT; 243 AA.
AC Q7TCM2; AC Q7TCM2;
DT 01-OCT-2003 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN IGH-6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Salivary Gland;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018315; AAR18315.1; -.
DR MGD; MGI:96448; IGH-6.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MEC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 613 AA; 67855 MW; 41A9384DD4C22862 CRC64;

Query Match 17.6%; Score 618.5; DB 11; Length 613;
Best Local Similarity 28.1%; Pred. No. 1.1e-30;
Matches 196; Conservative 90; Mismatches 211; Indels 201; Gaps 28;

QY 1 EVOLQSGPDLVKPGASVKISCKASYFTGYVMHWKSPGKLEWIGRINPNNGVTLY 60
Db 20 QVQLQSGELMPEPGASVKISCKATGTFSSYIEWKORPGHLEWIGELIIPGSGSTNY 79
QY 61 NQKFKDKATLVDRKSTTAYMELRSLTSDSAVYCARSTMTNYMDYWGQGSTVTVSS 120
Db 80 NEKFCKATFTADTSNTAYMQLSSLTSDSAVYCAR--RLGRWYFDVWGAGTIVTVSS 137
QY 121 AKTTPSVVPLAP-GSAAQTNSMTLGLVKGYFPEPVTVW---NSGSLSGVITFPFAV 176
Db 138 ESQSFFNPVPLVSCSEPLSKDLVANGCLARDFLPSTISFTWYQNTEVIQGIPTPL 197
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QY 177 LQSDLYTLSSSVTV-PSS--TWPSETVTCNVAH-----PA--SSTKVKKIYP 219
Db 198 RTGKYLATQSVLLSPKSIILEGSDEYLVCKIHYGGKRDHLVPIPAVAEMPNVNVFVPP 257
QY 220 RDS--GGPSEKSEEBINEKDLRKSELOQTALGNLQIYYIYNSKAITSEKSAQDLTTL 278
Db 258 RDGFGSGAP-----RKSXL-----ICEATNFTPKPITVS-----286
QY 279 PKGFTGHPWYND-LLVDLGSTA--ATSEYEGSSVDLYGAYYQCAGGTENKTACMYGG 335
Db 287 -----WLDGKLVESGFTDPVTIENKSGSPQFY-----315
QY 336 VTLHNNRLTBEKKVPINLWDGKQTTVPIDKVKTSKEVTQVQELDLQARHYLHGKFGLY 395
Db 316 -----KVIST--LTISEID-----WL 329
QY 396 NSDSFGKVGQGLIVFHSBEGSTVSYDLFDAQOYPTLLRIYRDNTTISLSISLYL 455
Db 330 NLNVTYTCRVDHRLTFLKNVSSSTCA-----ASPSTDI-----361
QY 456 YTTISVMTQPTSLVLSAGDRVTITCKASQSVND--VAWYQKQPGSKPKLLISYTSR 512
Db 362 ----LTFTIPESFADIPLSKANLTLCLVSNLATYETLINISWASQ--GEPLTKIKINESH 416
QY 513 YAGVPDRFSGSGYGTDTLTISVQAE-----AAVYFC---QQDYNPPTFGGKTKLEIKR 566
Db 417 PNGT----PSAKG-----VASVCVEDMNNRKEFVCTVTHRDLPSP-----QKKTISK 459
QY 567 ADAA-----PTVSIFFPPSSEQLT-SGGASVVCFLNFPKDKINVKWIDGS--ERQNGVLN 619
Db 460 PNEVHKHPPAVYLLPPAREQNLRESATVCLVKGFSPADISVQVWLQRLPQKLVTS 519
QY 620 SWTQDQSDSTYSMSSTLTLTCKDYERHNSYTCEATHK 657
Db 520 APMEPGAPGYFTHSILTVEEWNSEGYTCVVGHE 557

RESULT 41
Q7TCM2 PRELIMINARY; PRT; 243 AA.
ID Q7TCM2 AC Q7TCM2;
AC Q7TCM2; AC Q7TCM2;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE SCFV 6H8 protein (Fragment).
GN SCFV 6H8.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Balb/C;
RA Peter J.C., Eftekhari P., Billiald P., Wallukat G.;
RT "scfv single chain antibody variable fragment as inverse agonist for
RT the beta-2 adrenergic receptor."
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ574851; CAE00495.1; -.
FT NON TER 1
SQ SEQUENCE 243 AA; 25976 MW; BEFF64D2DC4F76 CRC64;

Query Match 17.2%; Score 606; DB 11; Length 243;
Best Local Similarity 28.0%; Pred. No. 1.9e-30;
Matches 158; Conservative 31; Mismatches 48; Indels 328; Gaps 7;

QY 1 EVOLQSGPDLVKPGASVKISCKASYFTGYVMHWKSPGKLEWIGRINPNNGVTLY 60
Db 1 QVQLQSGSELVPGASVKLSCKASGYTFTYVMHWKQKHGQGLEWIGNIGYIPSGITNY 60
QY 61 NQKFKDKATLVDRKSTTAYMELRSLTSDSAVYCARSTMTNYMDYWGQGSTVTVSS 120
Db 61 DEKFNKIGILTVDTSSTAYMHLSLASEDSAVYICARG----GRGLDVMWAGTTLTVSS 116
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DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein_481AA; 52964 MW; FL2068460B400B9D CRC64;
SQ SEQUENCE 488 AA; 52964 MW; 17.1%; Score 602.5; DB 11; Length 488;
Matches 184; Conservative 73; Mismatches 165; Indels 247; Gaps 21;
Query Match
Best Local Similarity 27.5%; Pred. No. 8e-30;
Matches 179; Conservative 73; Mismatches 167; Indels 246; Gaps 21;
QY 1 EVOLQSGPDLVKPGASVKISKASGYSTGYVMHWKQSPGKLEWIGRINPNNGVTLY 60
Db EVOLQSGPDLVKPGASVKISKASGYSTGYVMHWKQSPGKLEWIGRINPNNGVTLY 60
QY 61 NQKFKDKATLVDSSTTAYMELRSITSEDSAVYYCARSTMTINYYM----DYWGQGTSLV 116
Db NQKFKDKATLVDSSTTAYMELRSITSEDSAVYYCARSTMTINYYM----DYWGQGTSLV 116
QY 117 TVSSAKTTPSVVPLAPGSAQTNSMTLGLVKGYPE-PVTVTW-NSGSLSSGVHTPL 174
Db TVSSAKTTPSVVPLAPGSAQTNSMTLGLVKGYPE-PVTVTW-NSGSLSSGVHTPL 174
QY 140 TVSAEPAREPTIYPLTFPQALSSDPVI-IGCLIHDFPFGTMVTKGSKGDIITVNPFP 198
Db TVSAEPAREPTIYPLTFPQALSSDPVI-IGCLIHDFPFGTMVTKGSKGDIITVNPFP 198
QY 175 AVLQSDLYTLSSSVTPSPSTWP-SETVTCNVAHPASSTKVDKIVPRDGGPSEKSEIN 233
Db AVLQSDLYTLSSSVTPSPSTWP-SETVTCNVAHPASSTKVDKIVPRDGGPSEKSEIN 233
QY 234 EKDLRKSELOQTALGNLKOIYYNKAITSSEKSAQDLNTLLFKGFTGHPWVNDLL 293
Db EKDLRKSELOQTALGNLKOIYYNKAITSSEKSAQDLNTLLFKGFTGHPWVNDLL 293
QY 241 V-----NCPGIC---SPPTTPPPSCQPSLS-----LQRPALDILL 273
Db V-----NCPGIC---SPPTTPPPSCQPSLS-----LQRPALDILL 273
QY 294 VDLGTAATSEYEGSSVDLYGAYGYQCAGGTENKTAACMGVGTLDHNNRLTEKKVPIN 353
Db VDLGTAATSEYEGSSVDLYGAYGYQCAGGTENKTAACMGVGTLDHNNRLTEKKVPIN 353
QY 274 --LGSASIT-----CTLNG-----DSNPVQELN 286
Db --LGSASIT-----CTLNG-----DSNPVQELN 286
QY 354 LWDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKVQGLIVFHS 413
Db LWDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKVQGLIVFHS 413
QY 287 -----LRDPEG-----AVFTWEPS-----TG 302
Db -----LRDPEG-----AVFTWEPS-----TG 302
QY 474 GDRVTITCKASQSVNDVAWYQKPGQPKLLISYTSRYAGVPDRFSGSGYGTDTFTLI 533
Db GDRVTITCKASQSVNDVAWYQKPGQPKLLISYTSRYAGVPDRFSGSGYGTDTFTLI 533
QY 303 KDAV-----QKAVQNSCGCY-----VSSVLPGCAERWNS---GASFKCTV 341
Db KDAV-----QKAVQNSCGCY-----VSSVLPGCAERWNS---GASFKCTV 341
QY 534 SSVQAEAAVYFCQDYNSPPTFGGKLEIKRADAAPTIVSIFPPSSQOLTSGG-ASVVC 592
Db SSVQAEAAVYFCQDYNSPPTFGGKLEIKRADAAPTIVSIFPPSSQOLTSGG-ASVVC 592
QY 342 TPESDTLTGTIAKVTNTFP-----PQVHLLPPPSSEALNELVSLTC 385
Db TPESDTLTGTIAKVTNTFP-----PQVHLLPPPSSEALNELVSLTC 385
QY 593 FLNNFYPKDNVKKIDGSRONG-----VLNSWTQDSDKSTYSMSSTLTLTKDEYERN 648
Db FLNNFYPKDNVKKIDGSRONG-----VLNSWTQDSDKSTYSMSSTLTLTKDEYERN 648
QY 386 LVZAFPKKEVLVW-LHGNEELSPESYLVEPLKEPGEGATTIYLVTSVLRVSAEIKWQGD 444
Db LVZAFPKKEVLVW-LHGNEELSPESYLVEPLKEPGEGATTIYLVTSVLRVSAEIKWQGD 444
QY 649 SYTCEATHK 657
Db SYTCEATHK 657
QY 445 QYSCMVGHE 453
Db QYSCMVGHE 453
RESULT 44
Q91WT1 PRELIMINARY; PRT; 481 AA.
ID Q91WT1
AC Q91WT1
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;

RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013490; AAH13490.1; --
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 4.
DR PROSITE; PS00290; IG MHC; 2.
KW Hypothetical protein_481AA; 52105 MW; 97DF68DI59463F65 CRC64;
SQ SEQUENCE 481 AA; 52105 MW; 16.6%; Score 583; DB 11; Length 481;
Best Local Similarity 26.9%; Pred. No. 1.3e-28;
Matches 179; Conservative 73; Mismatches 167; Indels 246; Gaps 21;
QY 1 EVOLQSGPDLVKPGASVKISKASGYSTGYVMHWKQSPGKLEWIGRINPNNGVTLY 60
Db EVOLQSGPDLVKPGASVKISKASGYSTGYVMHWKQSPGKLEWIGRINPNNGVTLY 60
QY 61 NQKFKDKATLVDSSTTAYMELRSITSEDSAVYYCARSTMTINYYM----DYWGQGTSLV 120
Db NQKFKDKATLVDSSTTAYMELRSITSEDSAVYYCARSTMTINYYM----DYWGQGTSLV 120
QY 80 NEKFKGKTTLTADKSSSTAYMELSSLTSEDSAVYFCTRG---CGWAFDYMGGTTLTVSS 136
Db NEKFKGKTTLTADKSSSTAYMELSSLTSEDSAVYFCTRG---CGWAFDYMGGTTLTVSS 136
QY 121 AKTTPSVVPLAPGSAQTNSMTLGLVKGYPE-PVTVTW-NSGSLSSGVHTFPVLQ 178
Db AKTTPSVVPLAPGSAQTNSMTLGLVKGYPE-PVTVTW-NSGSLSSGVHTFPVLQ 178
QY 137 EPAREPTIYPLTFPQALSSDPVI-IGCLIHDFPFGTMVTKGSKGDIITVNPFPALAS 195
Db EPAREPTIYPLTFPQALSSDPVI-IGCLIHDFPFGTMVTKGSKGDIITVNPFPALAS 195
QY 179 SDLYTLSSSVTPSPSTWP-SETVTCNVAHPASSTKVDKIVPRDGGPSEKSEINEKDL 237
Db SDLYTLSSSVTPSPSTWP-SETVTCNVAHPASSTKVDKIVPRDGGPSEKSEINEKDL 237
QY 196 GGRYTMSSQLTLPAVECPGESVKCSVQH-----DSNPVQELN 234
Db GGRYTMSSQLTLPAVECPGESVKCSVQH-----DSNPVQELN 234
QY 238 RKSELOQTALGNLKOIYYNKAITSSEKSAQDLNTLLFKGFTGHPWVNDLL 297
Db RKSELOQTALGNLKOIYYNKAITSSEKSAQDLNTLLFKGFTGHPWVNDLL 297
QY 235 -----NCPGIC---SPPTTPPPSCQPSLS-----LQRPALDILL 268
Db -----NCPGIC---SPPTTPPPSCQPSLS-----LQRPALDILL 268
QY 298 STAATSEYEGSSVDLYGAYGYQCAGGTENKTAACMGVGTLDHNNRLTEKKVPINLWID 357
Db STAATSEYEGSSVDLYGAYGYQCAGGTENKTAACMGVGTLDHNNRLTEKKVPINLWID 357
QY 269 SDASIT-----CTLNG-----AVFTWEPS-----TG 279
Db SDASIT-----CTLNG-----AVFTWEPS-----TG 279
QY 358 GKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKVQGLIVFHSSEGS 417
Db GKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKVQGLIVFHSSEGS 417
QY 280 -----LRDPEG-----AVFTWEPS-----TGKDAV 299
Db -----LRDPEG-----AVFTWEPS-----TGKDAV 299
QY 478 TITCKASQSVNDVAWYQKPGQPKLLISYTSRYAGVPDRFSGSGYGTDTFTLISSVQ 537
Db TITCKASQSVNDVAWYQKPGQPKLLISYTSRYAGVPDRFSGSGYGTDTFTLISSVQ 537
QY 300 -----QKAVQNSCGCY-----VSSVLPGCAERWNS---GASFKCTVTHPE 338
Db -----QKAVQNSCGCY-----VSSVLPGCAERWNS---GASFKCTVTHPE 338
QY 538 AEDAAVYFCQDYNSPPTFGGKLEIKRADAAPTIVSIFPPSSQOLTSGG-ASVVCFLNN 596
Db AEDAAVYFCQDYNSPPTFGGKLEIKRADAAPTIVSIFPPSSQOLTSGG-ASVVCFLNN 596
QY 339 SDTLTGTTIAKVTNTFP-----PQVHLLPPPSSEALNELVSLTCLVRA 382
Db SDTLTGTTIAKVTNTFP-----PQVHLLPPPSSEALNELVSLTCLVRA 382
QY 597 FYPKDNVKKIDGSRONG-----VLNSWTQDSDKSTYSMSSTLTLTKDEYERN 652
Db FYPKDNVKKIDGSRONG-----VLNSWTQDSDKSTYSMSSTLTLTKDEYERN 652
QY 383 FNPKEVLVW-LHGNEELSPESYLVEPLKEPGEGATTIYLVTSVLRVSAEIKWQGDQYSC 441
Db FNPKEVLVW-LHGNEELSPESYLVEPLKEPGEGATTIYLVTSVLRVSAEIKWQGDQYSC 441
QY 653 EATHK 657
Db EATHK 657
QY 442 MVGHE 446
Db MVGHE 446
RESULT 45
Q8VCV5 PRELIMINARY; PRT; 481 AA.
ID Q8VCV5
AC Q8VCV5
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical protein.


```
Db 352 -----TF-----PPQHLLPPPEELALNELLSLCLVRA 381
QY 597 FYPKDNVWKIDGSRQNG---VLNSWTDQSDKSTYSMSSTLTLTCKDEYERHNSYTC 652
Db 382 FNPKEVLVRW-LHGNEELSPESYLVEPLKEPGEAGATTYLVTSVLRVSAETWKQDQISC 440
QY 653 EATHK 657
Db 441 MVGHE 445

RESULT 47
Q8VCX4 PRELIMINARY; PRT; 489 AA.
AC Q8VCX4;
DT 01-MAR-2002 (T-EMBLrel. 20, Created)
DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN IGH-VJ558 OR A1893585.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Colon;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC018322; AAI18322.1; -.
DR MGD; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00230; IG_MHC; 2.
KW Hypothetical protein.
SQ SEQUENCE 489 AA; 53208 MW; CC85B1194DAFE2C CRC64;

Query Match 16.0%; Score 565; DB 11; Length 489;
Best Local Similarity 26.3%; Pred. No. 1.8e-27;
Matches 176; Conservative 76; Mismatches 170; Indels 248; Gaps 21;

QY 1 EVQLQSGDPLVKPGASVKISCKASGYSTGYMHVWYKQSPGKLEWIGRINPNNGVTLY 60
Db 20 KVLQSGAEELVKPGASVKLSCKASGYSTFYHVIWIKQKSGGLEWIGWFGSGSIXF 79
QY 61 NQKFKDKATLTVDKSTTAYMELSLTSDSAVYVCARSTMITNY-----VMDYWGQGT 115
Db 80 NEKFKDKATLTADKSTTVYMDLSRLTSDSAVYFCARHEDRGNVDGSLAWFYWGQGT 139
QY 116 VTSSAKTTPPSVYPLAPGSAQTNSMTLGLCLVKGYPPE-PVTYTW-NSGSLSSGVHTF 173
Db 140 VTSSAPAREPTIYPLTFPQALSSDPI-IGCLIHDFPSGTMTVWGSKGDIITVNP 198
QY 174 PAVLQSDLYLTSSSVTPSSTWP-SFTVTCNVAHPASSTKVDKIVPRDSGSPSEKSEI 232
Db 199 PALASGRVTMSQLTLPAVECEGESVKSCVQH-----DSNPVQEL 240
QY 233 NEKDLKKSELOGTALGNLKQIYYNSKAITSSSEKSAQFLNTLLFKGFTTCHFWYNDL 292
Db 241 NV-----NCFGIC---SPPTTPPSCQPSLS-----LQRALEDL 273
QY 293 LVDLGSTAATSEVGSSVDLYGNAYGYQCAGGTPNKATCMYGVTLHDNNRUTEKKVPI 352
Db 274 L--LGSASAIT-----CTLNG----- 287
QY 353 NLWIDGKQTTPIDKVKTSKEVTVQELDQARHYLHGKFLGYNLSDSGFGKVQORGLIVFH 412
Db 288 ----- 287
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QY 413 SSEGSTVSYDLFDAQGOVDPDTLLRIYRDNITISLSLSISLYLYTTTIVMTQTPTSLIVS 472
Db 288 -----LRDEG-----AVTWEP-----T 302
QY 473 AGDRVTTICKASQSVNDVAVYQKQPGSPKLLISYTSRYAGVDFDRFSGSGYGTDTFLT 532
Db 303 GKDAV-----QKAVQNSCGYS-----VSSLPGCAERWS---GASFCKT 341
QY 533 ISSVQAADAAVYFCQDYNPPTFGGTGKLEIKRADAAPTIVSIPPPSEQLTSGG-ASVV 591
Db 342 VTHPESDTLTGTAIKVTNTFP-----PQVHLLPPPEELALNELSLT 385
QY 592 CFLNNFYPKDNVWKIDGSRQNG---VLNSWTDQSDKSTYSMSSTLTLTCKDEYERH 647
Db 386 CLVRAFNPKEVLVRW-LHGNEELSPESYLVEPLKEPGEAGATTYLVTSVLRVSAEIKQ 444
QY 648 NSYTCEATHK 657
Db 445 DQYSCWVGE 454

RESULT 48
Q96BB9 PRELIMINARY; PRT; 597 AA.
AC Q96BB9;
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=B-Cell;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC015760; AAI15760.1; -.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65039 MW; 4FCA3AD8ECE263D9 CRC64;

Query Match 15.9%; Score 561; DB 4; Length 597;
Best Local Similarity 26.2%; Pred. No. 4.3e-21;
Matches 183; Conservative 104; Mismatches 214; Indels 198; Gaps 28;

QY 1 EVQLQSGDPLVKPGASVKISCKASGYSTGYMHVWYKQSPGKLEWIGRINPNNGVTLY 60
Db 20 EVQLLEGGGLVQPGGSLRLSCAASGFSYFAMNVRQAPGKLEWVAISGSGSTYY 79
QY 61 NQKFKDKATLTVDKSTTAYMELSLTSDSAVYVCARS---TMITNYM-DYWGQGT 115
Db 80 ADSVKGRFTISRDNRSDTLQLQMSLRADTAVYICARDPRGYSASGNYTREDYWGQGT 139
QY 116 VTSSAKTTPPSVYPL--AFGSAATNSMTLGLCLVKGYPPEVPTVW---NSGSLSSGV 170
Db 140 VTSSGSGASAPTLFPLVSCNSPDSSTSS-VAVGCLAQDFLPDSITFSWKYKNSDISS-T 197
QY 171 HTFPAVQLSDLYLTSSSVTPVPS---TWPSETVCNVAHPASSTKVDKIVPRDSGSPSE 227
Db 198 RGFSVLRGKKYATQSVLLPFSKDWMOGTDEHVHVCKVQHP-NGNKEKNVPLPVIAPLPK 256
QY 228 KSEINEKDLKKSELOGTALGNLKQIYYNSKAITSSSEKSAQFLNTLLFKGFTTCH 287
Db 257 VSVFVPRD-----GFF-GNP 271
```

QY 288 WYNDLLVDLSTAATSEYEGSSVDLYGAYICYQACGTPNKTCACMGVGVTLHNNRLTBE 347
DB 272 RKSLIC-----QATGSP-----285
QY 348 KVPINLWIDQK--TVPIDKVTSKK-----VTQBLDQARHYLHKGFL 394
DB 286 RQIQVSLREKQGVGTTDQVQAEKESGPTTYKVTSLTKESD-----W 333
QY 395 YNSDSFGKQVGLVIFHSSGSGTVSDLPDAQQYDPTLLRIYRDNNTSSISLSISLY 454
DB 334 LSQMFCTRVDRHGLTFOQASSWCVD-----OPTAIRVF-----AIPPSASIFL- 380
QY 455 LYTSIVNTOPTSLLSAGDRVTITCKASVSNVAVYQKPGQPKLLISYTSRYA 514
DB 381 --TKSTKLTCLVTL--TTYDSVTI-----SWTRON-GEAVK--THTNISES 420
QY 515 GVPDRSGSGYGTDTLTISVQAEADAIVFCQDYNSTPTE-----GGGTKEIK 565
DB 421 HPNATFSAVG-----EASI--CEDMNSGERFTCTVTHDLPPLKQTIS 463
QY 566 RADA-----PTVSIFPSSSEQLT-SGGASVVCFLNFPKIDINVKWKIDGS--ERQNGVL 618
DB 464 RPKGVALHRPVDVLLPAREQLNRESATITCLVTGSPADVFQVMQGOPLSPKXYT 523
QY 619 NSWTDQSKDSTYSMSSTLTITKDEYERHNSYTCEATHK 657
DB 524 SAPMPEQAPGRYFAHSILTVEBWNVTGETYTCVVAHE 562

RESULT 49
Q7SZ36 PRELIMINARY; PRT; 237 AA.
AC Q7SZ36;
DT 01-OCT-2003 (TREMELrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Hypothetical protein.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22341132; PubMed=12454917;
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
RA Richardson P.;
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
RT initiative.";
RL Dev. Dyn. 225:384-391(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.N., Sodergren E.J., Lu X., Gibbs R.A.,
RA Farley J., Heltan E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnertch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Whole;
RA Klein S., Strausberg R.;
RA Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC054155; AAH54155.1; -.
KW Hypothetical protein.
SQ SEQUENCE 237 AA; 26300 MW; 47B8D0D2639CB436 CRC64;
Query Match 15.6%; Score 548; DB 13; Length 237;
Best Local Similarity 48.6%; Pred. No. 8e-27; Indels 6; Gaps 2;
Matches 105; Conservative 42; Mismatches 63;
QY 460 IVMTQPTSLLSAGDRVTITCKASQSVSN-----VAVYQKPGQPKLLISYTSRYAG 515
DB 22 IVLTQSPDYVSVPGETVTLTKASSSVAIGSTVILHWYQKSGVQPKLLIYLANRHTG 81
QY 516 VPDPSGSGYGTDTLTITSSVQAEADAIVFCQDYNSTPTEGGGTKEIKADAAPTVSI 575
DB 82 TPERISGSGSGTDTLTISRMEADAADYCCQGRSDLTFTGKTRVELKENDAKPAVFI 141
QY 576 PPSSEQLTSGGASVVCFLNFPKIDINVKWKIDGSRQNGVLSWTDQDSKSTYSMS 635
DB 142 FXPSDEQYKEGNPTAVCLINFFPREDLVTWKVDSQVSSSDVXTSDPMQESDSTYSQS 201
QY 636 TLTKDSEYERHNSYTCEATHKSTSPIVKSFNNE 671
DB 202 MLTLTKDWKADKPECLVGHK--TAQLTQSFKSQ 235

RESULT 50
Q9BQB8 PRELIMINARY; PRT; 597 AA.
AC Q9BQB8;
DT 01-JUN-2001 (TREMELrel. 17, Created)
DT 01-JUN-2001 (TREMELrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle, and Lymph;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC006180; AAH06180.1; -.
DR EMBL; BC001872; AAH01872.1; -.
DR HSSP; P01825; 7FAB.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IG; 5.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG LIKE; 5.
DR PROSITE; PS00290; IG_MHC; 3.
KW Hypothetical protein.
SQ SEQUENCE 597 AA; 65300 MW; 2DAFAD50A6375851 CRC64;
Query Match 15.5%; Score 545; DB 4; Length 597;
Best Local Similarity 25.9%; Pred. No. 4.4e-26;
Matches 182; Conservative 103; Mismatches 213; Indels 204; Gaps 29;
QY 1 EYVLOQSGPDLVPCGASVKISCKASGYSTGYVHWKQSPKGLWIGRINNGVTLY 60
DB 20 QVLOQWAGLKPSETLSLTGVTGSGFGYVSWIRQPPKGLWIGRIN-HSGIINY 78
QY 61 NOKFKDKATLTVDKSTTAYMELRLTSEDSAVVYCARSTMIT-----NYVMDYWGQ 112
DB 79 NPSLKSRTVISVDTSKQLSLKLSVNAADTAVVYCAR--VITRASPGTDGRYGDVWGQ 136

RESULT 55
092409

AC	Q924Q9;	PRELIMINARY;	PRT;	145 AA.
ID	Q924Q9			

DT	01-DEC-2001 (TREMBlrel, 19, Created)
DT	01-DEC-2001 (TREMBlrel, 19, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update
DE VHL86.2-D-J-C mu protein (Fragment)).

OS *Mus musculus* (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Mur
OX NCBI_TaxID=10090;

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97	97	97	97
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99	99	99	99
100	100	100	100

RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;

RT Affinity Maturation of B Cell Antigen Receptors

Hydroxy-3-Nitrophenyl)Acetyl (NP)";
Submitted (AUG-2001) to the EMBL/GenBank/DBJ database.

DR EMBL; AB067791; BAB63276.1; -.
DR PIR; F28833; F28833.

DR F33932; F33932.
DR PIR; PH105; PH1105.
DR PIR; PH105; PH1105.
DR PIR; PH105; PH1105.

DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.

[illegible]

DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.

DR PH129; PH129.
DR PH129; PH129.
DR PH131; PH131.
DR PH131; PH131.

DR PH1137; PH1137.
DR PH1134; PH1134.
DR PH1137; PH1137.

DR PIR; PH1139; PH1139.
DR PIR. PH1142. PH1142

DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1147; PH1147.

DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1150; PH1150.

DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.

DR PIR; PH1153; PH1153.
DR InterPro: IPR007110; Ig-like.

DR InterPro; IPR003596; IG_v.
DR Pfam; PF00047; ig: 1.

DR SMART; SM00406; IGv; 1.
DR PROSITE; PS50835; IG LIKE; 1.

FT	NON-TER	1	1
FT	NON-TER	145	145

SQ SEQUENCE 145 AA; 16001 MW; 0F409EB09FA333D2

Query Match	15.2%;	Score 535;	DB 11;
Best Local Similarity	75.6%;	Pred. No. 2.7e-26;	

Matches	99;	Conservative	15;	Mismatches	17
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Qy 1 EVQLQQSGPDLVKPGASVKISCKASGYSFTGYMHVVK

Db 1 QVQLQQPGAELVKPGASVKLSCKASGYTFTSYWMHWVK

QY 61 NQPKDKATLTVDKSSTTAYMELRSLTSEDSAVYYCAR

61 NEKFRSKATLTVDKPFSSSTAYMQLSSLTSEDSAVYYCAR

121 AKTTPPSVYPL 131 QY

DB 121 ESQSFNPVPL 131

Figure 1. The effect of the concentration of the *Agrobacterium* suspension on the transformation efficiency of *Agrobacterium* strains. The *Agrobacterium* strains were grown in YEA medium for 24 h at 28 °C. The cell concentration of the strains was adjusted to 10⁸ cells/ml. The cell suspension was then diluted to 10⁶, 10⁷, 10⁸, 10⁹, and 10¹⁰ cells/ml. The cell suspension was then inoculated into the plant tissue. The transformation efficiency was determined by the number of transformants per plant. The data were presented as the mean ± SD of three independent experiments. The asterisk (*) indicates a significant difference between the control and the treatment groups.

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RESULT 56
Q91WT3
ID Q91WT3 PRELIMINARY; PRT; 481 AA.
AC Q91WT3
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Hypothetical protein.
GN IGH-VJ558 OR A1893585.
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RC TISSUE=Colon;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC013488; AAI33488.1; -.
DR MGD; MGI:96486; Igh-VJ558.
DR InterPro; IPR007110; IG_LIKE.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; Ig; 4.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; 2.
KW Hypothetical protein.
SQ
SEQUENCE 481 AA; 52022 MW; 4EBBSC2530398718 CRC64;

Query Match 15.2%; Score 535; DB 11; Length 481;
Best Local Similarity 25.9%; Pred. No. 1.4e-25;
Matches 172; Conservative 79; Mismatches 168; Indels 246; Gaps 22;

QY 1 EVQLQSGPDLVKASVKISKAGSYFTGYNHWKQSPGKLEWIGRINPNNGVTLY 60
DB 20 QVQLQSGPDLVKASVKISKAGSYFTGYNHWKQSPGKLEWIGRINPNNGVTLY 79
QY 61 NQKFKDKATLVKDSSTTAYNMLRSLSLTSSEDSAVTYCARSTMITNYNDYMGQSTVTSS 120
DB 80 NQKFKG-TTLIVDTSSSAYMLLSLTSSEDSAVTYCARSTMITNYNDYMGQSTVTSS 136
QY 121 AKTPPSVYPLAGSAATNMTGLVKGYPPE-PVTVW-NSGSLSSGVHTFPAVLQ 178
DB 137 EPAREPTIYPLTFQALSSDVI-IGCLIHDPFSGTNVTVGSKGKDITTVNFPFALAS 195
QY 179 SDLYTLSSSVTPGSTWP-SSTVTCNVAHPASTKVDKVIIPRDSGGPSEKSEINEKDL 237
DB 196 GGRYTNSSQLIPAVECEGSVKCSVQH-----DSNPFVQELNV--- 234
QY 238 RKSELOGTALGNLQIYYNYSKAITSEKSGADQFLNTLLFKGFFTHCHPWYNDLLVDLG 297
DB 235 -----NCPGIC---SPPTTPPPSPCPSLS-----LQRFALDGL--LG 268
QY 298 STAATSEYEGSSVDLYGAYGVQCAGGTPNKTACMYGSGVTLDHNNRLTEKKVPEINLWID 357
DB 269 SDASIT-----CTLNG----- 279
QY 358 GKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFLYNSDSFGKVGQRLIVHFSSEGS 417
DB 280 ----- 279
QY 418 TVSYDLFPAQGPPTLARIYRDNTTISSTLSISLYITTSIVMTQTPTSLIIVSAGDRV 477
DB 280 -----LRPEG-----AVFTWPS-----TGKDAV 299
QY 478 TITCKASQSVNDVAVYQKPKQSPKLLISYTSRYAGVPDRFSGSGYGTDTLTITSSVQ 537
DB 300 -----QKXAVQNSCCYS-----VSSVLPQCAERWNS---GASFKCTVTHPE 338
QY 538 AEDAAVYFCQDYNPPTFGGTTKLEIKRAADAATVSIFFPSSQLTSGG-ASVVCFLNN 596

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Db 339 SDTLTGTTAKVTNTFP-----FQVHLLPPPSSEALNELVSLCLVRA 382
QY 597 FYPKIDINVKWIDGSEKONG-----VLNSWTQDQSKDSTYSMSSTLTTLTKDEYERHNSYTC 652
Db 383 FNPKEVLVVRW-LHGNEELSPESYLVFELKEFGEGATTYLVTSVLVRSAAEIKWQGDQYSC 441
QY 653 EATHK 657
Db 442 MVGHE 446

RESULT 57
Q924Q6
ID Q924Q6 PRELIMINARY; PRT; 145 AA.
AC Q924Q6
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE VHI86.2-D-J-C mu protein (Fragment).
OC Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RC STRAIN=C57BL/6;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067794; BAB63279.1; -.
DR PIR; F28833; F28833.
DR PIR; F33932; F33932.
DR PIR; PH1105; PH1105.
DR PIR; PH1108; PH1108.
DR PIR; PH1114; PH1114.
DR PIR; PH1118; PH1118.
DR PIR; PH1119; PH1119.
DR PIR; PH1125; PH1125.
DR PIR; PH1126; PH1126.
DR PIR; PH1128; PH1128.
DR PIR; PH1129; PH1129.
DR PIR; PH1131; PH1131.
DR PIR; PH1134; PH1134.
DR PIR; PH1137; PH1137.
DR PIR; PH1139; PH1139.
DR PIR; PH1142; PH1142.
DR PIR; PH1144; PH1144.
DR PIR; PH1147; PH1147.
DR PIR; PH1149; PH1149.
DR PIR; PH1150; PH1150.
DR PIR; PH1151; PH1151.
DR PIR; PH1152; PH1152.
DR PIR; PH1153; PH1153.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003596; IG_V.
DR Pfam; PF00047; IGV; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 1.
FT NON TER 1
FT NON TER 145
SQ SEQUENCE 145 AA; 16011 MW; 9BC0846D40DF97EA CRC64;

Query Match 15.2%; Score 534; DB 11; Length 145;
Best Local Similarity 75.6%; Pred. No. 3.1e-26;
Matches 99; Conservative 15; Mismatches 17; Indels 0; Gaps 0;

QY 1 EVQLQSGPDLVKASVKISKAGSYFTGYNHWKQSPGKLEWIGRINPNNGVTLY 60
DB 1 QVQLQSGPDLVKASVKISKAGSYFTGYNHWKQSPGKLEWIGRINPNNGVTLY 60

```



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Db      118 ESQSFNVPFL 128
       :|:|:|
RESULT 70
Q924P6 PRELIMINARY; PRT; 143 AA.
ID Q924P6 PRELIMINARY; PRT; 143 AA.
AC Q924P6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP)."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB069919; BAB63935.1; -.
DR PIR; F33932; F33932.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003596; Ig_V.
DR Pfam; PF00047; ig_1.
DR SMART; SM00406; IG; 1.
DR PROSITE; PS50835; IG_LIKE; 1.
FT NON TER 1
FT FT 143
FT NON TER 143
SQ SEQUENCE 143 AA; 15714 MW; 523385316C345A93 CRC64;

Query Match 14.4%; Score 507; DB 11; Length 143;
Best Local Similarity 73.3%; Pred. No. 1.5e-24;
Matches 96; Conservative 16; Mismatches 17; Indels 2; Gaps 0

QY 1 EVQLQQSGDPLVPGASVKISCKASYGFTGYHWKQSPGKLEWIGRIPNNGVG
DB 1 QVQLQQPTGLVLPFGASVKLSCTASGYFTSWHWKQRPGRGLEWIGRIDPSNGGG
   |||||
QY 61 NQKPKDKATLVDSSTTAYMEIRSLTSDSAVYYCARSTMITNYMDYWGQTSVT
DB 61 NEKFKTKATLVDPKPSTTAYMQSLTSDSAVYYCAR--RLDGVNDYWGQTSVT
   |||||
QY 121 AKTTPPSVYPFL 131
DB 119 ESQSFNVPFL 129
       :|:|:|
RESULT 71
Q924R2 PRELIMINARY; PRT; 140 AA.
ID Q924R2 PRELIMINARY; PRT; 140 AA.
AC Q924R2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE VH186.2-D-J-C mu protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Kozono Y., Kozono H., Azuma T.;
RT "Direct Estimation of Relative Affinity by Flow Cytometry Reveals
RT Affinity Maturation of B Cell Antigen Receptors in Response to (4-
RT Hydroxy-3-Nitrophenyl)Acetyl (NP)."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB067788; BAB63273.1; -.

```


Search completed: August 12, 2004, 13:32:24
Job time : 71.4605 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 12, 2004, 13:21:44 ; Search time 84.4429 Seconds
(without alignments)
2248.525 Million cell updates/sec

Title: US-09-900-766-1
Perfect score: 3522
Sequence: 1 EVQLQSGDPLVKPGASVKI.....EATHKTSIPVKSFNRES 672

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database: A_Geneseqp29Jan04:*

1: Genesecp1980s:*

2: Genesecp1990s:*

3: Genesecp2000s:*

4: Genesecp2001s:*

5: Genesecp2002s:*

6: Genesecp2003s:*

7: Genesecp2003bs:*

8: Genesecp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	3522	100.0	672	6	ABP58454
2	1644	46.7	573	4	AA654459
3	1218	34.6	233	6	ABP58455
4	1130	32.1	233	6	ABP58457
5	1113	31.6	245	2	AAW35375
6	1107	31.4	233	6	ABP58456
7	1107	31.4	227	4	AAU14103
8	1107	31.4	257	6	ABO10288
9	1096.5	31.1	720	4	AA655572
10	1093	31.0	230	4	AA673339
11	1091	31.0	245	2	AAW35374
12	1072	30.4	248	6	ABU79072
13	1069	30.4	592	4	AA638338
14	1069	30.4	595	2	AAW66003
15	1059.5	30.1	464	2	AA676088
16	1055.5	30.0	445	2	AA676085
17	1048	29.6	230	2	AA65012
18	1044	29.6	230	5	AA676235
19	1035	29.4	230	2	AA63204
20	1028	29.2	597	5	AA618377
21	1028	29.2	537	5	ABG76352
22	1025.5	29.1	464	3	AAW3041
23	1025.5	29.1	464	3	AA614747
24	1025.5	29.1	464	3	AAW30897
25	1025.5	29.1	464	5	ABB74912

26	1025.5	29.1	464	5	ABB74866
27	1024.5	29.1	613	5	AAE18380
28	1024.5	29.1	613	5	ABG76355
29	1023.5	29.1	456	5	AAE18370
30	1023.5	29.1	456	5	ABG76345
31	1023.5	29.1	493	5	AAE18379
32	1023.5	29.1	493	5	ABG76354
33	1023.5	29.1	510	5	AAE18378
34	1023.5	29.1	510	5	ABG76353
35	1022.5	29.0	438	5	AAE18372
36	1022.5	29.0	438	5	ABG76347
37	1018	28.9	206	2	AAV39452
38	1018	28.9	465	2	AA66758
39	980.5	27.8	711	2	AAW85692
40	979.5	27.8	223	7	ADE06766
41	977.5	27.8	626	3	AAV55081
42	972.5	27.6	243	2	AAW86002
43	972.5	27.6	243	2	AAV42294
44	972.5	27.6	243	2	AAV27407
45	972.5	27.6	243	4	AA63835
46	970	27.5	214	2	AAV44176
47	967.5	27.5	488	2	AAW86004
48	967.5	27.5	488	4	AA63836
49	967.5	27.5	488	6	ABU07262
50	967.5	27.5	488	6	ABU07253
51	966.5	27.4	209	6	ABP95772
52	966.5	27.4	209	6	ABP95771
53	966	27.4	468	2	AA613061
54	961.5	27.3	225	2	AA640385
55	960	27.3	212	2	AAW15932
56	960	27.3	233	2	AA613203
57	953.5	27.1	223	2	AA675456
58	953	27.1	220	2	AA653802
59	951.5	27.0	469	2	AA640384
60	948	26.9	214	3	AAU78253
61	948	26.9	233	6	ABP58458
62	948	26.9	257	4	AAU14104
63	948	26.9	257	6	ABO10269
64	948	26.9	257	7	AD44368
65	945	26.8	234	6	AAO29870
66	944.5	26.8	209	6	ABP96752
67	944.5	26.8	209	6	ABP96751
68	944.5	26.8	239	2	AA676087
69	944	26.8	233	2	AAW06738
70	942	26.7	233	2	AA645011
71	941.5	26.7	219	2	AA676086
72	941	26.7	233	2	AAW35373
73	941	26.7	233	4	AA676338
74	938	26.6	234	5	AAU72802
75	935	26.5	257	6	ABU79068
76	933	26.5	222	2	AAW15934
77	933	26.5	233	5	AB676234
78	932.5	26.5	218	7	ADD05274
79	931	26.4	223	1	AA640031
80	925	26.3	257	5	AB679501
81	925	26.3	257	6	ABU10081
82	925	26.3	257	6	ABU62324
83	925	26.3	257	7	AA637676
84	921	26.1	233	3	AAV54463
85	921	26.1	233	5	AB679502
86	921	26.1	233	6	ABU10082
87	921	26.1	233	7	ABU62325
88	921	26.1	233	7	AA637677
89	919.5	26.1	219	2	AA644495
90	917.5	26.1	219	6	ABP96777
91	917.5	26.1	219	6	ABP96778
92	917	26.0	233	6	ABU10099
93	916.5	26.0	238	2	AAW31752
94	916.5	26.0	238	2	AAW71889
95	916.5	26.0	238	3	AA612909
96	916	26.0	454	5	AB676124
97	916	26.0	462	5	AB676126
98	915.5	26.0	254	2	AAV30123

99 915.5 26.0 254 2 AAY30121 Murine an
100 915 26.0 238 2 AAW83042 Anti-Fas

ALIGNMENTS

RESULT 1
ASP58454
ID ABP58454 standard; protein; 672 AA.
XX AC ABP58454;
XX 14-APR-2003 (first entry)
XX Engineered superantigen for human cancer therapy.
XX Superantigen; staphylococcal enterotoxin; antibody; cancer; tumour;
KW cytostatic; vaccine; human; SEA/E-120; mutant; mutein.
XX Homo sapiens.
OS Staphylococcus sp.
OS Synthetic.
OS Chimeric.
XX Key Location/Qualifiers
XX 1. 120
XX Region /note= "574 variable heavy chain"
FT Misc-difference 41 /note= "wild-type His substituted by Pro"
FT Misc-difference 44 /note= "wild-type Ser substituted by Gly"
FT Misc-difference 69 /note= "wild-type Ile substituted by Thr"
FT Misc-difference 113 /note= "wild-type Val substituted by Gly"
FT Region 121. .222
FT Region /note= "C242 constant heavy chain"
FT Region 226. .458
FT Misc-difference 245 /note= "SEA/E-120"
FT Misc-difference 246 /note= "wild-type Arg substituted by Gly"
FT Misc-difference 246 /note= "wild-type Asn substituted by Thr"
FT Misc-difference 249 /note= "wild-type Ser substituted by Gly"
FT Misc-difference 252 /note= "wild-type Arg substituted by Lys"
FT Misc-difference 304 /note= "wild-type Lys substituted by Glu"
FT Misc-difference 306 /note= "wild-type Lys substituted by Glu"
FT Misc-difference 308 /note= "wild-type Lys substituted by Ser"
FT Misc-difference 309 /note= "wild-type Lys substituted by Ser"
FT Misc-difference 452 /note= "wild-type Asp substituted by Ser"
FT Region 459. .565
FT Misc-difference 469 /note= "574 variable light chain"
FT Misc-difference 504 /note= "wild-type Phe substituted by Ser"
FT Misc-difference 522 /note= "wild-type Thr substituted by Lys"
FT Misc-difference 532 /note= "wild-type Ile substituted by Ser"
FT Misc-difference 536 /note= "wild-type Phe substituted by Leu"
FT Misc-difference 537 /note= "wild-type Thr substituted by Ser"
FT Misc-difference 542 /note= "wild-type Leu substituted by Val"

FT Region /note= "wild-type Leu substituted by Ala"
FT 566. .672
FT /note= "C242 constant light chain"
XX WO2003002143-A1.
XX 09-JAN-2003.
XX 19-JUN-2002; 2002WO-SE001188.
XX 28-JUN-2001; 2001SE-00002327.
XX (ACTI-) ACTIVE BIOTECH AB.
XX Forsberg G, Brlandsson E, Antonsson P, Walse B;
XX WPI; 2003-201467/19.
XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
XX receptor and four regions to determine binding to class II major
XX histocompatibility complex, antibody to cancer associated cell surface
XX structure.
XX Claim 12; Fig 10; 102pp; English.
XX The present sequence is a conjugate of a bacterial superantigen and an
XX antibody moiety, and has been designed to target and destroy cancer
XX cells. The bacterial superantigen is SEA/E-120 (see also ABP58455), which
XX was derived from staphylococcal enterotoxin E (SEE) by the incorporation
XX of the following amino acid substitutions to reduce seroreactivity whilst
XX maintaining production levels and biological activity: R20G, N21F, S24G,
XX R27K, K79E, K81E, K83S and D227S. SEA/E-120 was genetically fused to the
XX Fab moiety of the tumour reactive antibody 5T4. Substitutions were made
XX in the 5T4 sequence to obtain higher yields: in the heavy chain, H41P,
XX S44G, I69T and V113G; and in the light chain, F10S, T45K, I63S, F73L,
XX T77S, L78V and L83A. An expression vector comprising DNA encoding the
XX conjugate can be used to transform host cells for recombinant production
XX of the conjugate. The conjugate is useful for treating cancer, including
XX cancer of the lung, breast, colon, kidney, pancreas, ovary, stomach,
XX cervix and prostate (claimed)
XX SQ Sequence 672 AA;
Query Match 100.0%; Score 3522; DB 6; Length 672;
Best Local Similarity 100.0%; Pred. No. 3e-201;
Matches 672; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 EVLOQSGDPLVKPGASVKISCKASGYGFTGYMHVWKQSPCKGLEWIGRINPNNGVTLV 60
Db 1 EVLOQSGDPLVKPGASVKISCKASGYGFTGYMHVWKQSPCKGLEWIGRINPNNGVTLV 60
QY 61 NQKFKDKATLVDKSSTTAYMELSLTSEDSAVVYCARSTMITNYMDYWGCGTSTVYSS 120
Db 61 NQKFKDKATLVDKSSTTAYMELSLTSEDSAVVYCARSTMITNYMDYWGCGTSTVYSS 120
QY 121 AKTTPPSVYPLAPGSAQTNSMVTGLCVKGFPEPVTVTWNSGLSSGVHTFPVAVLQSD 180
Db 121 AKTTPPSVYPLAPGSAQTNSMVTGLCVKGFPEPVTVTWNSGLSSGVHTFPVAVLQSD 180
QY 181 LYTSLSSVTPSPSTWPFSETVTCNVAHPASSTKVDKKIIVPRDSGGPSEKSEINEKDLRKK 240
Db 181 LYTSLSSVTPSPSTWPFSETVTCNVAHPASSTKVDKKIIVPRDSGGPSEKSEINEKDLRKK 240
QY 241 SELQGTALGNLKOIYYNSKAITSEKSAQDQPLTNLLPKGFPTGHPWYNDLLVDLGSTA 300
Db 241 SELQGTALGNLKOIYYNSKAITSEKSAQDQPLTNLLPKGFPTGHPWYNDLLVDLGSTA 300
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTACMGVGTLLHNNRLTEERKVPINLWIDGKQ 360
Db 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTACMGVGTLLHNNRLTEERKVPINLWIDGKQ 360
QY 361 TTVPIDKVTSKETVQBELDQAHHYHGFGLNSDSFGKVGQGLIVHSSSEGSTVS 420

Db 361 TTVPIDKVKTSKEVTVQSLDLQARHLYHGKFGLYNSDSFGGKVGRLIVPHSSEGSTVS 420
 QY 421 YDLFDAGGYPBTLRIYEDNTTISSTLSISLYLYTTISIVMTOTPTSLIYSAGDRVTIT 480
 Db 421 YDLFDAGGYPBTLRIYEDNTTISSTLSISLYLYTTISIVMTOTPTSLIYSAGDRVTIT 480
 QY 481 CKASQSVNDVAVYQKQKPSKLLISYSSRYAGVPDRFSGGYGTDFTLTISVQAE 540
 Db 481 CKASQSVNDVAVYQKQKPSKLLISYSSRYAGVPDRFSGGYGTDFTLTISVQAE 540
 QY 541 AAVYFCQDYNSPPTFGGKTKLEIKRADAAPTIVSIPPSSEOLTSGGASVVCFLNFPYK 600
 Db 541 AAVYFCQDYNSPPTFGGKTKLEIKRADAAPTIVSIPPSSEOLTSGGASVVCFLNFPYK 600
 QY 601 DINVKWKIDGSRQNGVLSWTDQSKDSTYSMSSTLTLTDEYERHNSYTCETHKST 660
 Db 601 DINVKWKIDGSRQNGVLSWTDQSKDSTYSMSSTLTLTDEYERHNSYTCETHKST 660
 QY 661 SPIVKSFRNES 672
 Db 661 SPIVKSFRNES 672

RESULT 2
 AAG64459
 ID AAG64459 standard; protein; 573 AA.

XX AAG64459;
 AC
 DT 21-SEP-2001 (first entry)
 XX Mouse 6D9 catalytic antibody.
 DE Mouse; 6D9; catalytic antibody; esterase activity.
 XX
 XX Mus sp.

Key Location/Qualifiers

FT Misc-difference 28 /note= "Encoded by GCCTGA"
 FT Misc-difference 35 /label= unknown
 FT /note= "Encoded by TNT"
 FT Misc-difference 46 /note= "Encoded by GAGTAA"
 FT Misc-difference 329 /note= "Encoded by GAGTAA"
 FT Misc-difference 572 /note= "Encoded by TGTAA"
 FT /note= "Encoded by TGTAA"

JP2001128681-A.

XX 15-MAY-2001.
 XX 04-NOV-1999; 99JP-00314259.
 XX 04-NOV-1999; 99JP-00314259.
 XX (NIBS) JAPAN TOBACCO INC.
 PA (SEIB-) SEIBUTSU BUNSHI KOGAKU KENKYUSHO KK.
 PA (TANP-) TANPAKU KOGAKU KENKYUSHO KK.

XX WPI; 2001-373026/39.
 XX N-PSDB; AAH47858.

XX A new catalytic antibody.

XX Claim 3; Page 14-17; 18pp; Japanese.

CC The present sequence is that of the mouse 6D9 catalytic antibody. The
 CC invention relates to an antibody in which 1 to 9 amino acids are
 CC replaced, deleted, inserted and/or added to substantially increase its
 CC catalytic esterase activity

XX Sequence 573 AA;
 SQ
 Query Match 46.7%; Score 1644; DB 4; Length 573;
 Best Local Similarity 51.2%; Pred. No. 1.4e-89;
 Matches 353; Conservative 52; Mismatches 78; Indels 206; Gaps 11;
 QY 1 EVQLQQSGPDLVKPGASVKISKASGYSTGYTHHWVKQSPGKGLWIGRINPNNGVTLY 60
 Db 71 QVQLLEGSGGLVKPGGSLKLSCAASGFTFSYAMSWRQTPEKLEWVVIS-SGGSIYY 129
 QY 61 NQKPKDKATUTVDKSTTAYMELRSLTSDSVAIVYCARSTMITNY-----VMDYWGQGT 114
 Db 130 LDSVKGFTVSRDNARNILYLQMTSLASEDTAMVFCAR---VSHYDGRDWMYFDVWAGT 186
 QY 115 SVTVSSAKTTPPSVYPLAPGSAQTNSMVTGLCLVKGYPPEPTVTWNSGSLSGGVHTFP 174
 Db 187 SVTVSSAKTTPPSVYPLAPGSAQTNSMVTGLCLVKGYPPEPTVTWNSGSLSGGVHTFP 246
 QY 175 AVLQSDLYTLSSSVTPSPSTWPTSETVTCNVAPASSTKVDKIVPRDSGSPSEKSEINE 234
 Db 247 AVLQSDLYTLSSSVTPSPSTWPTSETVTCNVAPASSTKVDKIVPRD----- 293
 QY 235 KDLRKKSELOGTALGNLKQIYYVNSKAITSEKSDAQFLTWLLFKGFFTHPWNLLV 294
 Db 294 -----CTSEAST----- 301
 QY 295 DLGSTAATSEYEGSSVDLYGAVYGYCAGGTPNKTACMYGVTLHNNRLTEKKVPINL 354
 Db 302 -----TVSKTENLSGGSSVIEFRAGY-----LFF 326
 QY 355 WIDG-KQTTVPIDKVKTSKEVTVQSLDLQARHLYHGKFGLYNSDSFGGKVGRLIVPHS 413
 Db 327 WMEAMKQSTI----- 336
 QY 414 SEGSTVSYDLFDAQGGYPTLLRIYRDNTTISSTLSISLYLVLT-----TSIVMTOTPT 467
 Db 337 -----LILLILLLLPTVKMAELVMTOTPL 362
 QY 468 SLVLSAGDRVITCKASQSV--SND---VAVYQKQKPSKLLISYSSRYAGVPDRFSG 522
 Db 363 SLVSLGDPQASISCRSSQTIYHNSGDTYLDWFLQKQKPSKLLIYKVSNEFSGVDPDRFSG 422
 QY 523 SGYGTDFTLTISVQAEADAAYVFCQDYNSPPTFGGKTKLEIKRADAAPTIVSIPPSSEQ 582
 Db 423 SSGTDFTLKLSRVEAEDLVYICFGSHVPTPTGGGKTKLEIKRADAAPTIVSIPPSSEQ 482
 QY 583 LTSGGASVVCFLNFPYKIDNVKWKIDGSRQNGVLSWTDQSKDSTYSMSSTLTITKD 642
 Db 483 LTSGGASVVCFLNFPYKIDNVKWKIDGSRQNGVLSWTDQSKDSTYSMSSTLTITKD 542
 QY 643 EYERHNSYTCETHKSTSTSPVKSFRNE 671
 Db 543 EYERHNSYTCETHKSTSTSPVKSFRNE 571

RESULT 3
ABP58455

ID ABP58455 standard; protein; 233 AA.

XX AC ABP58455;

XX 14-APR-2003 (first entry)

XX Engineered superantigen SEA/E-120 for human cancer therapy.

XX Superantigen; staphylococcal enterotoxin; antibody; cancer; tumour;
 KW cytostatic; vaccine; SEA/E-120; mutant; mutein.

XX Staphylococcus sp.

OS Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 20 /note= "wild-type Arg substituted by Gly"
 FT Misc-difference 21 /note= "wild-type Asn substituted by Thr"
 FT Misc-difference 24 /note= "wild-type Ser substituted by Gly"
 FT Misc-difference 27 /note= "wild-type Arg substituted by Lys"
 FT Misc-difference 79 /note= "wild-type Lys substituted by Glu"
 FT Misc-difference 81 /note= "wild-type Lys substituted by Glu"
 FT Misc-difference 83 /note= "wild-type Lys substituted by Ser"
 FT Misc-difference 84 /note= "wild-type Lys substituted by Ser"
 FT Misc-difference 227 /note= "wild-type Asp substituted by Ser"
 FT
 PN WO2003002143-A1.
 XX
 XX 09-JAN-2003.
 XX
 PF 19-JUN-2002; 2002WO-SE001188.
 XX
 PR 28-JUN-2001; 2001SE-00002327.
 XX
 PA (ACTI-) ACTIVE BIOTECH AB.
 XX
 PI Forsberg G, Erlandsson E, Antonsson P, Walse B;
 XX
 XX WPI; 2003-201467/19.
 XX
 XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
 PT receptor and four regions to determine binding to class II major
 PT histocompatibility complex, antibody to cancer associated cell surface
 PT structure.
 XX
 XX Claim 8; Fig 2; 102pp; English.
 PS
 CC The present sequence is the protein sequence of engineered staphylococcal
 CC superantigen SEA/E-120. The superantigen is derived from staphylococcal
 CC enterotoxin E (SEE) by the incorporation of the following amino acid
 CC substitutions to reduce seroreactivity whilst maintaining production
 CC levels and biological activity: R20G, N21T, S24G, R27K, K79E, K81E, K83S
 CC and D227S. SEA/E-120 has been genetically fused to the Fab moiety of the
 CC tumour reactive antibody 5T4 to form a claimed conjugate (see ABP58454)
 CC designed to target and destroy cancer cells, including cancer of the
 CC lung, breast, colon, kidney, pancreas, ovary, stomach, cervix and
 CC prostate (claimed)
 XX
 XX Sequence 233 AA;

Query Match 34.6%; Score 1218; DB 6; Length 233;
 Best Local Similarity 100.0%; Pred. No. 1e-64;
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITTSSEKSDQFLTNLLFKGFTG 285
 DB 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITTSSEKSDQFLTNLLFKGFTG 60
 QY 286 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 345
 DB 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 120
 QY 346 EEKVPINLWIDGKQTTVPIDKVTSSKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQ 405
 DB 121 EEKVPINLWIDGKQTTVPIDKVTSSKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQ 180
 QY 406 RGLIVFHSSEGSTVSDFDAQGGVPTDLLRIYRDNNTTISTSLISLYLTT 458
 DB 181 RGLIVFHSSEGSTVSDFDAQGGVPTDLLRIYRDNNTTISTSLISLYLTT 233

RESULT 4
 ABP58457
 ID ABP58457 standard; protein; 233 AA.
 XX
 AC ABP58457;
 XX
 DT 14-APR-2003 (first entry)
 XX
 DE Engineered superantigen SEA/E-18 for human cancer therapy.
 XX
 KW Superantigen; staphylococcal enterotoxin; antibody; cancer; tumour;
 KW cytostatic; vaccine; SEA/E-18; mutant; mutein.
 XX
 OS Staphylococcus sp.
 OS Synthetic.
 XX
 PN WO2003002143-A1.
 XX
 PD 09-JAN-2003.
 XX
 PF 19-JUN-2002; 2002WO-SE001188.
 XX
 PR 28-JUN-2001; 2001SE-00002327.
 XX
 PA (ACTI-) ACTIVE BIOTECH AB.
 XX
 PI Forsberg G, Erlandsson E, Antonsson P, Walse B;
 XX
 XX WPI; 2003-201467/19.
 XX
 XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
 PT receptor and four regions to determine binding to class II major
 PT histocompatibility complex, antibody to cancer associated cell surface
 PT structure.
 XX
 XX Example 3; Fig 3; 102pp; English.
 PS
 CC The present sequence is the protein sequence of engineered staphylococcal
 CC superantigen SEA/E-18. The superantigen is based on staphylococcal
 CC enterotoxin E (SEE, see ABP58456) except for 4 amino acid residues close
 CC to the N-terminal that were from enterotoxin A and one substitution in
 CC the C-terminal part, D227A. Models of new superantigen variants were
 CC constructed using the SEA/E-18 model as the template. These include the
 CC new engineered superantigen SEA/E-120 (see ABP58455), which has been
 CC genetically fused to the Fab moiety of the tumour reactive antibody 5T4
 CC to form a conjugate (see ABP58454) polypeptide. The conjugate is a
 CC claimed example of novel conjugates of the invention comprising an
 CC engineered bacterial superantigen and an antibody moiety. The conjugates
 CC are designed to target and destroy cancer cells, including cancer of the
 CC lung, breast, colon, kidney, pancreas, ovary, stomach, cervix and
 CC prostate (claimed)
 XX
 XX Sequence 233 AA;

Query Match 32.1%; Score 1130; DB 6; Length 233;
 Best Local Similarity 91.4%; Pred. No. 1.8e-59;
 Matches 213; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
 QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITTSSEKSDQFLTNLLFKGFTG 285
 DB 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITTSSEKSDQFLTNLLFKGFTG 60
 QY 286 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 345
 DB 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 120
 QY 346 EEKVPINLWIDGKQTTVPIDKVTSSKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQ 405
 DB 121 EEKVPINLWIDGKQTTVPIDKVTSSKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQ 180
 QY 406 RGLIVFHSSEGSTVSDFDAQGGVPTDLLRIYRDNNTTISTSLISLYLTT 458

Db 181 RGLIVFHSSEGSTVSYDLFDAQQYPTDLLRIYRDNKNTINSENHIALYLYTT 233

RESULT 5
AAW35375
ID AAW35375 standard; peptide; 245 AA.
XX AC AAW35375;
XX DT 20-APR-1998 (first entry)
XX DE Staphylococcus enterotoxin SEE modified superantigen.
XX KW SEE; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment;
XX KW cancer; infection; autoimmune disease; antibody; modified.
XX OS Staphylococcus sp.
XX FH Key Location/Qualifiers
FT Misc-difference 20 /label= R20G
FT /note= "wild-type Arg is replaced by Gly"
FT Misc-difference 21 /label= N21T
FT /note= "wild-type Asn is replaced by Thr"
FT Misc-difference 24 /label= S24G
FT /note= "wild-type Ser is replaced by Gly"
FT Misc-difference 27 /label= R27K
FT /note= "wild-type Arg is replaced by Lys"
XX PN WO9736932-A1.
XX PD 09-OCT-1997.
XX PE 26-MAR-1997; 97WO-SE000537.
XX PR 29-MAR-1996; 96SE-00001245.
XX PR 12-AUG-1996; 96US-00695692.
XX PA (PHAA) PHARMACIA & UPJOHN AB.
XX PI Antonsson P, Hansson J, Bjoerk P, Dohlsten M, Kalland T;
PI Abrahamsen L, Forsberg G;
XX WPI; 1997-503052/46.
XX Conjugate of target seeking moiety and modified superantigen - useful for
PT activating the immune system to treat cancer, viral infections, parasitic
PT infestations and autoimmune diseases.
XX Claim 5; Page; 58pp; English.
XX This is a modified Staphylococcus enterotoxin SEE superantigen. The wild-
CC type SEE superantigen is modified to be used in a novel conjugate. The
CC novel conjugate comprises a target seeking moiety and a modified wild
CC type superantigen. This modified superantigen retains its ability to
CC activate a subset of T cells, even though 1 or more wild-type amino acid
CC residues in at least 1 region which functions in determining binding to T
CC cell receptor (TCR) and activation of a subset of T cells has/have been
CC replaced. Such a modified superantigen can optionally be used as part of
CC a conjugate with a target seeking moiety, for activating the immune
CC system to treat a mammalian disease. A pharmaceutical composition can be
CC prepared comprising a modified antibody (preferably a Fab fragment fused
CC to a peptide moiety providing activation of T cells in Vbeta specific
CC manner) in which cysteines providing for interchain cysteine linkages in
CC the native antibody have been replaced (preferably by serine residues) to
CC prohibit cysteine formation. The modified wild-type superantigen is used
CC for treating cancer, viral infections, parasitic infestations and
CC autoimmune disease. The modified wild type superantigen has a lower
CC immunogenicity and reactivity with neutralising antibodies and has fewer
CC side-effects when used as a drug, compared to wild type superantigen.

CC Note: This sequence is not provided in the specification. It has been
CC created by modifying the wild-type SEE superantigen sequence in Pages 38-
CC 39 of the specification
XX SQ Sequence 245 AA;
Query Match 31.6%; Score 1113; DB 2; Length 245;
Best Local Similarity 86.9%; Pred. No. 1.9e-58;
Matches 213; Conservative 8; Mismatches 12; Indels 12; Gaps 1;
QY 226 SEKSEINEKDLRKSEHQGTALGNLQKIYYNKAITSSEKSADQFLNTLLFKGPTG 285
DB 1 SEKSEINEKDLRKSEHQGTALGNLQKIYYNKAITSSEKSADQFLNTLLFKGPTG 60
QY 286 HPWYNDLLVLDGSAATSEYEGSSVDLYGAYGYQCAGGTPNKACMYGGVTLHDNNRLT 345
DB 61 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTPNKACMYGGVTLHDNNRLT 120
QY 346 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGGKVQ 405
DB 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGGKVQ 180
QY 406 RGLIVFHSSEGSTVSYDLFDAQQYPTDLLRIYRDNKNTINSENHIALYLYTT 453
DB 181 RGLIVFHSSEGSTVSYDLFDAQQYPTDLLRIYRDNKNTINSENHIALYLYTT 240
QY 454 YLYTT 458
DB 241 YLYTT 245

RESULT 6
ABP58456
ID ABP58456 standard; protein; 233 AA.
XX AC ABP58456;
XX DT 14-APR-2003 (first entry)
XX DE Staphylococcal enterotoxin E.
XX KW Superantigen; staphylococcal enterotoxin E; antibody; cancer; tumour;
XX cytotstatic; vaccine.
XX OS Staphylococcus sp.
XX PN WO2003002143-A1.
XX PD 09-JAN-2003.
XX PF 19-JUN-2002; 2002WO-SE001188.
XX PR 28-JUN-2001; 2001SE-00002327.
XX (ACTI-) ACTIVE BIOTECH AB.
XX Forsberg G, Erlandsson E, Antonsson P, Walse B;
XX WPI; 2003-201467/19.
XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
PT receptor and four regions to determine binding to class II major
PT histocompatibility complex, antibody to cancer associated cell surface
PT structure.
XX Example 3; Fig 4; 102pp; English.
XX The present sequence is the protein sequence of staphylococcal
CC enterotoxin SEE. The invention provides novel conjugates (see ABP58454)
CC for human cancer therapy. These comprise an engineered bacterial
CC superantigen, such as novel SEA/E-120 (see ABP58455), which is based on
CC SEE, and an antibody moiety, such as tumour reactive antibody 5F4. The
CC superantigen is engineered to reduce seroreactivity whilst maintaining

CC biological activity and production levels. The conjugates are designed to
CC target and destroy cancer cells, including cancer of the lung, breast,
CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
XX
XX
SQ Sequence 233 AA;

Query Match 31.4%; Score 1107; DB 6; Length 233;
Best Local Similarity 89.7%; Pred. No. 4.1e-58;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSDAQFTNTLLFKGFTG 285
DB 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSDAQFTNTLLFKGFTG 60

QY 286 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYYGQAGGTPNKACMYGGVTLHDNNRLT 345
DB 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYYGQAGGTPNKACMYGGVTLHDNNRLT 120

QY 346 BEKKVPINLWDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKGLYNSDSFGGKVQ 405
DB 121 BEKKVPINLWDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKGLYNSDSFGGKVQ 180

QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNTTISSTLSISLYLYTT 458
DB 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNTTISSTLSISLYLYTT 233

RESULT 7
AAU14103
ID AAU14103 standard; peptide; 257 AA.

XX AC AAU14103;
XX
XX 21-NOV-2001 (first entry)

DE Peptide sequence from Staphylococcus aureus enterotoxin type E.
KW Anti-retroviral; DP178-like; DP107-like; enterotoxin type E;
KW antifusogenic; antiviral; HIV transmission.

OS Staphylococcus aureus.
XX
XX WO200151673-A2.

PD 19-JUL-2001.
XX
XX 05-JUL-2000; 2000WO-US035727.

PR 09-JUL-1999; 99US-00350841.
XX
XX (TRIM-) TRIMERIS INC.

PI Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
XX
XX WPI; 2001-442157/47.

XX Identifying a compound that inhibits the formation of or disrupts a
PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral
PT or intracellular modulatory activity, by detecting the formation of a
PT DP107/DP178 complex.

PS Disclosure; Fig 41; 259pp; English.

XX The present invention relates to peptides which exhibit anti-retroviral
CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
CC amino acids 639-673 of the transmembrane protein gp41 from human
CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
CC also relates to a method of identifying compounds that inhibit the
CC formation of or disrupts a DP107/DP178 complex. The method comprises
CC detecting the formation of a DP107/DP178 complex, both in the presence or
CC absence of a test compound, in a reaction mixture containing DP107 and

CC DP178 peptides. The method is useful for identifying compounds, including
CC small molecule compounds, which may themselves exhibit antifusogenic,
CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
CC peptides are useful to inhibit human and non-human retroviral,
CC particularly HIV, transmission to uninfected cells. The present sequence
CC represents a peptide sequence from Staphylococcus aureus enterotoxin type
CC E

XX
SQ Sequence 257 AA;

Query Match 31.4%; Score 1107; DB 4; Length 257;
Best Local Similarity 89.7%; Pred. No. 4.6e-58;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSDAQFTNTLLFKGFTG 285
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSDAQFTNTLLFKGFTG 84

QY 286 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYYGQAGGTPNKACMYGGVTLHDNNRLT 345
DB 85 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYYGQAGGTPNKACMYGGVTLHDNNRLT 144

QY 346 BEKKVPINLWDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKGLYNSDSFGGKVQ 405
DB 145 BEKKVPINLWDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKGLYNSDSFGGKVQ 204

QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNTTISSTLSISLYLYTT 458
DB 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNTTISSTLSISLYLYTT 257

RESULT 8
ABO10268
ID ABO10268 standard; protein; 257 AA.

XX AC ABO10268;
XX
XX 19-AUG-2003 (first entry)

DE S. aureus enterotoxin E.
XX
XX HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;
KW Epstein-Barr virus infection; heptad repeat motif.

XX Staphylococcus aureus.
XX
XX US6518013-B1.

PD 11-FEB-2003.
XX
XX 07-JUN-1995; 95US-00485546.

PR 07-JUN-1993; 93US-00073028.
PR 07-JUN-1994; 94US-00255208.
PR 20-DEC-1994; 94US-00360107.

XX (TRIM-) TRIMERIS INC.
PA
XX Barney SO, Lambert DM, Petteway SR;
PI
XX WPI; 2003-465599/44.

XX Inhibiting transmission of Epstein-Barr virus to a cell, by contacting
PT the cell with a peptide consisting of a region of Epstein-Barr virus
PT protein.
XX
XX Example; Fig 41; 716pp; English.

XX The invention relates to inhibiting (M) transmission of an Epstein-Barr
CC virus to a cell, comprising contacting the cell with an effective
CC concentration of a peptide consisting of a region of 16-39 consecutive
CC amino acids of an Epstein-Barr virus protein for an effective period of
CC time, where the region is recognised by one or more of A1MOT15,

CC 107X178x4 or PLZIP sequence search motifs, the peptide further comprises
 CC an amino terminal X, and a carboxy terminal Z in which X comprises an
 CC amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic
 CC group or macromolecular carrier group, and Z comprises a carboxyl group,
 CC amino group, hydrophobic group, or macromolecular carrier group, and
 CC fusion of the virus to the cell is inhibited. The peptides were
 CC identified by analysing the structure/motifs present in the HIV-1
 CC glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat
 CC motif containing peptides were used to design the motifs cited above,
 CC which in turn were used to analyse proteins from other pathogenic
 CC organisms and HIV isolates, looking for DP107/178 structural analogues.
 CC The method is useful for inhibiting transmission of Epstein-Barr virus to
 CC a cell and Epstein-Barr virus infection. The present sequence is a
 CC protein from a pathogenic organism analysed for regions analogous to
 CC DP107 or DP178
 XX
 SQ Sequence 257 AA;

Query Match 31.4%; Score 1107; DB 6; Length 257;
 Best Local Similarity 89.7%; Pred. No. 4.6e-58;
 Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
 QY 226 SEKSEBINEKDKRKKSELOQALGNLQIYYNKAITSSEKSAQOFLNTLLFKGFTG 285
 DB 25 SEKSEBINEKDKRKKSELOQALGNLQIYYNKAITSSEKSAQOFLNTLLFKGFTG 84
 QY 286 HPYNDLLVDLSTATSEVSGSSVDLYGAYGYOCAGTGNKTCMYGGVTLHDNNRLT 345
 DB 85 HPYNDLLVDLSTATSEVSGSSVDLYGAYGYOCAGTGNKTCMYGGVTLHDNNRLT 144
 QY 346 EEKVPINLWDGKQTTVPIDKVTSSKKEVTQELDQARHYLHGKFGLYNSDSFGKQV 405
 DB 145 EEKVPINLWDGKQTTVPIDKVTSSKKEVTQELDQARHYLHGKFGLYNSDSFGKQV 204
 QY 406 RGLIVFHSSEGSTVSVDLFDAGQVPTLLRIYRDNLTISSTLSISLYITT 458
 DB 205 RGLIVFHSSEGSTVSVDLFDAGQVPTLLRIYRDNLTISSTLSISLYITT 257

RESULT 9
 AAG65572
 ID AAG65572 standard; protein; 720 AA.
 AC AAG65572;
 DT 30-NOV-2001 (first entry)
 DE Amino acid sequence of a plasmid pFCAH9-B8d.
 XX Gene library; immunoglobulin; antibody library.
 XX Synthetic.
 XX WO200162907-A1.
 XX 30-AUG-2001.
 XX 22-FEB-2001; 2001WO-JP001298.
 XX 22-FEB-2000; 2000JP-00050543.
 XX (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
 XX Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinochara M, Takahashi M;
 PI Okuno Y, Shiraki K;
 DR WPI; 2001-565420/63.
 DR N-PSDB; AAH47738.

Producing gene libraries and antibody libraries, involves selecting a
 PT light chain that binds to a heavy chain product to produce a functional
 PT formation, and producing a gene library of the light chain variable
 PT regions.

XX
 PS Example; Fig 3-6; 181pp; Japanese.
 CC The invention relates to producing gene libraries, comprising
 CC immunoglobulin light and heavy variable region. The method involves
 CC selecting light chain that binds with the heavy chain product to produce
 CC a functional conformation, producing a gene library comprising a
 CC collection of these light chain variable genes, and combining with gene
 CC library of heavy chain variable genes. The method is used for production
 CC of gene and antibody libraries. The present sequence represents the amino
 CC acid sequence of a plasmid pFCAH9-B8d
 XX
 SQ Sequence 720 AA;

Query Match 31.1%; Score 1096.5; DB 4; Length 720;
 Best Local Similarity 37.9%; Pred. No. 6.7e-57;
 Matches 256; Conservative 39; Mismatches 55; Indels 325; Gaps 9;
 QY 1 EVQLQQSGPDLVKPGASVKISCKASGYFTGYMHVWYKQSPGKLEWIGINPNNGVTLY 60
 DB 23 QVQKQQSGAELVKGASVKLSCTASGPNIKDTYMHVWYKQSPGK----- 66
 QY 61 NQKPKDKATLTVDKSTTAYMELRSLTSEDSVYVYCARSTMITNY---VMDYMGQGTSTV 117
 DB 67 -----LTSEDTAVYCA-----CYDYGNFDYNGQGTSTV 95
 QY 118 VSSAKTTPPSVYPLAPGSAATQNSMVTGLCLVKGYPPEPVTVTNWSSLSGSHVTPPAVL 177
 DB 96 VSSASTKGPSVFPPLAPGSAATQNSMVTGLCLVKGYPPEPVTVTNWSSLSGSHVTPPAVL 155
 QY 178 QSD--LYTLSSSTVTPSPSTWPEVTVCNVAHPASSTKVKDKIVPRDSGGPSEKSEINEKD 236
 DB 156 QSSGLYLSSTVTPSPSSSLGTQYICNVNHPKNTKVDKVEPK----- 199
 QY 237 LRKKELOQTALGNLKOIYYNKAITSSEKSAQOFLNTLLFKGFTGHPYNDLLVDL 296
 DB 200 ----- 199
 QY 297 GSTAATSEYEGSSVDLYGAYGYOCAGTGNKTCMYGGVTLHDNNRLTBEKKVPINLWI 356
 DB 200 -----SCHH----- 203
 QY 357 DGKQTTVPIDKVTSSKKEVTQELDQARHYLHGKFGLYNSDSFGKQVQGLIVFHSSEG 416
 DB 204 -----HHHMKVLLPTAAA-----GLUL----- 221
 QY 417 STVSYDLFDAQQVPTLLRIYRDNLTISSTLSISLYITTSTIVMTQTSTLLVSAGDR 476
 DB 222 -----LAAQFAMATSDIELTQSPASLSASVGET 249
 QY 477 VTITCKASQSVNDVAVYQKQSPKLLISYTSRYAGVDFRPSGSGYGTDFTLTISV 536
 DB 250 VTITCRASGNIHNYLA----- 265
 QY 537 QAEDAAVYFCQDYNVPPTFGGKTKLEIKRADAAPTVSIFPPSSQITSGGASVVCFLNN 596
 DB 266 -----KLEIKRADAAPTVSIFPPSSQITSGGASVVCFLNS 301
 QY 597 FYPKDNVKKIDGSRQNGVLSNWTDDQSKSTYSVSSLTLLTKDEYEHNSVTCEATH 656
 DB 302 FYPKDNVKKIDGSRQNGVLSNWTDDQSKSTYSVSSLTLLTKDEYEHNSVTCEATH 656
 QY 657 KTSTSPIVKSFNRNE 671
 DB 362 KTSTSPIVKSFNRNE 376

RESULT 10
 AAB67339
 ID AAB67339 standard; peptide; 230 AA.
 XX
 AC AAB67339;
 XX

DT 23-APR-2001 (first entry)
 DE Staphylococcus aureus enterotoxin E protein.
 XX Tumour; cancer; immune; enterotoxin.
 OS Staphylococcus aureus.
 XX US6180097-B1.
 XX 30-JAN-2001.
 XX 30-OCT-1998; 98US-00183437.
 XX 03-OCT-1989; 89US-00416530.
 PR 17-JAN-1990; 90US-00466577.
 PR 17-JAN-1991; 91WO-US000342.
 PR 01-JUN-1992; 92US-00891718.
 PR 02-MAR-1993; 93US-00025144.
 PR 31-JAN-1994; 94US-00189424.
 PR 19-JUN-1995; 95US-00491746.
 XX (TERM/) TERMAN D S.
 PA Terman DS;
 PI WPI; 2001-158657/16.
 DR Tumor cell capable of stimulating antitumor immune reactivity in vitro or
 XX in vivo comprises exogenous nucleic acids encoding a superantigen and a
 PT costimulatory molecule.
 XX Disclosure; Fig 2; 16pp; English.
 PS The present invention relates to a tumour cell capable of stimulating
 CC antitumor immune reactivity in vitro or in vivo contains and expresses an
 CC exogenous nucleic acid molecule encoding a superantigen or its active
 CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
 CC molecule that activates T cells in conjunction with an antigenic
 CC stimulus. The invention may be used for cancer therapy by stimulating an
 CC anticancer immune response in vivo or ex vivo
 XX Sequence 230 AA;
 SQ Query Match 31.0%; Score 1093; DB 4; Length 230;
 Best Local Similarity 89.6%; Pred. No. 2.7e-57;
 Matches 206; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
 QY 229 SEINEKDLRKSELOGTALGNLQIYYNKAITSSEKSDQFLTNLLFKGFTGHPW 288
 DB 1 SEINEKDLRKSELOGTALGNLQIYYNKAITSSEKSDQFLTNLLFKGFTGHPW 60
 QY 289 YNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGTGNKTAACMYGGVTLHDNNRLTEK 348
 DB 61 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTAACMYGGVTLHDNNRLTEK 120
 QY 349 KVPINLWIDGQTTVPIDKVTSKVETVQBLDQARHYLHGKGLYNSDSFGKVGQRL 408
 DB 121 KVPINLWIDGQTTVPIDKVTSKVETVQBLDQARHYLHGKGLYNSDSFGKVGQRL 180
 QY 409 IVFHSSEGSTVSYDLFDAGQGPDTLLRIYRDNTTIGSTLSLSLYLTT 458
 DB 181 IVFHSSEGSTVSYDLFDAGQGPDTLLRIYRDNTTIGSTLSLSLYLTT 230
 RESULT 11
 ID AAW35374
 AC AAW35374 standard; peptide; 245 AA.
 XX AAW35374;
 XX 20-APR-1998 (first entry)
 DT Staphylococcus enterotoxin SEE wild-type superantigen.
 DE SEE; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment;
 KW cancer; infection; autoimmune disease; antibody.
 XX Staphylococcus sp.
 OS Staphylococcus sp.
 XX Key Location/Qualifiers
 FH Misc-difference 20 /note= "can be mutated at this position"
 FT Misc-difference 21 /note= "can be mutated at this position"
 FT Misc-difference 24 /note= "can be mutated at this position"
 FT Misc-difference 27 /note= "can be mutated at this position"
 FT Misc-difference 27 /note= "can be mutated at this position"
 XX WO9736932-A1.
 XX 09-OCT-1997.
 XX 26-MAR-1997; 97WO-SE000537.
 XX 29-MAR-1996; 96SE-00001245.
 PR 12-AUG-1996; 96US-00695692.
 XX (PHAA) PHARMACIA & UPJOHN AB.
 XX PA Antonsson P, Hansson J, Bjoerk P, Dohlsten M, Kalland T;
 PI Abraham L, Forsberg G;
 DR WPI; 1997-503052/46.
 XX Conjugate of target seeking moiety and modified superantigen - useful for
 PT activating the immune system to treat cancer, viral infections, parasitic
 PT infestations and autoimmune diseases.
 XX Claim 4; Page 38-39; 58pp; English.
 XX This is the wild-type Staphylococcus enterotoxin SEE superantigen. This
 CC SEE superantigen can be modified to be used in a novel conjugate. The
 CC novel conjugate comprises a target seeking moiety and a modified wild
 CC type superantigen. The modified superantigen retains its ability to
 CC activate a subset of T cells, even though 1 or more wild-type amino acid
 CC residues in at least 1 region which functions in determining binding to T
 CC cell receptor (TCR) and activation of a subset of T cells has/have been
 CC replaced. Such a modified superantigen can optionally be used as part of
 CC a conjugate with a target seeking moiety, for activating the immune
 CC system to treat a mammalian disease. A pharmaceutical composition can be
 CC prepared comprising a modified antibody (preferably a Fab fragment fused
 CC to a peptide moiety providing activation of T cells in Vbeta specific
 CC manner) in which cysteines providing for interchain cysteine linkages in
 CC the native antibody have been replaced (preferably by serine residues) to
 CC prohibit cysteine formation. The modified wild-type superantigen is used
 CC for treating cancer, viral infections, parasitic infestations and
 CC autoimmune disease. The modified wild type superantigen has a lower
 CC immunogenicity and reactivity with neutralising antibodies and has fewer
 CC side-effects when used as a drug, compared to wild type superantigen
 XX Sequence 245 AA;
 SQ Query Match 31.0%; Score 1091; DB 2; Length 245;
 Best Local Similarity 85.3%; Pred. No. 3.9e-57;
 Matches 209; Conservative 9; Mismatches 15; Indels 12; Gaps 1;
 QY 226 SEKSEINEKDLRKSELOGTALGNLQIYYNKAITSSEKSDQFLTNLLFKGFTG 285
 DB 1 SEKSEINEKDLRKSELOGTALGNLQIYYNKAITSSEKSDQFLTNLLFKGFTG 60
 QY 286 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGTGNKTAACMYGGVTLHDNNRLT 345
 DB 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTAACMYGGVTLHDNNRLT 120

QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHVLHGKFGLYNSDSFGGKVQ 405
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHVLHGKFGLYNSDSFGGKVQ 180
QY 406 RGLIVFHSSEGSTVSYDLFDAGQGYPTDILLRIYRDNT-----TISTSLISL 453
Db 181 RGLIVFHSSEGSTVSYDLFDAGQGYPTDILLRIYRDNTINSENHLIDLYTINSENHLID 240
QY 454 YLYTT 458
Db 241 YLYTT 245
RESULT 12
ABU79072
ID ABU79072 standard; protein; 248 AA.
XX AC ABU79072;
XX DT 18-JUN-2003 (first entry)
XX DE S. aureus SEE (staphylococcus enterotoxin E) protein.
XX KW Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis;
XX KW gene therapy; mammalian cell receptor; tumour associated lipid; anergy;
XX KW T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;
XX KW APC; antitumour.
XX OS Staphylococcus aureus.
XX PN US2002177551-A1.
XX PD 28-NOV-2002.
XX PF 30-MAY-2001; 2001US-00870759.
XX PR 31-MAY-2000; 2000US-0208128P.
XX PA (TERM/) Terman D S.
XX PI Terman DS;
XX DR WPI; 2003-361759/34.
XX DR N-PSDB; ACA64698.
XX PT A mammalian cell receptor, useful in the treatment of cancer by binding
XX PT to tumour associated lipids where the binding induces anergy or apoptosis
XX PS in T cells and antigen presenting cells.
XX PS Disclosure; Page; 167pp; English.

CC population ex vivo in a mammal (by allowing a tumour associated lipid to
CC contact APCs, in which receptors for the tumour associated lipids are
CC inactivated or deleted to produce a tumouricidally activated population,
CC and administering APCs to the host), producing a tumouricidal T cell
CC population ex vivo in a mammal) by allowing a tumour associated lipids to
CC contact T cells in which adaptor proteins, which inhibit T cell
CC activation by tumour associated antigens, are deleted or functionally
CC deactivated to produce a tumouricidal population of T cells, and
CC administering the tumouricidally activated T cells to the host, or
CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
CC administering the tumouricidally activated T cells to the host), treating
CC (M5) cancer in a mammal (by administering a lipid binding molecule which
CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
CC a tumouricidal T cell population in vivo in a mammal (by allowing a
CC tumour associated antigen to contact immunocytes in which adaptor
CC proteins which inhibit T cell activation by tumour associated antigens
CC are deleted or functionally deactivated) and producing (M7) a
CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
CC receptors, methods and compositions are useful for treating cancers and
CC tumours. Bacterial superantigens are co-administered or administered as
CC fusion constructs with anti-tumour proteins or motifs. The present
CC sequence represents a bacterial superantigen protein (e.g. a
CC staphylococcal enterotoxin). Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format from the US patent office website at
CC "seqdata.uspto.gov/sequence.html?DocID=20020177551"
XX
SQ Sequence 248 AA;
Query Match 30.4%; Score 1072; DB 6; Length 248;
Best Local Similarity 90.2%; Pred. No. 5.3e-56;
Matches 202; Conservative 9; Mismatches 13; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKSAQDPLTWLFLKGFPTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKSAQDPLTWLFLKGFPTG 84
QY 286 HPWYNDLLVLDLGTATSEYEGSSVDLYGAYGYQACAGTPTNCTACMYGGVTLHDNNRLT 345
Db 85 HPWYNDLLVLDLGTATSEYEGSSVDLYGAYGYQACAGTPTNCTACMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHVLHGKFGLYNSDSFGGKVQ 405
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHVLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSYDLFDAGQGYPTDILLRIYRDNTTISTSL 449
Db 205 RGLIVFHSSEGSTVSYDLFDAGQGYPTDILLRIYRDNTTISTSL 248
RESULT 13
AAB83838
ID AAB83838 standard; protein; 592 AA.
XX AC AAB83838;
XX DT 23-JUL-2001 (first entry)
XX DE Amino acid sequence of an Ig-5T4 fusion protein.
XX KW Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
XX KW hypersensitivity; autoimmune disease; central nervous system disorder;
XX KW Parkinson's disease; periodontal disease; cardiopulmonary disease;
XX KW cardiovascular disease; gastrointestinal disorder; infection; diabetes;
XX KW Helicobacter-related disease; immune disorder.
XX OS Synthetic.
XX OS Mus sp.
XX FH Key Location/Qualifiers
XX FT Misc-difference 503
XX FT /note= "Met encoded by CTG"

XX FN WO200136486-A2.
XX PD 25-MAY-2001.
XX PF 13-NOV-2000; 2000WO-GB004317.
XX PR 18-NOV-1999; 99WO-GB003859.
XX PR 15-FEB-2000; 2000GB-00003527.
XX PR 02-MAR-2000; 2000GB-00005071.
XX PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX PI Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;
XX PI Myers KA;
XX DR WPI; 2001-343805/36.
XX DR N-PSDB; AAF89733.
XX PT Use of single chain antibody capable of recognizing a disease associated
XX PT molecule for manufacturing a medicament for preventing and/or treating a
XX PT disease condition associated with disease associated molecule.
XX PS Disclosure; Fig 6; 118pp; English.
XX XX The specification describes the use of a single chain antibody (ScFv),
XX CC which is capable of recognizing a disease associated molecule in the
XX CC manufacture of a medicament for the prevention and treatment of a disease
XX CC condition. The ScFv antibody is useful in the manufacture of a
XX CC medicament, for affecting a disease in vivo, for preparing a
XX CC pharmaceutical composition, for in vivo imaging and/or for adjuvant
XX CC treatment of a disease. The ScFv antibody is also useful for treating
XX CC inflammatory diseases including arthritis, hypersensitivity, autoimmune
XX CC diseases, cancers, central nervous system disorders including Parkinson's
XX CC disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
XX CC diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
XX CC related diseases, and other immune disorders. The present sequence
XX CC represents an Ig-5T4 fusion protein
XX SQ Sequence 592 AA;

Query Match 30.4%; Score 1069; DB 4; Length 592;
Best Local Similarity 37.9%; Pred. No. 2.3e-55;
Matches 254; Conservative 20; Mismatches 60; Indels 336; Gaps 9;
1 EVQLQQSGPDLVKPCASVKISKASGYSFTGYMHWKQSPGKLEWIGRINPNNGVTLY 60
20 EVQLQQSGPDLVKPCASVKISKASGYSFTGYMHWKQSPGKLEWIGRINPNNGVTLY 79
61 NQKFKDKATLVDSSTAYVELSLTSEDSAVVYCARSTMTNYMDYWGQVTSVTS 120
80 NQKFKDKATLVDSSTAYVELSLTSEDSAVVYCARSTMTNYMDYWGQVTSVTS- 138
121 AKTTPSPVYPLAPGSAQTNSMTLGLVKGYFPEPTVTWNSGSLSGVHTFPAVLQSD 180
139 ----- 138
181 LYTLSSTVTPSSWTPSETVTCNVAHPASSTYKVDKKIVPRDSGSPSEKSEINEKLRKK 240
139 -----SGG----- 141
241 SELQGTALGNLKIYYNKAITSSEKSAQDQFLNTLLFKGFTGHPWYNDLLVDLGSTA 300
142 ----- 141
301 ATSEYEGSVLDYGYGYGQAGGTPNKTACWYGGVTLHDNNRLTEBKVPIINLWIDGKQ 360
142 -----GGSGGGGT-----GG----- 151
361 TVVPIDKVTSSKVEVVELDLQARHYLHGKFLGSLYNSDSFGKVQGRGLIVPHSSEGSTVS 420
152 -----GG----- 153

QY 421 YDLFDAQGGYPTDLLRIYRDNTTISSTLSISLYLYTTIWMQTPTSLVLSAGDRTVIT 480
DB 154 -----SSIVMTQTPTFLVLSAGDRTVIT 176
QY 481 CKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDRPFGSGYGTDTFTLTSSVQAE 540
DB 177 CKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDRPFGSGYGTDTFTLTSSVQAE 236
QY 541 AAVYECQDYNPPFTFGGKLEIKRADA-APTYSIRPPSEQLTSGGASVVCFLNNFYP 599
DB 237 LAVYECQDYNPPFTFGGKLEIKRADA-APTYSIRPPSEQLTSGGASVVCFLNNFYP 296
QY 600 KDINYKWK-----IDGSEKQNGVNSWTDQDSKSTYSMSSTLTLTKEYERHNSYTCAT 655
DB 297 EPTVTSWNSGALTSVHTFPAVLQS-----SGLYSLSSVTVTPSSSLGT-QTYICNVN 348
QY 656 HKTSTSPVK 665
DB 349 HKPSNTRKVDK 358
RESULT 14
AAW86003
ID AAW86003 standard; protein; 595 AA.
XX AC AAW86003;
XX DT 15-MAR-1999 (first entry)
XX DE Anti-5T4 single chain antibody 5T4Sabl.
XX KW Tumour interacting protein; cancer; gene therapy; vector; 5T4 antigen;
XX KW monoclonal antibody; single chain antibody; mouse; human; 5T4Sabl.
XX OS Mus sp.
XX OS Homo sapiens.
XX OS Synthetic.
XX OS Chimeric.
XX PN MO9855607-A2.
XX PD 10-DEC-1998.
XX PF 04-JUN-1998; 98WO-GB001627.
XX PR 04-JUN-1997; 97GB-00011579.
XX PR 20-JUN-1997; 97GB-00013150.
XX PR 04-JUL-1997; 97GB-00014230.
XX PA (OXFO-) OXFORD BIOMEDICA UK LTD.
XX PI Kingsman SM, Bebbington CR, Ellard FM, Carroll MW, Myers KA;
XX DR WPI; 1999-059910/05.
XX DR N-PSDB; AAW80291.
XX PT New vector encoding a tumour interacting protein for treating cancer -
XX PT contains a desired nucleotide sequence and/or protein which recognises
XX PT tumours, and is used as a gene delivery system to treat cancer.
XX PS Example 1; Fig 1B; 82pp; English.
XX XX This is the amino acid sequence of a single chain antibody (Sabl), termed
XX CC 5T4Sabl, comprising an scFv derived from murine monoclonal antibody 5T4
XX CC (see AAW86002) and the human gi constant region. cDNA (see AAW80291),
XX CC encoding the Sabl has been inserted into vector pCineo to allow expression
XX CC in mammalian cells. The trophoblast cell surface antigen defined by 5T4
XX CC is expressed at high levels on the cells of a wide variety of human
XX CC tumours. The invention relates to a vector comprising a nucleotide
XX CC sequence coding for a tumour interacting protein (TIP) and optionally a
XX CC nucleotide sequence of interest (NOI) which encodes a protein of interest
XX CC (POI), the vector being capable of delivering the NOI and/or POI to the
XX CC tumour recognised by the TIP. Delivery can be in vivo or ex vivo. The

Db 298 --DVEVHTAQTPREEQNSTFRSVSELPIMHQDLNGKEFKCRVNSAAPPAPIEK----- 351
Qy 411 FHSSEGSTSVYDLFDAQGYPTLLRIYRDNVTTSSTLSISLYLTVTTSIVMTQTPTSL 470
Db 352 -----TISK----- 356
Qy 471 VSAGRVITCKASQSVNSDVAMTQQKPGQSKLLISYTSRAGVDPDRSGSGYGTDF 530
Db 357 ----- 356
Qy 531 LTISVQAEDAAYVFCQDYNSPTFGGKLEIKRADAAPTVSIPPPSEQLTSGASV 590
Db 357 -----KGRPKAPQVYTPPPKEQAKKVS 382
Qy 591 VCFLNFPKIDINVKWIDGSRQGVNSWTDODSKDSTYSMSSTLTTLTKDYERHNSY 650
Db 383 TCMITDFFPEDITVEWQWNGQPAEN-YKNTQPIMDT-DGSYFVYVKLVNQSKEAGNTF 440
Qy 651 TCEATHK 657
Db 441 TCSVLHE 447

RESULT 16
AAR76085
ID AAR76085 standard; peptide; 445 AA.
XX AC AAR76085;
XX KW Antigen binding structure; complementarity determining region; CDR;
XX KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;
XX KW monoclonal antibody; Mab; immunotherapy; therapy; diagnosis;
XX KW transgenic animal; transgenic plant; antibody engineering;
XX KW humanized antibody; immunotoxin.
XX OS Mus sp.
XX FN W09515382-A1.
XX PD 08-JUN-1995.
XX PF 29-NOV-1994; 94WO-GB002610.
XX PR 03-DEC-1993; 93GB-00024819.
XX PR 03-JUN-1994; 94GB-00011089.
XX PA (ZENE) ZENECA LTD.
XX PI Rose MS, Boot C, Copley CG, Paterson DS, Hall SM, Wright AF;
XX PI Blakey DC;
XX DR WPI; 1995-215262/28.
XX PT Antigen binding structures containing CDR's recognising the CA55.1
XX PT antigen - produced by hybridomas and host cells, for use in the diagnosis
XX PT and therapy of cancer.
XX PS Claim 3; Page 97-98; 121pp; English.
XX CC An antigen binding structure is based on the CDRs (given in AAR76078- 84)
XX CC of the heavy (AAR76085) and light (AAR76086) chains of Mab 55.1 (SCACC
XX CC 93051901), which recognises the colorectal tumor-associated antigen
XX CC CA55.1. It is optionally humanized and in the form F(ab')2, F(ab)', Fab,
XX CC Fv, scFv or V-min, and is produced in transgenic animals or plants.
XX CC (Updated on 25-MAR-2003 to correct FN field.)
XX SQ Sequence 445 AA;

Query Match 30.0%; Score 1055.5; DB 2; Length 445;
Best Local Similarity 37.5%; Pred. No. 1e-54;
Matches 250; Conservative 60; Mismatches 108; Indels 249; Gaps 14;

Qy 1 EYLOQSGPDLVKPGASVKISKASGYSFTGYGMHVKQSPKGLWIGRINPNNGVTLY 60
Db 1 QVLOQPGAEVLKPGASVQLSCASGYFTGYGMHVKQSPKGLWIGRINPNNGVTLY 60

Qy 61 NOKFKDKATLTVDKSTTAYMELSLRSLSEDSAVYCARSTMI-TNYMDYKQCGTSTVTS 119
Db 61 NEKFENKATLTVDKSTTAYMQLSLRSLSEDSAVYCARERAYGYDDADMDYKQCGTSTVTS 120

Qy 120 SAKTTPPSVPLAPGSAQAQTNMTVTLGCLVKGYPEPVTVTWNSGSLSSGVTTPAVLQS 179
Db 121 SAKTTPPSVPLAPGSAQAQTNMTVTLGCLVKGYPEPVTVTWNSGSLSSGVTTPAVLQS 180

Qy 180 DLYTLSSSVTPSSWTPSETVTCNVHPASSTKVDKTIIVPRDSGSPSEKSEINEKDLRK 239
Db 181 DLYTLSSSVTPSSWTPSETVTCNVHPASSTKVDKTIIVPRDCG----- 224

Qy 240 KSELQGTALGNLKQIYYNNSKAITSSSEKSAQDFLNTLLFKGFFTGHPWYNDLLVDLGS 299
Db 225 -CKPCITVPEVSVVIFPPK-----PKDVLITLL----- 253

Qy 300 AATSEYEGSSVDLYGAYYGYCAGGTPNKTACTMYGGVTLHDNNRLTEKKYVINLWIDGK 359
Db 254 -----TP-KVTCVVVDIS-----KDDPEVQFSWFD-- 278

Qy 360 QTTVPIDKVTSKKEV-----TVQELDLQARHVLHGK-FGL-YNSDSFGKQVORGLIV 410
Db 279 --DVEVHTAQTPREEQNSTFRSVSELPIMHQDLNGKEFKCRVNSAAPPAPIEK----- 332

Qy 411 FHSSEGSTSVYDLFDAQGYPTLLRIYRDNVTTSSTLSISLYLTVTTSIVMTQTPTSL 470
Db 333 -----TISK----- 337

Qy 471 VSAGRVITCKASQSVNSDVAMTQQKPGQSKLLISYTSRAGVDPDRSGSGYGTDF 530
Db 338 ----- 337

Qy 531 LTISVQAEDAAYVFCQDYNSPTFGGKLEIKRADAAPTVSIPPPSEQLTSGASV 590
Db 338 -----KGRPKAPQVYTPPPKEQAKKVS 363

Qy 591 VCFLNFPKIDINVKWIDGSRQGVNSWTDODSKDSTYSMSSTLTTLTKDYERHNSY 650
Db 364 TCMITDFFPEDITVEWQWNGQPAEN-YKNTQPIMDT-DGSYFVYVKLVNQSKEAGNTF 421

Qy 651 TCEATHK 657
Db 422 TCSVLHE 428

RESULT 17
AAR45012
ID AAR45012 standard; protein; 230 AA.
XX AC AAR45012;
XX XX
XX XX
XX XX 25-MAR-2003 (revised)
XX XX 08-JUN-1994 (first entry)
XX XX
XX DE Staphylococcal enterotoxin SEE.
XX XX
XX KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
XX KW autoimmune disease; toxicity; Protein A; perfusion system.
XX XX
XX OS Staphylococcus aureus.
XX XX
XX XX Location/Qualifiers
XX FT Misc-difference 120
XX FT /note= "Given in the specification as J, no further
XX FT details given"

FT Misc-difference 121 /note= "Given in the specification as J, no further
 FT details given"
 FT Misc-difference 123 /note= "Given in the specification as O, no further
 FT details given"
 FT Misc-difference 124 /note= "Given in the specification as U, no further
 FT details given"
 FT Misc-difference 125 /note= "Given in the specification as V, no further
 FT details given"
 PN WO9324136-A1.
 XX
 XX 09-DEC-1993.
 XX
 XX 01-JUN-1993; 93WO-US005213.
 XX
 XX 01-JUN-1992; 92US-00891718.
 XX
 XX (TERM/) Terman D S.
 PA (STON/) STONE J L.
 XX
 XX Terman DS, Stone JL;
 PI
 XX
 XX WPI; 1993-405418/50.
 DR
 XX
 XX Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
 PT in a patient or for the treatment of auto-immune diseases.
 FT
 XX
 XX Disclosure; Fig 1; 90pp; English.
 PS
 XX
 XX The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer in
 CC a patient. These SEs, and homologues of them, can be used as tumouricidal
 CC agents for treating cancers and autoimmune disease. They exhibit
 CC tumouricidal activity and toxicity identical to that observed for the
 CC Protein A perfusion system. They may be administered by i.v. injection.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 CC
 XX Sequence 230 AA;
 SQ
 Query Match 29.8%; Score 1048; DB 2; Length 230;
 Best Local Similarity 85.7%; Pred. No. 1.3e-54;
 Matches 197; Conservative 12; Mismatches 21; Indels 0; Gaps 0;
 QY 229 SEINEKDLRKKELOGLTALGNLQIYYNKAITSSEKSAQOFLNTLLFKGFTGHPW 288
 Db 1 SEINEKDLRKKELOGLTALGNLQIYYNKAITSSEKSAQOFLNTLLFKGFTGHPW 60
 QY 289 YNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNRITTEK 348
 Db 61 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNRITTEK 120
 QY 349 KVPINLWIDGKQTVPIDKVTSKKEVTVQELDLQARHLYHGKFGLYNSDSFGKVGQGL 408
 Db 121 XVXXBKWDGKQTVPIDKVTSKKEVTVQELDLQARHLYHGKFGLYNSDSFGKVGQGL 180
 QY 409 IVFHSSEGSVSYDLFDAQOQYPTLLIRYRDNNTTSSLSLSLYTT 458
 Db 181 IVFHSSEGSVSYDLFDAQOQYPTLLIRYRDNNTTSSLSLSLYTT 230
 RESULT 18
 ABB76235
 ID ABB76235 standard; protein; 230 AA.
 XX
 XX ABB76235;
 AC
 XX
 XX 09-AUG-2002 (first entry)
 DT
 XX
 XX Staphylococcus aureus enterotoxin E.
 DE
 XX
 XX Enterotoxin E; SEE; superantigen; antigen; tumour; cancer; antitumour;
 KW therapy.

XX Staphylococcus aureus.
 OS
 XX
 XX Key Location/Qualifiers
 PH Misc-difference 120 /note= "given as 'J' in the specification"
 FT Misc-difference 121 /note= "given as 'J' in the specification"
 FT Misc-difference 123 /note= "given as 'O' in the specification"
 FT Misc-difference 124 /note= "given as 'U' in the specification"
 FT Misc-difference 125 /note= "given as 'V' in the specification"
 FT
 XX US2002051765-A1.
 PN
 XX 02-MAY-2002.
 PD
 XX 19-DEC-2000; 2000US-00741503.
 PF
 XX 03-OCT-1989; 89US-00416530.
 PR 17-JAN-1990; 90US-00466577.
 PR 17-JAN-1991; 91WO-US000342.
 PR 01-JUN-1992; 92US-00891718.
 PR 02-MAR-1993; 93US-00025144.
 PR 31-JAN-1994; 94US-00189424.
 PR 19-JUN-1995; 95US-00491746.
 XX
 XX (TERM/) Terman D S.
 PA
 XX Terman DS;
 PI
 XX WPI; 2002-415198/44.
 DR
 XX Reagent for treating cancer without the need for e.g. radiotherapy,
 PT comprises a specific V beta subset of T cells sensitized to a growing
 PT tumor and stimulated with superantigens.
 PT
 XX Disclosure; Fig 2; 17pp; English.
 PS
 XX The present sequence is the protein sequence of enterotoxin E (SEE) of
 CC Staphylococcus aureus. Similarity is shown, in several stretches of
 CC sequence, between staphylococcal enterotoxins, streptococcal pyrogenic
 CC exotoxins and staphylococcal exfoliative toxins (see AB376234-44). In the
 CC present invention, synthetic polypeptides useful in tumour therapy and in
 CC blocking or destroying autoreactive T and B lymphocyte populations are
 CC characterised by substantial structural homology to staphylococcal
 CC enterotoxin A and enterotoxin B, and to streptococcal pyrogenic
 CC exotoxins, with statistically significant sequence homology and
 CC similarity (Z value of Lipman and Pearson algorithm in Monte Carlo
 CC analysis exceeding 6) to include alignment of cysteine residues and
 CC similar hydropathy profiles. These superantigens are used to treat solid
 CC tumours, including their metastases, without radiation, surgery or
 CC standard chemotherapeutic agents. A claimed method of human cancer
 CC treatment involves contacting haematopoietic cells from a patient with
 CC one or more superantigens ex vivo to generate stimulated cells, selecting
 CC a specific V beta subset of cells, and reintroducing these cells into the
 CC patient to induce an in vivo therapeutic, tumouricidal reaction
 XX
 XX Sequence 230 AA;
 SQ
 Query Match 29.6%; Score 1044; DB 5; Length 230;
 Best Local Similarity 85.7%; Pred. No. 2.3e-54;
 Matches 197; Conservative 11; Mismatches 22; Indels 0; Gaps 0;
 QY 229 SEINEKDLRKKELOGLTALGNLQIYYNKAITSSEKSAQOFLNTLLFKGFTGHPW 288
 Db 1 SEINEKDLRKKELOGLTALGNLQIYYNKAITSSEKSAQOFLNTLLFKGFTGHPW 60
 QY 289 YNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNRITTEK 348
 Db 61 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNRITTEK 120

QY 349 KVPINLWIDGKQTTVPIDKVKTSKKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQVQGL 408
DB 121 XVXXKKWIDGKQTTVPIDKVKTSKKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQVQGL 180
QY 409 IVFHSSEGSTVSYDLFDAQGQVPTLLRIYRDNKTINSNNHIDIYLYTT 458
DB 181 IVFHSSEGSTVSYDLFDAQGQVPTLLRIYRDNKTINSNNHIDIYLYTT 230

RESULT 19
AAR13204
ID AAR13204 standard; protein; 230 AA.
AC AAR13204;
DT 15-OCT-1991 (first entry)
DE Staphylococcal enterotoxin E.
KW SEE; cancer treatment; pyrogen; tumouricide.
XX Staphylococcus aureus.
OS Staphylococcus aureus.
PN WO9110680-A.
PD 25-JUL-1991.
PF 17-JAN-1990; 90US-00466577.
PR 17-JAN-1990; 90US-00466577.
XX (TERM/) Terman D S.
PA Terman DS;
PI WPI; 1991-237984/32.
DR
XX Treating cancer with enterotoxin from Staphylococcus aureus -
PT administered by IV injection, having same tumoricidal activity as
PT Staphylococcal protein A without potential toxic reactions.
XX
PS Disclosure; Fig 1; 74pp; English.
XX
CC SEE was isolated and purified from S.aureus. It can be used for treating
CC cancer, activating cytokine mediators and procoagulant systems,
CC augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be
CC administered intravenously, optionally with ibuprofen to attenuate toxic
CC reaction to SEE. Synthetic polypeptides having structural homology to
CC Staphylococcal exotoxins are claimed, provided the homology includes
CC statistically significant sequence homology, alignment of Cysteine
CC residues and similar hydropathy profiles. See AAR13203-R13211
XX
SQ Sequence 230 AA;
Query Match 29.4%; Score 1035; DB 2; Length 230;
Best Local Similarity 84.3%; Pred. No. 7,7e-54;
Matches 194; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 229 SEINEKDLRKXSELOGTALGNLKOIYYNYSKATTSSEKSDQFLTWLFLKGFPTGHPW 288
DB 1 SEINEKDLRKXSELOGTALGNLKOIYYNYSKATTSSEKSDQFLTWLFLKGFPTGHPW 60
QY 289 YNDLIVDVGSTAAATSEYEGSSVDLYGAYGVCAGGTPNKTACMYGGVTLHDNNRLTEEX 348
DB 61 YNDLIVDVGSKDANKYKGVLDLYGAYGVCAGGTPNKTACMYGGVTLHDNNRLTEEX 120
QY 349 KVPINLWIDGKQTTVPIDKVKTSKKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQVQGL 408
DB 121 XVXXKKWIDGKQTTVPIDKVKTSKKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQVQGL 180
QY 409 IVFHSSEGSTVSYDLFDAQGQVPTLLRIYRDNKTINSNNHIDIYLYTT 458
DB 181 IVFHSSEGSTVSYDLFDAQGQVPTLLRIYRDNKTINSNNHIDIYLYTT 230

DB 181 IVFHSSEGSTVSYDLFDAQGQVPTLLRIYRDNKTINSNNHIDIYLYTT 230

RESULT 20
AAE18377
ID AAE18377 standard; protein; 597 AA.
XX AAE18377;
AC AAE18377;
DT 07-MAY-2002 (first entry)
XX
DE Human N-terminal DAV-1 heavy chain-mature TNF-alpha fusion protein.
XX
KW Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer;
KW vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder;
KW hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain;
KW cytotstatic; vasotropic; ophthalmological; tumour necrosis factor-alpha;
KW TNF-alpha; fusion protein.
XX
OS Homo sapiens.
OS Synthetic.
OS Chimeric.
XX
XX Key Location/Qualifiers
FT Region 1..439
FT /note= "N-terminal portion of DAV-1 heavy chain"
FT Region 441..597
FT /note= "Human mature TNF-alpha"
XX
PN WO200204522-A2.
XX
PD 17-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-BP007878.
XX
PR 10-JUL-2000; 2000US-00613017.
XX
XX (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PA (SCRI) SCRIPS RES INST.
XX
PI Nemerow GR, Li E;
XX
XX WPI; 2002-171707/22.
XX
XX New bifunctional molecules comprising an antibody or its antigen-binding
XX portion, and a targeting agent, useful for e.g. gene therapy, or for
XX promoting Adenoviral vector-mediated gene delivery to cells lacking av
XX integrins.
XX
PS Claim 15; Page 98-99; 106pp; English.
XX
CC The present invention relates to a bifunctional molecule comprising an
CC antibody or its antigen-binding portion, and a targeting agent where the
CC antibody specifically binds to an antigen in a protein that binds to av
CC integrin, and the targeting agent specifically binds to a cell surface
CC protein that activates the phosphatidylinositol 3 (PI3K) signalling
CC pathway. The bifunctional molecules are useful for gene therapy, for
CC promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking
CC av integrins, for enhancing Ad binding and internalisation, and in gene
CC delivery of by fibreless adenovirus particles. The bifunctional molecules
CC permit targeting of viral and bacterial vectors to cells that express
CC targeted receptors. Diseases that can be targeted include cancers,
CC vascular disorders, diabetic retinopathies, restenosis, ophthalmic
CC disorders, hyperproliferative disorders, and hormonal disorders. The
CC present sequence is human N-terminal DAV-1 heavy chain-mature tumour
CC necrosis factor-alpha (TNF-alpha) fusion protein which is used in the
XX invention
XX
SQ Sequence 597 AA;
Query Match 29.2%; Score 1028; DB 5; Length 597;
Best Local Similarity 37.2%; Pred. No. 6.4e-53;

```
Matches 253; Conservative 53; Mismatches 115; Indels 260; Gaps 15;
QY 1 EVQLQSGPDLVKPGASVKISKASGYSTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60
Db 20 EVQLQSGPELVKPGASVKISKASGYSTGYMHVWKQSHGKSLWIGIYIYPYKGGTGY 79
QY 61 NQKFKDKATLTVDKSTTAYMELSLTSDSAVYICARSTMTITNYVMDYWGOGTSVTYSS 120
Db 80 NQKFKSKATLTVDSSNTAYMELSLTSDSAVYICARG-----IAYWGGTGLVTVA 132
QY 121 AKTTPPSVYPLAPGSAATNSMTLGLVKGYFPEPVTVTWNSGSLSSGVHTFPVAVLQSD 180
Db 133 AKTTPPSVYPLAPGSAATNSMTLGLVKGYFPEPVTVTWNSGSLSSGVHTFPVAVLQSD 192
QY 181 LYTLSSSVTPSPSTWPESETVTCNVAPASSTKVDKIVPRDSDGSGPSEKSEINEKDLRKK 240
Db 193 LYTLSSSVTPSPSTWPESETVTCNVAPASSTKVDKIVPRDCG-----KDDPEVQFSWFVD 235
QY 241 SELQGTALGNLKOIYYNKAITSSEKSAQDFLTNTLLFKGFTGHPWYNDLLVDLGSTA 300
Db 236 CKPICITVPEVSSVFIIPPCK-----PKDVLITL-----IAYWGGTGLVTVA 264
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNRLTEEEKVPIINLWIDGKQ 360
Db 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--- 289
QY 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVQGLIVF 411
Db 290 -DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLNGKEFKCRVNSAAPPAPIEK----- 343
QY 412 HSSEGSTVSYDLFDAGQYPTDLLRIYRDNMTTISSTLSISLYLYTTSIVMTQTPTSLLV 471
Db 344 -----TISK----- 348
QY 472 SAGDRVTITCKASQSVNDVAVYQKPGQPKLLISYTSRRVAGVYDRFSGSGYGTDFTL 531
Db 349 ----- 348
QY 532 TISSVQAEAAVYFCQDYNSPTTGGGTKLEIKRADAAPTYSIIPPSSEQTSGGASVV 591
Db 349 -----KGRPKAPQVYVTPPPKQMAKDKVSLT 375
QY 592 CFLNRPYKDNVWKIDGSRQNGVLNWTQDQSKDSTYSMSSTLTLTCKDYERHNSYT 651
Db 376 CMITDFPEDITVEWOMQPAEN-YKNTQPMDT-DGSYFYVSKLVNQKSNWEAGNTFI 433
QY 652 CEATHKTSPIVKSFNRES 672
Db 434 CSVLHE-----FVRSSTRTPS 449

RESULT 21
ABG76352
ID ABG76352 standard; protein; 597 AA.
XX
AC ABG76352;
XX
DT 23-OCT-2003 (revised)
DT 10-MAY-2003 (first entry)
DE
DE Mouse DAV-1 heavy chain-mature human TNF-alpha fusion protein.
XX
XX Human; bifunctional molecule; antigen-binding portion; alpha integrin;
XX cell surface protein; phosphatidylinositol-3-OH kinase, PI3K;
XX signalling pathway; targeted gene therapy; delivery vector;
XX adenoviral gene delivery particle; viral infection; cancer;
XX rheumatoid arthritis; cardiovascular disorder; diabetic retinopathy;
XX restenosis; ophthalmic disorder; hyperproliferative disorder;
XX hormonal disorder; varicicide; antiinflammatory; antirheumatic;
XX antiarthritic; ophthalmological; DAV-1 antibody heavy chain; TNF-alpha;
XX tumour necrosis factor-alpha; mouse.
XX
XX Homo sapiens.
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OS Mus sp.
OS Chimeric.
XX US2002164333-A1.
XX
XX PD 07-NOV-2002.
XX
XX PF 10-JUL-2001; 2001US-00903327.
XX
XX PR 10-JUL-2000; 2000US-00613017.
XX
XX PR 10-JUL-2000; 2000US-0325781P.
XX
XX PA (SCRI ) SCRIPPS RES INST.
XX
XX PI Nemerow GR, Li E;
XX
XX DR WPI; 2002-171707/22.
XX
XX PT New bifunctional molecules comprising an antibody or its antigen-binding
XX PT portion, and a targeting agent, useful for e.g. gene therapy, or for
XX PT promoting Adenoviral vector-mediated gene delivery to cells lacking av
XX PT integrins.
XX
XX PS Example 2; Page 38-39; 49pp; English.
XX
XX CC The present invention relates to a bifunctional molecule comprising an
XX CC antibody or its antigen-binding portion, and a targeting agent. The
XX CC antibody specifically binds to an antigen in a protein that binds to
XX CC alpha integrin, and the targeting agent specifically binds to a cell
XX CC surface protein that activates the phosphatidylinositol-3-OH kinase
XX CC (PI3K) signalling pathway. The bifunctional molecules are useful for
XX CC targeted gene therapy using targeting delivery vectors, such as
XX CC adenoviral gene delivery particles. The bifunctional molecules are useful
XX CC for treating viral infections, rheumatoid arthritis, cancers,
XX CC cardiovascular disorders, diabetic retinopathies, restenosis, ophthalmic
XX CC disorders, hyperproliferative disorders, and hormonal disorders. The
XX CC present sequence represents a fusion protein with mouse DAV-1 antibody
XX CC heavy chain. (Updated on 23-OCT-2003 to standardise OS field)
XX
XX SQ Sequence 597 AA;

Query Match 29, 28; Score 1028; DB 5; Length 597;
Best Local Similarity 37.2%; Pred. No. 6.4e-53;
Matches 253; Conservative 53; Mismatches 115; Indels 260; Gaps 15;
QY 1 EVQLQSGPDLVKPGASVKISKASGYSTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60
Db 20 EVQLQSGPELVKPGASVKISKASGYSTGYMHVWKQSHGKSLWIGIYIYPYKGGTGY 79
QY 61 NQKFKDKATLTVDKSTTAYMELSLTSDSAVYICARSTMTITNYVMDYWGOGTSVTYSS 120
Db 80 NQKFKSKATLTVDSSNTAYMELSLTSDSAVYICARG-----IAYWGGTGLVTVA 132
QY 121 AKTTPPSVYPLAPGSAATNSMTLGLVKGYFPEPVTVTWNSGSLSSGVHTFPVAVLQSD 180
Db 133 AKTTPPSVYPLAPGSAATNSMTLGLVKGYFPEPVTVTWNSGSLSSGVHTFPVAVLQSD 192
QY 181 LYTLSSSVTPSPSTWPESETVTCNVAPASSTKVDKIVPRDSDGSGPSEKSEINEKDLRKK 240
Db 193 LYTLSSSVTPSPSTWPESETVTCNVAPASSTKVDKIVPRDCG-----KDDPEVQFSWFVD 235
QY 241 SELQGTALGNLKOIYYNKAITSSEKSAQDFLTNTLLFKGFTGHPWYNDLLVDLGSTA 300
Db 236 CKPICITVPEVSSVFIIPPCK-----PKDVLITL----- 264
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKATCMYGGVTLHDNRLTEEEKVPIINLWIDGKQ 360
Db 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--- 289
QY 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVQGLIVF 411
Db 290 -DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLNGKEFKCRVNSAAPPAPIEK----- 343
```

QY 412 HSEGSTVSYDLFDAQGYPTLLRIYRDNNTTISSTLSLSLYLYTTSIVMTQPTSLV 471
 Db 344 -----TISK----- 348
 QY 472 SAGDRVTITCKASQSVNDVAWYQKQKQSPKLLISYTSRYAGVDPFRPSGSGVGTDFTL 531
 Db 349 ----- 348
 QY 532 TISSVQAEAAVFCQDYNPPTFGGKLEIKRADAAPTISFPSSSGLTSGGASVV 591
 Db 349 -----XGRKAPQVYTIPTPKQMAKDKVSLT 375
 QY 592 CFLNNFYKIDINVKWIDGSRQNGVLSWTDQSKSTYSMSSTLTLYTDEVERHNSYT 651
 Db 376 CMITDFPFDITVBMQNGQPAEN-YKNTQPIMDT-DGSYFVYSKLVNQKSNWEAGNTFI 433
 QY 652 CEATHKTSPIVSFNRNES 672
 Db 434 CSVLHE-----FVRSSTRTPS 449
 RESULT 22
 ID AAW83041
 XX AAW83041 standard; protein; 464 AA.
 AC AAW83041;
 DT 25-MAR-2003 (revised)
 DT 15-MAR-1999 (first entry)
 XX
 DE Anti-Fas Mab HFE7A heavy chain.
 KW HFE7A; monoclonal antibody; mouse; Fas; humanised antibody; apoptosis;
 KW HFE7A; autoimmune disease; Hashimoto's disease;
 KW Sjogren syndrome; pernicious anaemia; Addison's disease; scleroderma;
 KW Goodpasture syndrome; Crohn's disease; sterility; rheumatoid arthritis;
 KW autoimmune haemolytic anaemia; myasthenia gravis; multiple sclerosis;
 KW Basedow's disease; thrombopenia purpura; insulin-dependent diabetes;
 KW allergy; atopy; arteriosclerosis; myocardiitis; cardiomyopathy;
 KW glomerular nephritis; hypoplastic anaemia; hepatitis; AIDS;
 KW transplant rejection; therapy; complementarity determining region; CDR.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..19
 FT Protein /label= Sig_peptide
 FT 20..464
 FT Region /label= Mat_protein
 FT 20..140
 FT Region /label= Variable
 FT 50..54
 FT Region /label= CDR H1
 FT /note= "claim 9"
 FT 69..84
 FT Region /label= CDR H2
 FT /note= "claim 9"
 FT 118..128
 FT Region /label= CDR H3
 FT /note= "claim 9"
 FT 141..464
 FT Region /label= Constant
 FT
 XX AU9859701-A.
 PN 08-OCT-1998.
 XX
 PF 30-MAR-1998; 98AU-00059701.
 XX
 PR 01-APR-1997; 97JP-00082953.
 PR 25-JUN-1997; 97JP-00169088.
 PR 08-OCT-1997; 97JP-00276064.

(SANY) SANKYO CO LTD.
 Nobufusa S, Kimihisa I, Jun O, Masahiko O, Hideyuki H, Tohru T;
 Hiroko Y, Akio S, Shin Y;
 WPI: 1998-543440/01.
 N-PSDB; AAV71029.
 New antibodies and proteins bind conserved epitope of Fas antigen - used
 to evaluate drugs in animal models and to treat Fas-associated diseases
 e.g. autoimmune disease, allergy, atopy, arteriosclerosis, myocarditis,
 hepatitis and AIDS.
 Example 4; Page 187-188; 292pp; English.
 This is the amino acid of the heavy chain of murine anti-human Fas
 monoclonal antibody HFE7A. CDNA (see AAV70129) encoding the heavy chain
 was obtained from HFE7A-secreting hybridoma (PERM BP-5828) RNA by RT-PCR
 (see AAV70125-26). The invention provides humanised HFE7A antibodies (see
 AAW83031-37) produced by CDR grafting. These antibodies are capable of
 inducing apoptosis in abnormal cells expressing Fas, and of inhibiting
 Fas-induced apoptosis in normal cells. They are used to evaluate, in
 animal models, treatments of diseases that involve Fas/Fas ligand
 interactions, and also to treat such diseases, including autoimmune
 disease (e.g. systemic lupus erythematosus, Hashimoto's disease, graft
 versus host disease, Sjogren syndrome, pernicious anaemia, Addison's
 disease, scleroderma, Goodpasture syndrome, Crohn's disease, rheumatoid
 arthritis, autoimmune haemolytic anaemia, sterility, myasthenia gravis,
 multiple sclerosis, Basedow's disease, thrombopenia purpura and insulin-
 dependent diabetes), allergies, atopy, arteriosclerosis, myocarditis,
 cardiomyopathy, glomerular nephritis, hypoplastic anaemia, hepatitis,
 AIDS and transplant rejection (all claimed). (Updated on 25-MAR-2003 to
 correct DR field.)
 XX Sequence 464 AA;
 SQ
 Query Match 29.1%; Score 1025.5; DB 2; Length 464;
 Best Local Similarity 36.2%; Pred. No. 6.6e-53;
 Matches 243; Conservative 64; Mismatches 106; Indels 259; Gaps 14;
 QY 1 EYVLOQSGPDLVKPCASVKISKASGYSTGYVYHMKQSPCKGLEWIGRINPNNVTLY 60
 Db 20 QVQLQPGAEELVKPGASVKLSCKASGYTFTSYMMQWVKQKQGLEWIGEDIPDSYNY 79
 QY 61 NQKFKDKATLTVDKSTTAYMELRLTSEDSESAVYVCARS-TMITNYMDYWGQGTSTVTS 119
 Db 80 NQKFKGKATLTVDTSSTAYMQLSSLTSEDSAVYVCARNRDYNNWYFDVWGTTVTVS 139
 QY 120 SAKTTPPSVYPLAPGSAQTNSMTLGLVKGYPPEPTVTWNSGLSSGVTTPAVLQS 179
 Db 140 SAKTTPPSVYPLAPGSAQTNSMTLGLVKGYPPEPTVTWNSGLSSGVTTPAVLQS 199
 QY 180 DLYTLSSSVTPSPSTWPSSTVTCNVHPASSTKVDKIVPRDSGGPSEKSEINEKDLRK 239
 Db 200 DLYTLSSSVTPSPSTWPSSTVTCNVHPASSTKVDKIVPRDCG----- 243
 QY 240 KSELOGTALGNLKOIYYNNSKAITSEKSAQDFLNTLLFKGFFTHGHPWYNDLLVDLGS 299
 Db 244 -CKPCICTVPEVSSVFIPPK-----PKDVLITL----- 272
 QY 300 AATSEYEGSSVDLYGAYGYQCAGGTPNKTKACMYGVTLDHNNRLTEEKVPIINLWDGK 359
 Db 273 -----TP-KVTCVVVDIS-----KDDPEVQFSFVVD-- 297
 QY 360 QTTVPIDKVTSKKEV-----TQEELDLQARHYLHGK-FGL-YNSDSFGKVGQRLIV 410
 Db 298 --DVEVHTAQTQPREEQFNSTFRSVSELPIMHQWNLGKFKCRVNSAFAPIEK----- 351
 QY 411 FHSSEGSTVSYDLFDAQGYPTLLRIYRDNNTTISSTLSLSLYLYTTSIVMTQPTSLV 470
 Db 352 -----TISK----- 356

QY 471 VSAGDRVTITCKASQSVNSDVAMVQKPGQPKLLISYTSRAGYVDPDRFSGSGYGTDT 530
 Db 357 ----- 356
 QY 531 LTSSVQAEADAAVYFCQDYNSPPTFGGPKLEIKRADAAPTIVSIFPPSEQLTSGGASV 590
 Db 357 ----- KGRKAPQVYTIPTTPPEQMAKDKVSL 382
 QY 591 VCFLLNFPKIDINVWKIDGSEON-----GVLSNWTDDQSDKSTYSMSSTLTLTCKDEYE 645
 Db 383 TCMITDFPFDITVEMQNGQPAENYKNTQPIMT-----NGSYFYVSKLVNQSWE 435
 QY 646 RHNSYTCEATHK 657
 Db 436 AGNTFTCSVLHE 447

RESULT 23
 AAB14747
 ID AAB14747 standard; protein; 464 AA.
 AC AAB14747;
 DT 24-NOV-2000 (first entry)
 XX Mouse anti-Fas antibody HFE7A heavy chain.
 XX Anti-Fas antibody; monoclonal antibody HFE7A; FERM-BP-5828; murine;
 KW complementarity determining region; CDR; human Fas; Fas ligand;
 KW apoptosis modulator; programmed cell death; autoimmune disease; allergy;
 KW atopy; arteriosclerosis; myocarditis; cardiomyopathy; glomerulonephritis;
 KW aplastic anemia; pancytopenia; hepatitis; AIDS; graft rejection;
 KW heavy chain.
 XX Mus musculus.
 OS JP2000159393-A.
 PN 20-JUN-2000.
 PD 30-SEP-1999; 99JP-00278301.
 PF 30-SEP-1998; 98JP-00276883.
 PR (SANY) SANKYO CO LTD.
 PA WPI; 2000-495645/43.
 XX N-PSDB; AAA72108.
 DR Preventive or treating agent for the diseases caused by an abnormality in
 PT the Fas/Fas ligand system e.g. autoimmune diseases, contains anti-Fas
 PT antibody.

Example 4; Page 67-68; 139pp; Japanese.
 The invention relates to compositions for the prevention or treatment of
 diseases caused by an abnormality in the Fas/Fas ligand system containing
 an anti-Fas antibody as the active component. The anti-Fas antibody is
 either the murine anti-human Fas monoclonal antibody HFE7A, or a
 humanised version of HFE7A containing identical CDRs (complementarity
 determining regions) to antibody HFE7A. Via its interaction with Fas, the
 antibody of the invention acts as a modulator of apoptosis. The
 compositions of the invention may therefore be used in the treatment or
 prevention of conditions such as autoimmune diseases, allergy, atopy,
 arteriosclerosis, myocarditis, cardiomyopathy, glomerulonephritis,
 CC aplastic anaemia (panmyelopenia), hepatitis, AIDS and organ graft
 CC rejection. The present sequence represents the heavy chain of the murine
 CC anti-human Fas monoclonal antibody HFE7A, which is produced by hybridoma
 CC HFE7A (FERM-BP-5828)
 XX Sequence 464 AA;
 SQ Query Match 29.1%; Score 1025.5; DB 3; Length 464;

Best Local Similarity 36.2%; Pred. No. 6.6e-53;
 Matches 243; Conservative 64; Mismatches 106; Indels 259; Gaps 14;
 QY 1 EVQQQSGPDLVFKPGASVKISKASGYSTGYMHVQKSPKGLWIGRINPNNGVTLY 60
 Db 20 QVQLQQPQGAELVKGASVKLSCKASGYTFTSYMQWVKQRPQGGLWIGIDPSDSYNY 79
 QY 61 NQKFKDKATLVDSSTTAYMELSLTSEDSADVVCARS-TMIINYVMDYQGQTSVTVS 119
 Db 80 NQKFKGKATLVDSSTTAYMELSLTSEDSADVVCARNRDYSNNYVDFVWGTGTITVS 139
 QY 120 SAKTTPPSVYPLAPGSAQAQNSMVTGLGVKGYPEPVTVTWNSGSLSSGSHVHTPAVLQS 179
 Db 140 SAKTTPPSVYPLAPGSAQAQNSMVTGLGVKGYPEPVTVTWNSGSLSSGSHVHTPAVLQS 199
 QY 180 DLYTLSSSVTPSPSTWPSSETVTCNVAHPASSTKVKKIVPRDSDGSPKSEINEKDLRK 239
 Db 200 DLYTLSSSVTPSPSTWPSSETVTCNVAHPASSTKVKKIVPRDCG----- 243
 QY 240 KSELQGTALGNLKOIYYNYSKAITSEKSDAQELTNTLLPKGFTTGHVWYNLLVLDLST 299
 Db 244 -CKPCICTVPEVSVVFIPPK-----PKDVLITL----- 272
 QY 300 AATSEYEGSSVDLYGAYGYQACGTPNKTACMYGGVTLHNNRLTBKVPINLWIDGK 359
 Db 273 -----TP-KVTCVVVDIS-----KODPEVQFSWFVD-- 297
 QY 360 QTTVPIDKVTSSKEV-----TVQELDLQARHYLEGK-FGL-YNSDSFGGKVQORGLIV 410
 Db 298 --DVEHTAQTPREQFNSTFRSVSELPINHQWLNKGEFKCRVNSAAPPAPIEK---- 351
 QY 411 FHSSEGSTSVSDLEDAQCGYPTDILLRIYRDNNTTISSTLSLSLYLYTTSIVMTPTSL 470
 Db 352 -----TISK----- 356
 QY 471 VSAGDRVTITCKASQSVNSDVAMVQKPGQPKLLISYTSRAGYVDPDRFSGSGYGTDT 530
 Db 357 ----- 356
 QY 531 LTSSVQAEADAAVYFCQDYNSPPTFGGPKLEIKRADAAPTIVSIFPPSEQLTSGGASV 590
 Db 357 -----KGRKAPQVYTIPTTPPEQMAKDKVSL 382
 QY 591 VCFLLNFPKIDINVWKIDGSEON-----GVLSNWTDDQSDKSTYSMSSTLTLTCKDEYE 645
 Db 383 TCMITDFPFDITVEMQNGQPAENYKNTQPIMT-----NGSYFYVSKLVNQSWE 435
 QY 646 RHNSYTCEATHK 657
 Db 436 AGNTFTCSVLHE 447
 RESULT 24
 AAW90897
 ID AAW90897 standard; protein; 464 AA.
 AC AAW90897;
 DT 08-AUG-2000 (first entry)
 XX Murine anti-Fas antibody HFE7A heavy chain protein.
 KW Fas; antibody; murine; anti-inflammatory; anti-anemic; antidiabetic;
 KW anti-allergic; anti-arthritic; antiviral; immunomodulatory; cardiant;
 KW dermatological; immunosuppressive; thyromimetic; antirheumatic; anti-Fas;
 KW nephrotropic; antiinfertility; neuroprotective; antiarteriosclerotic;
 KW hepatotropic; humanized; apoptosis; systemic lupus erythematosus; HFE7A;
 KW Hashimoto disease; rheumatoid arthritis; graft versus host disease;
 KW Sjogren's syndrome; anemia; Addison's disease; scleroderma; sterility;
 KW Goodpasture syndrome; Crohn's disease; sterility; myasthenia gravis;
 KW multiple sclerosis; Basedow's disease; thrombopenia purpura; allergy;
 KW insulin dependent diabetes mellitus; arteriosclerosis; myocarditis;
 KW cardiomyopathy; glomerulonephritis; hepatitis; transplant rejection.

QY 531 LTISSVQAEADAAVYFCQDYNSTPFGGTTKLEIKRADAAPTVSIIPPSSEQLTSGASV 590
 Db 357 -----KGRPKAPQVYVTPPPKEQVAKDKVSL 382
 QY 591 VCFNNFVKDINVKWKIDGSEON-----GVLSNWTDDQSKDSTYSMSSTLTLTDEYE 645
 Db 383 TCMITDFPEDIIVVQWNGQPAENYKNTQPIWNT-----NGSYFVYSLNVLQKSNWE 435
 QY 646 RHNSYTCETHK 657
 Db 436 AGNFTCSVLHE 447

RESULT 27
 ID AAE18380 standard; protein; 613 AA.
 AC AAE18380;
 XX 07-MAY-2002 (first entry)

DE Human N-terminal DAV-1 heavy chain-mature SCF fusion protein.
 KW Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer;
 KW vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder;
 KW hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain;
 KW cytostatic; vasotropic; ophthalmological; stem cell factor; SCF;
 KW fusion protein.
 XX Homo sapiens.
 OS Synthetic.
 OS Chimeric.

FT Key Location/Qualifiers
 FT Region 1..438
 FT /note= "N-terminal portion of DAV-1 heavy chain"
 FT Region 439..449
 FT /note= "Linker peptide"
 FT Region 450..613
 FT /note= "Human mature SCF"
 XX WO200204522-A2.
 XX 17-JAN-2002.
 XX 09-JUL-2001; 2001WO-EP007878.
 XX 10-JUL-2000; 2000US-00613017.
 XX (NOVS) NOVARTIS AG.
 XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX (SCRI) SCRIPPS RES INST.
 XX Nemerow GR, Li B;
 XX WPI; 2002-171707/22.

XX New bifunctional molecules comprising an antibody or its antigen-binding
 PT portion, and a targeting agent, useful for e.g. gene therapy, or for
 PT promoting Adenoviral vector-mediated gene delivery to cells lacking av
 PT integrins.
 XX Claim 15; Page 102-103; 106pp; English.
 PS The present invention relates to a bifunctional molecule comprising an
 CC antibody or its antigen-binding portion, and a targeting agent where the
 CC antibody specifically binds to an antigen in a protein that binds to av
 CC integrin, and the targeting agent specifically binds to a cell surface
 CC protein that activates the Phosphatidylinositol 3 (PI3K) signalling
 CC pathway. The bifunctional molecules are useful for gene therapy, for
 CC promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking
 CC av integrins, for enhancing Ad binding and internalisation, and in gene
 CC delivery of by fibreless adenovirus particles. The bifunctional molecules

CC permit targeting of viral and bacterial vectors to cells that express
 CC targeted receptors. Diseases that can be targeted include cancers,
 CC vascular disorders, diabetic retinopathies, restenosis, ophthalmic,
 CC disorders, hyperproliferative disorders, and hormonal disorders. The
 CC present sequence is human N-terminal DAV-1 heavy chain-mature stem cell
 CC factor (SCF) fusion protein which is used in the invention
 XX Sequence 613 AA;
 SQ

Query Match 29.1%; Score 1024.5; DB 5; Length 613;
 Best Local Similarity 37.3%; Pred. No. 1.1e-52;
 Matches 250; Conservative 51; Mismatches 115; Indels 255; Gaps 14;

QY 1 EVLOQSGPDLVKPGASVKISKASGYFTGYVHWKQSPKGLWIGRINPNNGVTLY 60
 Db 20 EVLOQSGPELVKPGASVKISKASGYFTGYVHWKQSPKGLWIGRINPNNGVTLY 79
 QY 61 NQFKDKATLTVDKSTTAYMELSLTSEDASVYCARSTMTNVMYDYGQGTSTVSS 120
 Db 80 NQFKDKATLTVDKSTTAYMELSLTSEDASVYCARSTMTNVMYDYGQGTSTVSS 132
 QY 121 AKTTPSVYPLAPGSAQTNSMTLGLVKGVEPEPTVTWNSSGLSSGVHTFAVLQSD 180
 Db 133 AKTTPSVYPLAPGSAQTNSMTLGLVKGVEPEPTVTWNSSGLSSGVHTFAVLQSD 192
 QY 181 LYTSSSVTPSSSTWPSSTVTCNVAHPASSTKVDKVIYPRDSGGPSEKSEINEKDLKK 240
 Db 193 LYTSSSVTPSSSTWPSSTVTCNVAHPASSTKVDKVIYPRDSGGPSEKSEINEKDLKK 235
 QY 241 SELQGTALGNLKQIYYNSKAITSEKSAQDQFLNTLLFKGFTTCHPHYNDLLVDLGSTA 300
 Db 236 CKPCICTVPEVSSVFIFPK-----PKDVLITL----- 264
 QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTACWGVGTVLHNNRLTEKKVPINLWIDGKQ 360
 Db 265 -----TP-KVTCVVDIS-----KDDPEVQSFWEVD--- 289
 QY 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGRLIVF 411
 Db 290 -DVEVHTAQTPREQFNSTFRSVELPFIMHQDLWNGKEFKRCVNSAAFPAPIEK----- 343
 QY 412 HSEGSTVSYDLFDAQGOYPTDLLRIYRDNTTISTSLISLYLYTTSIVMTQPTSLLV 471
 Db 344 -----TISKT----- 348
 QY 472 SAGDRAVITCKASQSVNDVAWYQKQSPKLLISYTSRYAGVDPDRFSGSGYGTDTL 531
 Db 349 ----- 348
 QY 532 TISSVQAEADAAVYFCQDYNSTPFGGTTKLEIKRADAAPTVSIIPPSSEQLTSGASV 591
 Db 349 -----KGRPKAPQVYVTPPPKEQVAKDKVSLT 375
 QY 592 CFLNNFVKDINVKWKIDGSEONGVLSNWTDDQSKDSTYSMSSTLTLTDEYERHNSYT 651
 Db 376 CMTIDFPEDIIVVQWNGQPAEN-YKNTQPIWNT-DGSYFVYSLNVLQKSNWEAGNTFI 433
 QY 652 CEATHTSTSP 662
 Db 434 CSVLHEFCRYP 444

RESULT 28
 ABG76355
 ID ABG76355 standard; protein; 613 AA.
 XX AC ABG76355;
 XX DT 23-OCT-2003 (revised)
 XX DT 10-MAY-2003 (first entry)
 XX Mouse DAV-1 heavy chain-mature human SCF fusion protein.
 XX

KW Human; bifunctional molecule; antigen-binding portion; alpha integrin;
 KW cell surface protein; phosphatidylinositol-3-OH kinase; PI3K;
 KW signalling pathway; targeted gene therapy; delivery vector;
 KW adenoviral gene delivery particle; viral infection; cancer;
 KW rheumatoid arthritis; cardiovascular disorder; diabetic retinopathy;
 KW restenosis; ophthalmic disorder; hyperproliferative disorder;
 KW hormonal disorder; virucide; antiinflammatory; antineumatic;
 KW antiarthritic; ophthalmological; DAV-1 antibody heavy chain; SCF;
 KW stem cell factor; mouse.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 XX
 XX US2002164333-A1.
 XX
 XX 07-NOV-2002.
 XX
 XX 10-JUL-2001; 2001US-00903327.
 XX
 XX 10-JUL-2000; 2000US-00613017.
 XX 10-JUL-2000; 2000US-0325781P.
 XX
 XX (SCRI) SCRIPPS RES INST.
 XX
 XX Nemerow GR, Li E;
 XX
 XX WPI; 2002-171707/22.
 XX
 XX
 XX New bifunctional molecules comprising an antibody or its antigen-binding
 XX portion, and a targeting agent, useful for e.g. gene therapy, or for
 XX promoting Adenoviral vector-mediated gene delivery to cells lacking av
 XX integrins.

Example 2; Page 42-44; 49pp; English.

XX The present invention relates to a bifunctional molecule comprising an
 XX antibody or its antigen-binding portion, and a targeting agent. The
 XX antibody specifically binds to an antigen in a protein that binds to
 XX alpha integrin, and the targeting agent specifically binds to a cell
 XX surface protein that activates the phosphatidylinositol-3-OH kinase
 XX (PI3K) signalling pathway. The bifunctional molecules are useful for
 XX targeted gene therapy using targeting delivery vectors, such as
 XX adenoviral gene delivery particles. The bifunctional molecules are useful
 XX for treating viral infections, rheumatoid arthritis, cancers,
 XX cardiovascular disorders, diabetic retinopathies, restenosis, ophthalmic
 XX disorders, hyperproliferative disorders, and hormonal disorders. The
 XX present sequence represents a fusion protein with mouse DAV-1 antibody
 XX heavy chain. (Updated on 23-OCT-2003 to standardise OS field)

XX Sequence 613 AA;

Query Match 29.1%; Score 1024.5; DB 5; Length 613;
 Best Local Similarity 37.3%; Pred. No. 1.1e-52;
 Matches 250; Conservative 51; Mismatches 115; Indels 255; Gaps 14;

QY 1 EVLOQSGPDLVKPGASVKISCKASYSTGYMHWKSPGKLEWIGRINPNNGVTLY 60
 Db EVQLQSGPELVKPGASVKISCKASGYTFTDYNMHWKSPGKLEWIGVYPIYKGGTGY 79
 QY 61 NQKFKDKALITVDKSTTAYMELRSITSDSAVYICARSTMTINMYDMWGQTSVTYSS 120
 Db 80 NQKFKSKALITDSSNTAYMELRSITSDSAVYICARG-----IAYWGQGLTIVTSA 132
 QY 121 AKTTPSVVPLAPGSAQNSMTVLCGLVKGFPEPVTVTWNSGSLSSGVHTFPAVLQSD 180
 Db 133 AKTTPSVVPLAPGSAQNSMTVLCGLVKGFPEPVTVTWNSGSLSSGVHTFPAVLQSD 192
 QY 181 LYTLLSSVTPSSSTWPSSTVTCNVAHPASTKVKDKIIVPRDGGPSEKSEENEXDLRKK 240
 Db 193 LYTLLSSVTPSSSTWPSSTVTCNVAHPASTKVKDKIIVPRDGG----- 235
 QY 241 SELQGTALGNLKIYYYNKAITSSSEKSAQDLFTNLLFKGFTTGHFWYNDLLVDLGSTA 300

Db 236 CKPCICTVPESSVFIPPK-----PKDVLITL----- 264
 QY 301 ATSEVEGSSVDLYGAYGYQCAGGTENKACMGVTLHDNNRLTEKKVPIINLWIDGKQ 360
 Db 265 -----TP-KVTCVVVDIS-----KDPPEVQFSFVD--- 289
 QY 361 TTVPIDKVTSKKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGKQGLIVF 411
 Db 290 -DVEVHTAQTPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAFPAPIEK----- 343
 QY 412 HSEGGSTVSVDLFDPAQGYPTDLLRIYRDNNTISSTLSLSLYLYTTSIVMTQPTSLLV 471
 Db 344 -----TISKT----- 348
 QY 472 SAGDRVTITTKASQSVSNDAVYQKQKPGSPKLLISYTSRYAGVDPDRFSGSGYGTDTFL 531
 Db 349 ----- 348
 QY 532 TISSVQAEADAAYFCQDYNSTPFTGGTGLEIKRADAAPTSTVSPSSSQTSGGASVV 591
 Db 349 -----KGRPKAPQVYTIPTPKSQMAKDKVSLT 375
 QY 592 CFLNNFYPKDINVKWKIDGSRQGNVLNSWTDQDSKDYSSMSSTLTLTDEYERHNSYT 651
 Db 376 CMITDFPEDITVENQWNGQPAEN-YKNTQPIMDT-DGSYFVYSKLVNQKSNWEAGNTFI 433
 QY 652 CEATHKSTSTSP 662
 Db 434 CSVLHFCRYP 444

RESULT 29
 AAE18370

ID AAE18370 standard; protein; 456 AA.

XX AAE18370;

DT 07-MAY-2002 (first entry)

DE Human penton base monoclonal antibody, DAV-1 heavy chain.

XX Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer;
 XX vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder;
 XX hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain;
 XX cytostatic; vasotropic; ophthalmological.

XX Homo sapiens.

PH Key Location/Qualifiers
 FT Region 230..242
 FT /note= "Hinge region"

XX WO200204522-A2.

XX 17-JAN-2002.

XX 09-JUL-2001; 2001WO-EP007878.

XX 10-JUL-2000; 2000US-00613017.

XX (NOVS) NOVARTIS AG.

XX (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX (SCRI) SCRIPPS RES INST.

XX Nemerow GR, Li E;

XX WPI; 2002-171707/22.

XX N-PSDB; AAD29308.

XX New bifunctional molecules comprising an antibody or its antigen-binding
 XX portion, and a targeting agent, useful for e.g. gene therapy, or for
 XX promoting Adenoviral vector-mediated gene delivery to cells lacking av

PT integrins.
XX Claim 10; Page 91-92; 106pp; English.
XX The present invention relates to a bifunctional molecule comprising an antibody or its antigen-binding portion, and a targeting agent where the antibody specifically binds to an antigen in a protein that binds to an integrin, and the targeting agent specifically binds to a cell surface protein that activates the phosphatidylinositol 3 (PI3K) signalling pathway. The bifunctional molecules are useful for gene therapy, for promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking an integrin, for enhancing Ad binding and internalisation, and in gene delivery of by fibroless adenovirus particles. The bifunctional molecules permit targeting of viral and bacterial vectors to cells that express targeted receptors. Diseases that can be targeted include cancers, vascular disorders, diabetic retinopathies, restenosis, ophthalmic disorders, hyperproliferative disorders, and hormonal disorders. The present sequence is human penton base monoclonal antibody, DAV-1 heavy chain

XX SQ Sequence 456 AA;
Query Match 29.1%; Score 1023.5; DB 5; Length 456;
Best Local Similarity 37.4%; Pred. No. 8.5e-53;
Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;

QY 1 EVQLQSGPDLVPGASVKISKASGYFTGYMHWKQSPGKLEWIGRINPNNGVTLV 60
DB EVQLQSGPDLVPGASVKISKASGYFTGYMHWKQSPGKLEWIGIYIPYKGGTGY 79

QY 61 NQKFKDKATLVDSKSTTAYMELSLTSDSAVYVCARSTMTNVMYDYGQGTSTVSS 120
DB NQKFKDKATLVDSKSTTAYMELSLTSDSAVYVCARSTMTNVMYDYGQGTSTVSS 132

QY 121 AKTTPSPVPLAPGSAAGTNSMTLGLVKGYPPEVTVTWNSGSLSSGVHTTTPAVLQSD 180
DB AKTTPSPVPLAPGSAAGTNSMTLGLVKGYPPEVTVTWNSGSLSSGVHTTTPAVLQSD 192

QY 181 LYTSSSVTPSPSTWPTVTCNVAHPASSTKVDKXIVPRDSGGPSEKSEINEKDLRKK 240
DB LYTSSSVTPSPSTWPTVTCNVAHPASSTKVDKXIVPRDSGGPSEKSEINEKDLRKK 235

QY 241 SELQGTALGNLKQIYYNYSKAITSEKSDQFLNTLLFKGFFHGHFWYNDLVDLGSTA 300
DB SELQGTALGNLKQIYYNYSKAITSEKSDQFLNTLLFKGFFHGHFWYNDLVDLGSTA 264

QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPIINLWIDGKQ 360
DB ATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPIINLWIDGKQ 289

QY 361 TVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKQVQGLIVF 411
DB TVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKQVQGLIVF 343

QY 412 HSSEGSTVSYDLFDAQGGVPTLLRIYRDNTTISTSLISLYLTTTSIVMTQTPTSLV 471
DB HSSEGSTVSYDLFDAQGGVPTLLRIYRDNTTISTSLISLYLTTTSIVMTQTPTSLV 348

QY 472 SAGDRVTITCKASVSNDAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDFTL 531
DB SAGDRVTITCKASVSNDAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDFTL 348

QY 532 TISSVQAEADAAYFCQQDYNSPPTFGGQTKLEIKRAADAAPTSTVFPPSSQLTSGGASV 591
DB TISSVQAEADAAYFCQQDYNSPPTFGGQTKLEIKRAADAAPTSTVFPPSSQLTSGGASV 375

QY 592 CFLANNYPKIDINVKWIDGSRQGNLSWTDQSDSTYSMSSTLTTLTKDEYERHNSYT 651
DB CFLANNYPKIDINVKWIDGSRQGNLSWTDQSDSTYSMSSTLTTLTKDEYERHNSYT 376

QY 652 CEATHK 657
DB CEATHK 439

RESULT 30
ABG76345
ID ABG76345 standard; protein; 456 AA.
XX AC ABG76345;
XX DT 10-MAY-2003 (first entry)
XX DE Mouse DAV-1 heavy chain monoclonal antibody.
XX KW Mouse; bifunctional molecule; antigen-binding portion; alpha integrin; cell surface protein; phosphatidylinositol-3-OH kinase; PI3K; signalling pathway; targeted gene therapy; delivery vector; adenoviral gene delivery particle; viral infection; cancer; rheumatoid arthritis; cardiovascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder; hyperproliferative disorder; hormonal disorder; virucide; antinflammatory; antirheumatic; antiarthritic; ophthalmological; DAV-1 heavy chain;
XX KW penton base monoclonal antibody.
XX OS Mus sp.
XX US2002164333-A1.
XX PD 07-NOV-2002.
XX PF 10-JUL-2001; 2001US-00903327.
XX PR 10-JUL-2000; 2000US-00613017.
XX PR 10-JUL-2000; 2000US-0325781P.
XX PA (SCRI) SCRIPPS RES INST.
XX PI Nemerow GR, Li E;
XX WPI; 2002-171707/22.
XX DR N-PSDB; ABX12744.
XX PT New bifunctional molecules comprising an antibody or its antigen-binding portion, and a targeting agent, useful for e.g. gene therapy, or for promoting Adenoviral vector-mediated gene delivery to cells lacking av integrins.
XX PS Claim 10; Page 30-31; 49pp; English.
XX The present invention relates to a bifunctional molecule comprising an antibody or its antigen-binding portion, and a targeting agent. The antibody specifically binds to an antigen in a protein that binds to alpha integrin, and the targeting agent specifically binds to a cell surface protein that activates the phosphatidylinositol-3-OH kinase (PI3K) signalling pathway. The bifunctional molecules are useful for targeted gene therapy using targeting delivery vectors, such as adenoviral gene delivery particles. The bifunctional molecules are useful for treating viral infections, rheumatoid arthritis, cancers, cardiovascular disorders, diabetic retinopathies, restenosis, ophthalmic disorders, hyperproliferative disorders, and hormonal disorders. The present sequence represents mouse DAV-1 heavy chain, penton base monoclonal antibody
XX SQ Sequence 456 AA;
Query Match 29.1%; Score 1023.5; DB 5; Length 456;
Best Local Similarity 37.4%; Pred. No. 8.5e-53;
Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;

QY 1 EVQLQSGPDLVPGASVKISKASGYFTGYMHWKQSPGKLEWIGRINPNNGVTLV 60
DB EVQLQSGPDLVPGASVKISKASGYFTGYMHWKQSPGKLEWIGIYIPYKGGTGY 79

QY 61 NQKFKDKATLVDSKSTTAYMELSLTSDSAVYVCARSTMTNVMYDYGQGTSTVSS 120

Db 80 NQKFKSKATLTSSSNTAYMELRLTSDASAVYYCARG-----IAYWGQGLTVTVSA 132
 QY 121 AKTTPPSVYPLAPGSAQAQNSMTLGLVKGYFPPEPVTVTNWSSGLSSGVHTFPFVQLQSD 180
 Db 133 AKTTPPSVYPLAPGSAQAQNSMTLGLVKGYFPPEPVTVTNWSSGLSSGVHTFPFVQLQSD 192
 QY 181 LYTSSSVTPSPSTWPSSETVTCNVAHPASSTKVDKVIIPRDSDGGPSEKSEINEKDLRKK 240
 Db 193 LYTSSSVTPSPSTWPSSETVTCNVAHPASSTKVDKVIIPRDSDGGPSEKSEINEKDLRKK 235
 QY 241 SELQGTALGNLQIYYNNSKAITSEKSAQDFLTNTLLFKGFTGHPWYNDLLVDLGSTA 300
 Db 236 CKPCICTVPEVSSVFIIPPCK-----PKDVLITL----- 264
 QY 301 ATSEYEGSSVDLYGAYGYQCAGTGNKTAQMYGGVTLHDNNRLTEKKVPIINLWIDGKQ 360
 Db 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--- 289
 QY 361 TTVPIDKVKTSKKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVQGLIVF 411
 Db 290 -DVEVHTAQTPREEQNFSTRSVSELPIMHQDLNGKEFKCRVNSAAPPAPIEK----- 343
 QY 412 HSESGSTVSYDLFDAGQGYPTLLRIYRDNTTISSTLSISLYLYTTSIVMTQTPTSLV 471
 Db 344 -----TISK----- 348
 QY 472 SAGDRVTITCKASQSVNSDVANVQKPGQSPKLLISYSSRVAGVDPDRFSGSGYCTDTL 531
 Db 349 ----- 348
 QY 532 TISSVQAEAAVFCQDYNSPTFGGKLEIKRADAAPTYSIFPPSSQELTSGGASV 591
 Db 349 -----KGRPKAPQYVITPPKEQWAKDKVBLT 375
 QY 592 CFLNFPKIDINVKWIDGSEKQVNLNWSWTDQSDKSTYSMSLTTLTKDYEYRHSYT 651
 Db 376 CMITDFPFDITVQWQNGQPAEN-YKNTQPTMDT-DGSYFYVYSKLVNPKNSWEAGNTFI 433
 QY 652 CEATHK 657
 Db 434 CSVLHE 439

RESULT 31
 AAE18379
 ID AAE18379 standard; protein; 493 AA.
 AC AAE18379;
 DE 07-MAY-2002 (first entry)
 DT Human N-terminal DAV-1 heavy chain-mature EGF fusion protein.
 DE Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer;
 KW vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder;
 KW hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain;
 KW cytostatic; vasotropic; ophthalmological; epidermal growth factor; EGF;
 KW fusion protein.
 OS Homo sapiens.
 OS Synthetic.
 OS Chimeric.
 XX
 FH Key
 FT Region
 FT 1. .439
 FT /note= "N-terminal portion of DAV-1 heavy chain"
 FT 441. .493
 FT /note= "Human mature EGF"
 XX
 PN WC0200204522-A2.
 XX
 PD 17-JAN-2002.
 XX

PF 09-JUL-2001; 2001WO-EP007878.
 XX
 XX 10-JUL-2000; 2000US-00613017.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 PA (SCRI) SCRIPPS RES INST.
 XX
 XX Nemerow GR, Li E;
 XX WPI; 2002-171707/22.
 DR
 XX
 XX
 PT New bifunctional molecules comprising an antibody or its antigen-binding
 PT portion, and a targeting agent, useful for e.g. gene therapy, or for
 PT promoting Adenoviral vector-mediated gene delivery to cells lacking av
 PT integrins.
 PS
 PS Claim 15; Page 101-102; 106pp; English.
 XX
 XX The present invention relates to a bifunctional molecule comprising an
 CC antibody or its antigen-binding portion, and a targeting agent where the
 CC antibody specifically binds to an antigen in a protein that binds to av
 CC integrin, and the targeting agent specifically binds to a cell surface
 CC protein that activates the phosphatidylinositol 3 (PI3K) signalling
 CC pathway. The bifunctional molecules are useful for gene therapy, for
 CC promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking
 CC av integrins, for enhancing Ad binding and internalisation, and in gene
 CC delivery of by fibroless adenovirus particles. The bifunctional molecules
 CC permit targeting of viral and bacterial vectors to cells that express
 CC targeted receptors. Diseases that can be targeted include cancers,
 CC vascular disorders, diabetic retinopathies, restenosis, ophthalmic
 CC disorders, hyperproliferative disorders, and hormonal disorders. The
 CC present sequence is human N-terminal DAV-1 heavy chain-mature epidermal
 CC growth factor (EGF) fusion protein which is used in the invention
 XX
 XX Sequence 493 AA;
 Query Match 29.1%; Score 1023.5; DB 5; Length 493;
 Best Local Similarity 37.4%; Pred. No. 9.3e-53;
 Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;
 QY 1 EVQLQQSGDPLVKPGASVKISCKASGYSTFTGYNMHWVKQSPGKLEWIGRINPNNGVTLY 60
 Db 20 EVQLQQSGDPLVKPGASVKISCKASGYSTFTGYNMHWVKQSPGKLEWIGRINPNNGVTLY 79
 QY 61 NQKFKSKATLTSSSNTAYMELRLTSDASAVYYCARG-----IAYWGQGLTVTVSA 120
 Db 80 NQKFKSKATLTSSSNTAYMELRLTSDASAVYYCARG-----IAYWGQGLTVTVSA 132
 QY 121 AKTTPPSVYPLAPGSAQAQNSMTLGLVKGYFPPEPVTVTNWSSGLSSGVHTFPFVQLQSD 180
 Db 133 AKTTPPSVYPLAPGSAQAQNSMTLGLVKGYFPPEPVTVTNWSSGLSSGVHTFPFVQLQSD 192
 QY 181 LYTSSSVTPSPSTWPSSETVTCNVAHPASSTKVDKVIIPRDSDGGPSEKSEINEKDLRKK 240
 Db 193 LYTSSSVTPSPSTWPSSETVTCNVAHPASSTKVDKVIIPRDSDGGPSEKSEINEKDLRKK 235
 QY 241 SELQGTALGNLQIYYNNSKAITSEKSAQDFLTNTLLFKGFTGHPWYNDLLVDLGSTA 300
 Db 236 CKPCICTVPEVSSVFIIPPCK-----PKDVLITL----- 264
 QY 301 ATSEYEGSSVDLYGAYGYQCAGTGNKTAQMYGGVTLHDNNRLTEKKVPIINLWIDGKQ 360
 Db 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD--- 289
 QY 361 TTVPIDKVKTSKKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVQGLIVF 411
 Db 290 -DVEVHTAQTPREEQNFSTRSVSELPIMHQDLNGKEFKCRVNSAAPPAPIEK----- 343
 QY 412 HSESGSTVSYDLFDAGQGYPTLLRIYRDNTTISSTLSISLYLYTTSIVMTQTPTSLV 471
 Db 344 -----TISK----- 348

QY 472 SAGDRVTITCKASQSVNDVAVYQKPGQPKLLISVTSRYAGVDPDRFSGSGYGTDFTL 531
 Db 349 ----- 348
 QY 532 TISSVQAEADAAYFCQDYNPPTFGGKLEIKRADAAPTIVSIFPPSSQLTSGASVV 591
 Db 349 -----KGRPKAPQVVTIPPPKEQMAKDVSILT 375
 QY 592 CFLNFPKIDINVKKIDGSRQNGVLSNWTQDSDKSTYSMSSTLTLTDEYERHNSYT 651
 Db 376 CMITDFPEDITVEQWNGQPAEN-YKNTQPIMDT-DGSYFVYSKLVNOKSNWEAGNTFI 433
 QY 652 CEATHK 657
 Db 434 CSVLHE 439

RESULT 32
 ABG76354
 ID ABG76354 standard; protein; 493 AA.
 AC ABG76354;
 XX
 XX 23-OCT-2003 (revised)
 DT 10-MAY-2003 (first entry)
 DE Mouse DAV-1 heavy chain-mature human EGF fusion protein.
 XX Human; bifunctional molecule; antigen-binding portion; alpha integrin;
 KW cell surface protein; phosphatidylinositol-3-OH kinase; PI3K;
 KW signalling pathway; targeted gene therapy; delivery vector;
 KW adenoviral gene delivery particle; viral infection; cancer;
 KW rheumatoid arthritis; cardiovascular disorder; diabetic retinopathy;
 KW restenosis; ophthalmic disorder; hyperproliferative disorder;
 KW hormonal disorder; virucide; antiinflammatory; antirheumatic;
 KW antiarthritic; ophthalmological; DAV-1 antibody heavy chain; EGF;
 KW epidermal growth factor; mouse.
 XX
 OS Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 XX
 XX US2002164333-A1.
 PN
 XX
 PD 07-NOV-2002.
 XX
 PF 10-JUL-2001; 2001US-00903327.
 XX
 PR 10-JUL-2000; 2000US-00613017.
 PR 10-JUL-2000; 2000US-0325781P.
 XX
 XX (SCRI) SCRIPPS RES INST.
 PA
 XX
 PI Nemerow GR, Li B;
 XX
 DR WPI; 2002-171707/22.
 XX
 XX New bifunctional molecules comprising an antibody or its antigen-binding
 PT portion, and a targeting agent, useful for e.g. gene therapy, or for
 PT promoting Adenoviral vector-mediated gene delivery to cells lacking av
 PT integrins.
 XX
 PS Example 2; Page 41-42; 49pp; English.
 XX
 CC The present invention relates to a bifunctional molecule comprising an
 CC antibody or its antigen-binding portion, and a targeting agent. The
 CC antibody specifically binds to an antigen in a protein that binds to
 CC alpha integrin, and the targeting agent specifically binds to a cell
 CC surface protein that activates the phosphatidylinositol-3-OH kinase
 CC (PI3K) signalling pathway. The bifunctional molecules are useful for
 CC targeted gene therapy using targeting delivery vectors, such as
 CC adenoviral gene delivery particles. The bifunctional molecules are useful
 CC for treating viral infections, rheumatoid arthritis, cancers,

CC cardiovascular disorders, diabetic retinopathies, restenosis, ophthalmic
 CC disorders, hyperproliferative disorders, and hormonal disorders. The
 CC present sequence represents a fusion protein with mouse DAV-1 antibody
 CC heavy chain. (Updated on 23-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 493 AA;
 Query Match 29.1%; Score 1023.5; DB 5; Length 493;
 Best Local Similarity 37.4%; Pred. No. 9.3e-53;
 Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;
 QY 1 EVQLQQSGPDIIVKPGASVKISCKASGYFTQYMHVWKQSPKGLGWIGRINPNNGVTL 60
 Db 20 EVQLQQSGPELVKPGASVKISCKASGYFTFDYNNHVKQSHGKSLWIGYIYPKGTGY 79
 QY 61 NQKPKDKATLTVDKSTTAYNELSLTSEDASVYVCARSTMTNVMYDYGQGTSTVTS 120
 Db 80 NQKFKSKATLTDDSSNTAYNELSLTSDASVYVCARG-----IAYWQGTLTIVSA 132
 QY 121 AKTTPPSVYPLAPGSAQAQNSMTLGLVKGYFPEPVTVTWNSGSLSSGVHTFPVAVLQSD 180
 Db 133 AKTTPPSVYPLAPGSAQAQNSMTLGLVKGYFPEPVTVTWNSGSLSSGVHTFPVAVLQSD 192
 QY 181 LYTLSSTVTPSSSTWPSSTVTCNVAHPASSTKVDDKIVPRDSGGPSEKSEINEKDLRKK 240
 Db 193 LYTLSSTVTPSSSTWPSSTVTCNVAHPASSTKVDDKIVPRDCG----- 235
 QY 241 SELQGTALGNLKIYYNYSKAITSEKSAQDLNTLLFKGFTTGHWPYNDLLVLDLSTA 300
 Db 236 CKPCICTVPESSVFIFFPK-----PKDVLITL----- 264
 QY 301 ATSEYEGSSVDLYGAYGYQACAGTPNTAKCMYGGVTLHDNRLTEKKVPINLWIDCKQ 360
 Db 265 -----TP-KVTCVVDIIS-----KDDPEVQFSWFDV--- 289
 QY 361 TTVPIDKVKTSKEV-----TVQELDLQARHVLHGK-FGL-YNSDSFGGKVQGRILVF 411
 Db 290 -DVEVHTAQTQPREQPNSTFRSVSELPIMHQDLNGLKEFKCRVNSAFAPIEK----- 343
 QY 412 HSSEGSTVSYDLFDAQGGYPTLLRIYRDNTTISTSLISLYLYTTSIVMTQPTSLLV 471
 Db 344 -----TISKT----- 348
 QY 472 SAGDRVTITCKASQSVNDVAVYQKPGQPKLLISVTSRYAGVDPDRFSGSGYGTDFTL 531
 Db 349 ----- 348
 QY 532 TISSVQAEADAAYFCQDYNPPTFGGKLEIKRADAAPTIVSIFPPSSQLTSGASVV 591
 Db 349 -----KGRPKAPQVVTIPPPKEQMAKDVSILT 375
 QY 592 CFLNFPKIDINVKKIDGSRQNGVLSNWTQDSDKSTYSMSSTLTLTDEYERHNSYT 651
 Db 376 CMITDFPEDITVEQWNGQPAEN-YKNTQPIMDT-DGSYFVYSKLVNOKSNWEAGNTFI 433
 QY 652 CEATHK 657
 Db 434 CSVLHE 439

RESULT 33
 AAE18378
 ID AAE18378 standard; protein; 510 AA.
 XX
 AC AAE18378;
 XX
 DT 07-MAY-2002 (first entry)
 XX Human N-terminal DAV-1 heavy chain-mature IGF-1 fusion protein.
 DE
 XX Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer;
 KW vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder;
 KW hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain;

KW cytotstatic; vasotropic; ophthalmological; insulin growth factor-1; IGF-1;
 XX fusion protein.
 OS Homo sapiens.
 OS Synthetic.
 OS Chimeric.
 XX
 XX Key Location/Qualifiers
 XX 1 439
 FT Region /note= "N-terminal portion of DAV-1 heavy chain"
 FT 441..510
 FT Region /note= "Human mature IGF-1"
 FT
 PN WO200204522-A2.
 XX
 XX 17-JAN-2002.
 XX
 XX 09-JUL-2001; 2001WO-EPC07878.
 XX
 XX 10-JUL-2000; 2000US-00613017.
 XX
 XX (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 PA (SCRI) SCRIPPS RES INST.
 XX
 XX Nemerow GR, Li E;
 XX WPI; 2002-171707/22.
 XX
 XX New bifunctional molecules comprising an antibody or its antigen-binding
 PT portion, and a targeting agent, useful for e.g. gene therapy, or for
 PT promoting Adenoviral vector-mediated gene delivery to cells lacking av
 PT integrins.
 XX
 XX Claim 15; Page 100; 106pp; English.
 XX
 XX The present invention relates to a bifunctional molecule comprising an
 CC antibody or its antigen-binding portion, and a targeting agent where the
 CC antibody specifically binds to an antigen in a protein that binds to av
 CC integrin, and the targeting agent specifically binds to a cell surface
 CC protein that activates the phosphatidylinositol 3 (PI3K) signalling
 CC pathway. The bifunctional molecules are useful for gene therapy, for
 CC promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking
 CC av integrins, for enhancing Ad binding and internalisation, and in gene
 CC delivery of by fibreless adenovirus particles. The bifunctional molecules
 CC permit targeting of viral and bacterial vectors to cells that express
 CC targeted receptors. Diseases that can be targeted include cancers,
 CC vascular disorders, diabetic retinopathies, restenosis, ophthalmic
 CC disorders, hyperproliferative disorders, and hormonal disorders. The
 CC present sequence is human N-terminal DAV-1 heavy chain-mature insulin
 CC growth factor-1 (IGF-1) fusion protein which is used in the invention
 XX
 XX Sequence 510 AA;
 SQ
 Query Match 29.1%; Score 1023.5; DB 5; Length 510;
 Best Local Similarity 37.4%; Pred.No. 9.7e-53;
 Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;
 QY 1 EVQLQSGDPLVKPGASVKISKASGYFTGYMHWKQSPGKLEWIGRINPNNGVTLY 60
 DB 20 EVQLQSGDPLVKPGASVKISKASGYFTGYMHWKQSPGKLEWIGRINPNNGVTLY 79
 QY 61 NQKFKDKATLTVDKSSSTAYMELRSLTSDSAVYVCARSTMTNVMYWGQGTSTVYS 120
 DB 80 NQKFKDKATLTVDKSSSTAYMELRSLTSDSAVYVCARSTMTNVMYWGQGTSTVYS 132
 QY 121 AKTTPSPVYPLAPGSAQAQNSMTVGLCLVKGFPPPTVTVNWSGLSSGVHFFPAVLQSD 180
 DB 133 AKTTPSPVYPLAPGSAQAQNSMTVGLCLVKGFPPPTVTVNWSGLSSGVHFFPAVLQSD 192
 QY 181 LYTLSSTVTPGSTWPSSTVTCNVAHPASSTKVDKIVPRDGGSPSEKSEENEXDLRKK 240
 DB 193 LYTLSSTVTPGSTWPSSTVTCNVAHPASSTKVDKIVPRDGGSPSEKSEENEXDLRKK 235

QY 241 SELQGTALGNLKQIYYNYSKAITSEKSAQDQFLINTLLFKGFTTGHFWYNDLLVLDGSTA 300
 DB 236 CKPCICTVPEVSSVFPPPK-----PKDVLITL----- 264
 QY 301 ATSEYEGSSVDLYGAYGYQCAGGTENKTAQWGGVTLHDNNRLTEKKVPINLWIDGKQ 360
 DB 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFDV----- 289
 QY 361 TTVFIDKVKTSKKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVGQGLIVF 411
 DB 290 -DVEVHTAQTQPREEQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAPPAPIEK----- 343
 QY 412 HSSGSGTVSYDLFDAQGOYPTLLRIYRDNTTISTSLISLYLYTTSIVMTQTPTSLLV 471
 DB 344 -----TISKT----- 348
 QY 472 SAGDRVITITKASQSVNDVAVYQQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTFTL 531
 DB 349 ----- 348
 QY 532 TISSVQAEAAVYFCQDYNSPPTFGGKLEIKRAAAPTIVSIPFPSSBQLTSGGASVV 591
 DB 349 -----KGRPKAPQVYTIPTPPKQMAKDKVSLT 375
 QY 592 CFLNNEPKDINVKWKIDGSEKQNGVLSNWDQSDKSTYSMSSTLTLTDKDEYERHNSYT 651
 DB 376 CMITDFFPEDITVWQWNGQPAEN-YKNTQPIMDT-DGSIFFVYSKLVQKSNWEAGNTFI 433
 QY 652 CEATHK 657
 DB 434 CSVLHE 439
 RESULT 34
 ABG76353
 ID ABG76353 standard; protein; 510 AA.
 XX
 XX AC ABG76353;
 XX
 XX DT 23-OCT-2003 (revised)
 XX DT 10-MAY-2003 (first entry)
 XX
 XX DE Mouse DAV-1 heavy chain-mature human IGF-1 fusion protein.
 XX
 XX KW Human; bifunctional molecule; antigen-binding portion; alpha integrin;
 KW cell surface protein; phosphatidylinositol-3-OH kinase; PI3K;
 KW signalling pathway; targeted gene therapy; delivery vector;
 KW adenoviral gene delivery particle; viral infection; cancer;
 KW rheumatoid arthritis; cardiovascular disorder; diabetic retinopathy;
 KW restenosis; ophthalmic disorder; hyperproliferative disorder;
 KW hormonal disorder; virucide; antiinflammatory; antirheumatic;
 KW antiarthritic; ophthalmological; DAV-1 antibody heavy chain; IGF-1;
 KW insulin-like growth factor-1; mouse.
 XX
 XX OS Homo sapiens.
 OS Mus sp.
 OS Chimeric.
 XX
 XX PN US2002164333-A1.
 XX
 XX PD 07-NOV-2002.
 XX
 XX PF 10-JUL-2001; 2001US-00903327.
 PR
 PR 10-JUL-2000; 2000US-00613017.
 PR 10-JUL-2000; 2000US-0325781P.
 XX
 XX PA (SCRI) SCRIPPS RES INST.
 XX
 XX PI Nemerow GR, Li E;
 XX WPI; 2002-171707/22.
 DR

XX	Db	434	CSVLHE 439
PT	RESULT 35		
PT	AAE18372		
PT	ID AAE18372	standard; protein; 438 AA.	
XX	XX	AAE18372;	
XX	AC	AAE18372;	
XX	DT	07-MAY-2002	(first entry)
XX	DE	Human penton base monoclonal antibody, DAV-1 heavy chain fragment.	
XX	DE	Human; bifunctional molecule; monoclonal antibody; gene therapy; cancer;	
XX	KW	vascular disorder; diabetic retinopathy; restenosis; ophthalmic disorder;	
XX	KW	hyperproliferative disorder; hormonal disorder; DAV-1 heavy chain;	
XX	KW	cytostatic; vasotropic; ophthalmological.	
XX	OS	Homo. sapiens.	
XX	OS	WO200204522-A2.	
XX	PN	17-JAN-2002.	
XX	PD	09-JUL-2001; 2001WO-EP007878.	
XX	PF	10-JUL-2000; 2000US-00613017.	
XX	PR	(NOVS) NOVARIS AG.	
XX	PA	(NOVS) NOVARIS-ERFINDUNGEN VERW GES MBH.	
XX	PA	(SCRI) SCRIPPS RES INST.	
XX	PA	Nemerow GR, Li E;	
XX	PI	WPI; 2002-171707/22.	
XX	DR	N-PSDB; AAE18372.	
XX	XX	New bifunctional molecules comprising an antibody or its antigen-binding	
XX	PT	portion, and a targeting agent, useful for e.g. gene therapy, or for	
XX	PT	promoting Adenoviral vector-mediated gene delivery to cells lacking av	
XX	PT	integrins.	
XX	XX	Claim 10; Page 96; 106pp; English.	
XX	PS	The present invention relates to a bifunctional molecule comprising an	
XX	CC	antibody or its antigen-binding portion, and a targeting agent where the	
XX	CC	antibody specifically binds to an antigen in a protein that binds to av	
XX	CC	integrin, and the targeting agent specifically binds to a cell surface	
XX	CC	protein that activates the phosphatidylinositol 3 (PI3K) signalling	
XX	CC	pathway. The bifunctional molecules are useful for gene therapy, for	
XX	CC	promoting Adenoviral (Ad) vector-mediated gene delivery to cells lacking	
XX	CC	av integrins, for enhancing Ad binding and internalisation, and in gene	
XX	CC	delivery of by fibreless adenovirus particles. The bifunctional molecules	
XX	CC	permit targeting of viral and bacterial vectors to cells that express	
XX	CC	targeted receptors. Diseases that can be targeted include cancers,	
XX	CC	vascular disorders, diabetic retinopathies, restenosis, ophthalmic	
XX	CC	disorders, hyperproliferative disorders, and hormonal disorders. The	
XX	CC	present sequence is human penton base monoclonal antibody, DAV-1 heavy	
XX	CC	chain fragment	
XX	XX	Sequence 438 AA;	
XX	XX	Query Match 29.0%; Score 1022.5; DB 5; Length 438;	
XX	XX	Best Local Similarity 37.4%; Pred. No. 9.3e-53;	
XX	XX	Matches 249; Conservative 50; Mismatches 111; Indels 255; Gaps 14;	
XX	QY	1 EVOLQSGPDLVKPGASVKISKASGYSTGYMHWKQSPGKLEWIGRINPNNGVTLY 60	
XX	Db	20 EVOLQSGPDLVKPGASVKISKASGYSTGYMHWKQSPGKLEWIGYIPYKGGTGY 79	
XX	QY	61 NQFKDKATLTVDKSTTAYMELSLTSDSAVYVCARSTMTINYMDYMGQGSTVTVSS 120	

Db 349 -----KGRPKAPQVVTIPPPKEQMAKDVKSLT 375

QY 592 CFLNFPKIDINVKWIDGSRQGVLSWTDQDSKDYMSSTLTTLTKDEYERHNSYT 651

Db 376 CMTIDFFPEDITVQWNGQPAEN-YKNTQPIMDT-DGSYFVYSKLVNOKSNWEAGNTFI 433

QY 652 CEATH 656

Db 434 CSVLH 438

RESULT 37

AAV39452

ID AAV39452 standard; protein; 206 AA.

XX AAV39452;

XX 19-NOV-1999 (first entry)

XX Antibody ABX-CBL light chain sequence.

XX Antibody; CD147; IgM; ABX-CBL; activated T-cell killing; leukaemia;

KW activated B-cell; monocytic; graft versus host disease; therapy; cancer;

KW organ transplant rejection disease; lymphoma; pancreatic disease;

KW autoimmune disease; inflammatory disease; arthritis; binding site.

XX Homo sapiens.

XX WO9945031-A2.

XX 10-SEP-1999.

XX 03-MAR-1999; 99WO-US004583.

PR 03-MAR-1998; 98US-00034607.

PR 03-FEB-1999; 99US-00244253.

XX (ABGE-) ARGENIX INC.

XX Davis CG, Blacher RW, Corvalan JR, Culwell AR, Green LL, Hales J;

PI Havrilla N, Ivanov VE, Lipani JA, Liu Q, Weber RF, Yang X;

XX WPI; 1999-540816/45.

XX New monoclonal antibody, used for treating e.g. graft versus host

PT disease, cancers, autoimmune diseases and inflammatory diseases.

XX Disclosure; Page 58; 245pp; English.

XX This sequence represents the light chain of the antibody ABX-CXL. The

CC invention relates to a monoclonal antibody (Mab) with an isotype that

CC fixes complement and a variable region that binds to the epitope on CD147

CC bound by the IgM Mab ABX-CBL, providing that the antibody is not CBL1.

CC The Mab can selectively kill activated T-cells, activated B-cells or

CC resting or activated monocytes. The products and methods can be used for

CC treating diseases involving activated T-cells or B-cells or monocytes,

CC e.g. graft versus host disease (GVHD), organ transplant rejection

CC diseases (e.g. renal transplant, ocular transplant), cancers (e.g.

CC cancers of the blood (e.g. leukaemia's and lymphomas) and pancreatic),

CC autoimmune diseases (e.g. lupus), and inflammatory diseases (e.g.

CC arthritis)

XX Sequence 206 AA;

SQ Query Match 28.9%; Score 1018; DB 2; Length 206;

Best Local Similarity 95.1%; Pred. No. 7e-53; Indels 0; Gaps 0;

Matches 193; Conservative 4; Mismatches 6;

QY 469 LLVSGADRVTITCKASQSVNDVAVYQKPGQSPKLLISYTSRRYAGVDPDRFGSGYGTG 528

Db 3 LLVSGADRVTITCKASQSVNDVAVYQKPGQSPKLLIYASNYTGVDPDRFGSGYGTG 62

QY 529 FTLTISVQAEADAVYFCQDYSSPYTFGGGTGKLEIKRADAAPTIVSIPPPSSEQLTSGGA 589

Db 63 FTFITISTVQAEADAVYFCQDYSSPYTFGGGTGKLEIKRADAAPTIVSIPPPSSEQLTSGGA 122

QY 589 SVVCFLNFPKIDINVKWIDGSRQGVLSWTDQDSKDYMSSTLTTLTKDEYERHN 648

Db 123 SVVCFLNFPKIDINVKWIDGSRQGVLSWTDQDSKDYMSSTLTTLTKDEYERHN 182

QY 649 SYTCEATHKTSPTSPVKSFNENE 671

Db 183 SYTCEATHKTSPTSPVKSFNENE 205

RESULT 38

AAV66758

ID AAV66758 standard; protein; 465 AA.

XX AAV66758;

XX 01-SEP-1995 (first entry)

XX Anti-tobacco mosaic virus monoclonal Ab heavy chain.

XX Tobacco mosaic virus; TMV; monoclonal antibody; heavy chain;

KW virus-resistant plants; biofarming.

XX Synthetic.

XX Key Location/Qualifiers

FT Peptide 1..19

FT /label= leader

FT Peptide 20..465

FT /label= mat_peptide

FT Domain 20..128

FT /note= "variable heavy domain"

FT Domain 129..141

FT /note= "J heavy 4 domain"

FT Domain 142..465

FT /note= "constant heavy domain"

XX JP06319396-A.

XX 22-NOV-1994.

XX 07-MAY-1993; 93JP-00131208.

XX 07-MAY-1993; 93JP-00131208.

XX (NISE) JAPAN TOBACCO INC.

PA (KURS) KURARAY CO LTD.

XX WPI; 1995-040220/06.

XX N-PSDB; AAQ79930.

XX Transformed plant producing animal-derived anti-virus antibody - esp.

PT tobacco plants producing anti-tobacco mosaic virus monoclonal antibody.

XX Example 2; Page 14-15; 26pp; Japanese.

XX AAQ79929 and AAQ79930 encode AAV66757 and AAV66758, the light and heavy

CC chains of an animal derived anti-tobacco mosaic virus (TMV) monoclonal

CC antibody. The cDNAs were incorporated into a TI plasmid vector, which was

CC incorporated into A. tumefaciens. The resultant plant expression vector

CC was used to transform tobacco plants, making them TMV resistant, the

CC plants could also be biofarmed for the prodn. of anti-virus antibodies

XX Sequence 465 AA;

SQ Query Match 28.9%; Score 1018; DB 2; Length 465;

Best Local Similarity 36.3%; Pred. No. 1.9e-52;

Matches 244; Conservative 60; Mismatches 109; Indels 260; Gaps 14;

QY 1 EVOLQSGPDLVKPGASVKISCKASGYSTGYMHVKQSPGKLGLEWIGRINPNNGVTLY 60


```

Db 20 QVQLQSGAEELARPGASVKLSCKASGYTFTSYVMQWVKORPGGLEWIGAIYPSGNDTRY 79
QY 61 NQKFKDKATLTVDKSTTAYMELRSITSDSAVYICAR--STMITNYVMYDYGQGTSTVTV 118
FT 61 NQKFKDKATLTVDKSTTAYMELRSITSDSAVYICAR--STMITNYVMYDYGQGTSTVTV 118
Db 80 TQKFKGKATLTADKSSASTAYMQLSALASDSAVYICAREGGYSWSDYANDYWGQGTSTVTV 139
QY 119 SSAKTTTPPSVYPLAPGSAQAQTSMTVLGCLVKGYPPEPVTVTWNSGSLSSGVTHTTFAVLQ 178
Db 140 SSAKTTTPPSVYPLAPGSAQAQTSMTVLGCLVKGYPPEPVTVTWNSGSLSSGVTHTTFAVLQ 199
QY 179 SDLYTLSSSVTPSSVPSTETVCNVAHPASSTKVDKIVPRDSDGSPSEKSEINEKDLR 238
Db 200 SDLYTLSSSVTPSSVPSTETVCNVAHPASSTKVDKIVPRDSDGSPSEKSEINEKDLR 244
QY 239 KXSELOGTALGNLKOIYIYNSKAITSSKASDAQFNTLLFKGFTTGHFWYNDLLVDLGS 298
Db 245 --CKPCICTVPEVSSVFIPPK-----PKDVLITL----- 273
QY 299 TAATSEYEGSSVDLYGAYGYOCAGCTPNKTCMVGVTLDHNNRLTEKKYPINLWIDG 358
Db 274 -----TP-KVTCVVVDIS-----KDDPEVQFQFWVD- 298
QY 359 KQTVTPIDKVTSKKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVRQGLI 409
Db 299 --DVEVHTAQTOPREEQFNSTFRSVSELPIMHQDWLNGKFKCRVNSAAFPAPTEK--- 352
QY 410 VFHSSEGSVVDLFDQAQGYDPTLLRIYDNTTISSTLSLSLYLYTTSIVMTQTPSL 469
Db 353 -----TISKT----- 357
QY 470 LVSAGDRVITTCASQSNVDVAWYQKPGQPKLLISYTSRYAGVPDRFSGSGVTD 529
Db 358 ----- 357
QY 530 TLTISVQAEADAAYPCQDYNSPPTFGGKLEIKRADAAPTISFPPSSBQLTSGGAS 589
Db 358 -----KGRPKAPQVYVTPPPKEQMAKDKVS 382
QY 590 VVCFLNAYPKDINVKWKIDGSEKON-----GVLSNWTQDQSKDSTYSMSSTLTITKDEY 644
Db 383 LTCMTIDFPDFTVQWNGQPAENYKQTPIMNT-----NGSIFYSKLNIVQKSNW 435
QY 645 ERHNSYTCETHK 657
Db 436 EAGNTFTCSVLHE 448

RESULT 39
AAW85692
ID AAW85692 standard; protein; 711 AA.
AC AAW85692;
XX
XX
DT 12-AUG-1999 (first entry)
XX
DE
XX
XX Antibody; humanised; variable region; heavy chain; light chain;
KW interferon gamma; IFN; treatment; prevention; septic shock; cachexia;
KW immune disease; multiple sclerosis; Crohn's disease; skin disorders;
KW inflammation; neoplasia; dermatitis; monoclonal antibody; diabody; scFv;
KW multivalent; ruminant.
XX
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Peptide 1..20
FT Peptide /label= Mouse_D9D10_light_chain_signal_peptide
FT Domain 21..137
FT /notes= "Humanised heavy chain variable domain of D9D10"
FT Domain 138..467
FT /note= "Human IgG1 heavy chain constant domain"
FT Misc-difference 468

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FT Region /note= "Leu added by cloning strategy"
FT 469..472
FT /label= Gly(3)Ser_linker
FT 473..711
FT /label= Humanised_D9D10_ScFv
XX
PN WO9909055-A2.
XX
PD 25-FEB-1999.
XX
XX 14-AUG-1998; 98WO-EP005165.
XX
XX 18-AUG-1997; 97EP-00870122.
XX 18-JUN-1998; 98EP-00870139.
XX (INNO-) INNOGENETICS NV.
XX
XX Buyse M, Sablon E;
XX
XX WPI; 1999-180969/15.
XX N-PSDB; AAW85692.
XX
XX New engineered antibodies which bind and neutralise interferon-gamma -
XX useful for prevention and treatment of septic shock, cachexia, immune
XX diseases and skin disorders.
XX
XX Disclosure; Fig 20; 134pp; English.
XX
XX New antibodies which bind and neutralise interferon-gamma (IFN gamma) can
XX be used as a medicant, for preventing or treating septic shock, cachexia,
XX immune diseases including multiple sclerosis and Crohn's disease and skin
XX disorders including bullous, inflammatory and neoplastic dermatoses. The
XX antibody is selected from a single chain antibody (scFv), a chimeric
XX antibody or diabody comprising the humanised variable domain of the
XX monoclonal mouse anti-IFN gamma antibody 9D10; a multivalent antibody;
XX or a ruminant antibody. The antibodies are also useful for determining
XX IFN gamma levels in a sample
XX
XX Sequence 711 AA;
XX
XX Query Match 27.8%; Score 980.5; DB 2; Length 711;
XX Best Local Similarity 35.3%; Pred. No. 5.2e-50;
XX Matches 254; Conservative 103; Mismatches 180; Indels 183; Gaps 23;
XX
QY 1 EVQLQSGSDPLVKPGASVKISCKASGYFTGYVMHWKQSPGKLEWIGINPNNGVTLY 60
Db 21 QVQLVQSGSELKPGASVKISCKASGYFTDYGVMHWKQAPGQGLKRWGINTVTGSTY 80
QY 61 NQKFKDKATLTVDKSTTAYMELRSITSDSAVYICARSTMITNYVMYDYGQGTSTVTVSS 120
Db 81 VDDEKGRFVPSLDTSVSAAYLIQISLKAEDTATYFCARRGF---YAMDYWGQGTSTVTVSS 137
QY 121 AKTTTPPSVYPLAPGSAQAQTSMTVLGCLVKGYPPEPVTVTWNSGSLSSGVTHTTFAVLQSD 180
Db 138 ASTKGPVFPPLAPSSKSTSGTAAALGCLVKDYPPPEPVTVSWNSGALTSVHTTFAVLQSS 197
QY 181 -LYTLSSSVTPSSVPSTETVCNVAHPASSTKVDKIVPRDS-----GG 224
Db 198 GLYSLSSTVTPSSSLGTQYICNVNHPKNTKVDKEVEPKSCDKTHTCPCPAPELGG 257
QY 225 PS-----EKSEBI-----NKKDLKKSELOGTALGNLK---QIYYN 258
Db 258 PSVFLFPFKPDKTLMISRTPEVTCTVVVDVSHEDPEKFNWYVDGVEVHNKTKPREQYN 317
QY 259 S-----KAITSS-EK-----SADQ 271
Db 318 STYRVSVTLVTHQDWLNGKEYKCKVSNKALPASIETISKAKGQPREPOVYITLPPSREE 377
QY 272 FLTN-----TLTFKGFHTGHPWYNDLLVDLGSTA-ATSEYEGSS--VDLYGAYGYQCAGG 324
Db 378 MTKNQVSLTCLVKGYF-----SDIAVEWESNGPENNYKTTPEVLDSGDSFFLYSKL-- 430
QY 325 TPNTKACMYGGV----TLHD--NNRLETEK-----KVINLWIDGKQITVPIDVK 368

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Db 431 TVDKSRWQGNVFCSCVNHAEALHHYTKSLSLSPGKLGGSQVQLVQSGSELKPKGASV 490
 QY 369 KTSKKEVTVQELDLQARHYLHGKGLNNSDSFGKVGORGLIVHSHSGSTVSYDLFDAQG 428
 Db 491 KISK-----ASGYTPTDYGMMVVKQAPGQGLKMGWINTYGTSTYVD--DFKG 538
 QY 429 QYPTLLRIYRDNNTTISTSLIS-----LYLVT----- 457
 Db 539 RF-----VFLSDTSVAAYLQISLKAEDTATVFCARRGFYADYWGQTTVTVSQGG 592
 QY 458 -----TSIVMTQPTSLVLSAGDRVTITCKASQSVNSNDVAWQKPGQSPKLLI 506
 Db 593 GSGGGSGGGSDIVLTQSPATMSAPGERVTLTCSASSISY-MFYWHQRPQSPRLI 651
 QY 507 SYTSRVAGVDPRESGSGYGHDFLTITSSVQAEADAAVYFCQDDVNSPPTFGGKLEIKR 566
 Db 652 YDTNLSAGVPAFPFSGSGSGTSLTISRMEPEDFATYFCHQSSSYPTFGQGTLEIKR 711

RESULT 40

ADE06766

ID ADE06766 standard; protein; 223 AA.

XX ADE06766;

XX 29-JAN-2004 (first entry)

DE D18 heavy chain protein SEQ ID NO:36.

XX hybrid polypeptide; protein aggregation; prion polypeptide;
 KW neuroprotective; nontropic; antidiabetic; anticonvulsant;
 KW cerebroprotective; antiparkinsonian; cytostatic; nephrotropic; cardiatic;
 KW antiinflammatory; antiarteriosclerotic; gene therapy;
 KW Creutzfeldt-Jakob disease; scrapie and bovine spongiform encephalopathy;
 KW Alzheimer's disease; Type II diabetes; Huntington's disease;
 KW immunoglobulin amyloidosis; amyloidosis; chronic inflammatory disease;
 KW amyotrophic lateral sclerosis; Pick's disease; Parkinson's disease;
 KW Frontotemporal dementia; multiple myeloma; plasma cell dyscrasia;
 KW familial amyloidotic polyneuropathy; medullary carcinoma;
 KW chronic renal failure; congestive heart failure; chronic inflammation;
 KW atherosclerosis.

OS Synthetic.

XX WO2003085086-A2.

XX 16-OCT-2003.

XX 08-APR-2003; 2003WO-US010856.

XX 09-APR-2002; 2002US-0371610P.

XX (SCRI) SCRIPPS RES INST.

XX Burton DR, Williamson RA, Moroncini G;

XX WPI, 2003-877028/81.

XX N-PSDB; ADE06765.

XX New motif-grafted hybrid polypeptides binding to the infectious form of a
 PT prion, useful for diagnosing or treating diseases of protein aggregation
 PT or conformation, e.g. amyloidosis, Alzheimer's disease, renal failure or
 PT diabetes.

XX Disclosure; SEQ ID NO 36, 115pp; English.

XX The present invention describes a hybrid polypeptide (I) comprising: (a)
 CC a polypeptide motif containing a sufficient number of contiguous amino
 CC acid residues from a polypeptide associated with a disease of protein
 CC aggregation or conformation to bind an aggregating form of the
 CC polypeptide or to a disease-associate conformer of the polypeptide; and
 CC (b) an additional amino acids from a polypeptide other than the

CC polypeptide from which the motif is derived, where the resulting hybrid
 CC polypeptide binds with greater affinity to a disease causing or
 CC infectious conformer of the polypeptide that is the source of the
 CC polypeptide motif compared to a benign form of the polypeptide. Also
 CC described: (1) a nucleic acid molecule encoding (1); (2) a vector
 CC comprising the nucleic acid molecule; (3) a cell comprising the vector;
 CC (4) detecting an isoform or a PrPsc form of a prion polypeptide or a
 CC polypeptide associated with a disease of protein aggregation, in a sample
 CC; (5) a solid support comprising a plurality of polypeptides described
 CC above; (6) detecting cells that contain a protein conformer associated
 CC with a disease of protein aggregation; (7) preparing a hybrid molecule
 CC that specifically interacts with one conformer of a protein involved in
 CC the disease mentioned above; and (8) an anti-idiotype antibody that
 CC specifically binds to an infectious form of a prion protein. (I) has
 CC neuroprotective, nontropic, antidiabetic, anticonvulsant,
 CC cerebroprotective, antiparkinsonian, cytostatic, nephrotropic, cardiatic,
 CC antiinflammatory and antiarteriosclerotic activities, and can be used in
 CC gene therapy. The composition and methods of the present invention can be
 CC used in diagnosing or treating diseases of protein aggregation or
 CC conformation, such as Creutzfeldt-Jakob disease, scrapie and bovine
 CC spongiform encephalopathy, Alzheimer's disease, Type II diabetes,
 CC Huntington's disease, immunoglobulin amyloidosis, reactive amyloidosis
 CC associated with chronic inflammatory disease, hereditary systemic
 CC amyloidosis associated with autosomal dominant inheritance of variant
 CC transthyretin gene, amyotrophic lateral sclerosis, Pick's disease,
 CC Parkinson's disease, frontotemporal dementia, multiple myeloma, plasma
 CC cell dyscrasias, familial amyloidotic polyneuropathy, medullary carcinoma
 CC of thyroid, chronic renal failure, congestive heart failure, senile
 CC cardiac and systemic amyloidosis, chronic inflammation, atherosclerosis
 CC or familial amyloidosis. The present sequence is used in the
 CC exemplification of the present invention.

XX Sequence 223 AA;

XX Query Match 27.8%; Score 979.5; DB 7; Length 223;

XX Best Local Similarity 87.4%; Pred. NO. 1.5e-50;

XX Matches 194; Conservative 7; Mismatches 16; Indels 5; Gaps 2;

QY 1 EVQ-LQSGPDLVKPGASVKISKASGYSFTGYMHVWKQSPGKLEWIGRINPNNGVTL 59

Db 3 EVCLLEQSGPELVKPGSSVKISKASRYTFDDNDWVKQHGKRLWIGIYFNTGTG 62

QY 60 YNQKFKRATLTVDKSSTTAYMELRSLTSEDSAVYTCARSTMITNVMYMDYWGQGTSTVTS 119

Db 63 YNQRFKGRATLTVDKSSSTAYMELRSLTSEDSAVYTCAG---FYGMDYWGQGTSTVTS 118

QY 120 SAKTTPPSVYPLAPGSAQAQTNSMTLGLVKGYPPEPTVTWNSSGLSSGVTTPAVLQS 179

Db 119 SAKTTPPSVYPLAPGSAQAQTNSMTLGLVKGYPPEPTVTWNSSGLSSGVTTPAVLQY 178

QY 180 DLYTLSSSVTPSPSTPSETVTCNVAHPASSTKVDKIVPRD 221

Db 179 DLYTWSSSVTPSPSTPSETVTCNVAHPASSTKVDKIVPRD 220

RESULT 41

AAV55081

ID AAV55081 standard; protein; 626 AA.

XX AAV55081;

XX 25-FEB-2000 (first entry)

DE Single chain Fv protein sequence sHPM1-kappa-BvGS3.

XX Gene isolation; membrane-bound protein; fusion protein; drug production;
 KW antigen-binding cell; secretable functional protein; antigenic protein;
 KW protein isolation; diagnosis; scfv.

OS Synthetic.

XX WO9960113-A1.

CC treat cancer, and may also used as a gene delivery system for introducing
CC at least 1 gene encoding a TRP (preferably a tumour binding protein) into
CC a haematopoietic cell lineage
XX
SQ Sequence 243 AA;

Query Match 27.6%; Score 972.5; DB 2; Length 243;
Best Local Similarity 40.1%; Pred. No. 4.3e-50;
Matches 227; Conservative 3; Mismatches 13; Indels 323; Gaps 5;
QY 1 EVQLQQSGPDLVKGASVKISKAGSYFTGYMHWKQSPGKLEWIGRINPNNGVTL 60
DB 1 EVQLQQSGPDLVKGASVKISKAGSYFTGYMHWKQSPGKLEWIGRINPNNGVTL 60
QY 61 NQKFKDKATLTVDKSSITAYMELSLTSEDASVYCARSTMTNYMDYWGQGSVTVS 120
DB 61 NQKFKDKATLTVDKSSITAYMELSLTSEDASVYCARSTMTNYMDYWGQGSVTVS 119
QY 121 AKTTPPSVYPLAPGSAQAQNSMTLGLVKGYPPEPVTVTWNSGSLSSGVHTFPVAVLQSD 180
DB 120 ----- 119
QY 181 LYTLSSTVTPSSVTPSETVTCNVAHPASSTKVDKIVPRDSGGPSEKSEINEKDLRKK 240
DB 120 ----- 122
QY 241 SELOQTALGNLQIYYNSKAITSEKSAQDLNTLLFKGFTGHPWYNDLLVGLGSA 300
DB 123 ----- 122
QY 301 ATSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
DB 123 ----- 132
QY 361 TTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQGLIVFHSSEGSTVS 420
DB 133 ----- 134
QY 421 YDLFDAQGYPTLLRIYRDNNTTISLSLYLXTTSIVMTQTPTSLVLSAGDRVIT 480
DB 135 ----- 157
QY 481 CKASQSVNDVAVYQKPGQPKLLISYTSRVAGVDPDFSGSGYGTDFLTLLTSSVQAE 540
DB 158 CKASQSVNDVAVYQKPGQPKLLISYTSRVAGVDPDFSGSGYGTDFLTLLTSSVQAE 217
QY 541 AAVYFCQDYNSPTFFGGTGLEIKR 566
DB 218 LAVYFCQDYNSPTFFGGTGLEIKR 243

RESULT 43
ID AAY42294
XX AAY42294 standard; protein; 243 AA.
AC AAY42294;
XX
DT 06-DEC-1999 (first entry)
XX
DE Anti-5T4 secreted single chain antibody Fv fragment.
XX
KW Cytochrome; targeting; localisation; cancer; tumour; prodrug; reduction;
XX nucleus.
OS Homo sapiens.
OS Synthetic.
XX
FN WO9945127-A2.
XX
PD 10-SEP-1999.
XX
PF 05-MAR-1999; 99WO-GB000674.
XX

PR 06-MAR-1998; 98GB-00004841.
PR 19-AUG-1998; 98GB-00018103.
PR 29-JAN-1999; 99GB-00002081.
XX
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
XX Stratford IJ, Patterson AV, Kingsman SM, Kan O, Griffiths L;
PI Mitrophanous X;
XX
XX WPI: 1999-551046/46.
DR N-PSDB; AAZ19786.
XX
XX New prodrug activating agent targeted to selected cells or tissues,
PT particularly hypoxic cells, for treating e.g. tumors.
PT
PS Example 9; Fig 3; 187pp; English.
XX

CC This sequence represents an example of a secreted single chain antibody
CC Fv fragment (in this case, directed against the 5T4 antigen), which is
CC involved in transcellular localisation. A secreted single chain antibody
CC Fv fragment can be fused to cytochrome P450 reductase (P450R) derivatives
CC such as anchorless P450R (AAY42287) or Fv fragment (AAY42288). This
CC enables the fusion protein to be delivered to other cells where it is
CC then transported to the nucleus. Many drugs' sites of action are in the
CC nucleus, rather than the cytoplasm, where P450R normally functions. P450R
CC or its derivatives can be used to activate prodrugs to their active form
CC via reduction. Administration of a prodrug is useful where the active
CC drug may be metabolised before it reaches its site of action or where the
CC active drug is cytotoxic, e.g., anticancer drugs. Targeted delivery of
CC such prodrug activators allows a reduction in dose of the prodrug, and
CC thus of systemic side-effects. P450R derivative fusion proteins, or
CC vectors that express them, are specifically used to treat tumours,
CC inflammation, atherosclerosis and muscular dystrophy, but may also be
CC used to treat many other conditions, e.g., cerebral malaria, rheumatoid
CC arthritis, or conditions associated with hypoxia, ischaemia or
CC hypoglycemia, or to deliver antibiotics, antiviral agents, analgesics,
CC anaesthetics, anti-inflammatories, antineoplastic agents and diagnostic
CC agents

XX SQ Sequence 243 AA;
Query Match 27.6%; Score 972.5; DB 2; Length 243;
Best Local Similarity 40.1%; Pred. No. 4.3e-50;
Matches 227; Conservative 3; Mismatches 13; Indels 323; Gaps 5;
QY 1 EVQLQQSGPDLVKGASVKISKAGSYFTGYMHWKQSPGKLEWIGRINPNNGVTL 60
DB 1 EVQLQQSGPDLVKGASVKISKAGSYFTGYMHWKQSPGKLEWIGRINPNNGVTL 60
QY 61 NQKFKDKATLTVDKSSITAYMELSLTSEDASVYCARSTMTNYMDYWGQGSVTVS 120
DB 61 NQKFKDKATLTVDKSSITAYMELSLTSEDASVYCARSTMTNYMDYWGQGSVTVS 119
QY 121 AKTTPPSVYPLAPGSAQAQNSMTLGLVKGYPPEPVTVTWNSGSLSSGVHTFPVAVLQSD 180
DB 120 ----- 119
QY 181 LYTLSSTVTPSSVTPSETVTCNVAHPASSTKVDKIVPRDSGGPSEKSEINEKDLRKK 240
DB 120 ----- 122
QY 241 SELOQTALGNLQIYYNSKAITSEKSAQDLNTLLFKGFTGHPWYNDLLVGLGSA 300
DB 123 ----- 122
QY 301 ATSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
DB 123 ----- 132
QY 361 TTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQGLIVFHSSEGSTVS 420
DB 133 ----- 134

QY 421 YDLFDAQGYPTLLRIYRDNTTISTSLISLYYTSIVMTQPTSLVAGDRVTIT 480
 Db 135 -----SSIVMTQPTFLVAGDRVTIT 157
 QY 481 CKASQSVNDVAVYQKPGQSKLLISYTSRYAGVDFSGGYGTPTLTISVQAE 540
 Db 158 CKASQSVNDVAVYQKPGQSKLLISYTSRYAGVDFSGGYGTPTLTISVQAE 217
 QY 541 AAVYFCQDYNPPTFGGKTLEIKR 566
 Db 218 LAVYFCQDYNPPTFGGKTLEIKR 243

RESULT 44
 AAY27407
 ID AAY27407 standard; protein; 243 AA.
 XX AC AAY27407;
 XX DT 23-NOV-1999 (first entry)
 XX DE 5T4 scFv antibody signal peptide.
 XX KW Prodrug; localization domain; tumor-selective antibody; cytochrome P450;
 KW prodrug activating domain; modified hematopoietic stem cell; MHC; tumor;
 KW inflammation; atherosclerosis; muscular dystrophy; cerebral malaria;
 KW rheumatoid arthritis; hypoxia; ischemia; hypoglycemia; tumor antigen;
 KW 5T4 scFv.
 XX OS Unidentified.
 XX PN WO9945126-A2.
 XX PD 10-SEP-1999.
 XX PF 05-MAR-1999; 99WO-GB000672.
 XX PR 06-MAR-1998; 98GB-00004841.
 XX PR 19-AUG-1998; 98GB-00018103.
 XX PR 29-JAN-1999; 99GB-00002081.
 XX PA (OXFO-) OXFORD BIOMERICA UK LTD.
 XX PI Stratford IJ, Patterson AV, Kingsman SM, Kan O, Griffiths L;
 PI Mitrophanous K;
 DR WPI: 1999-540852/45.
 DR N-PSDB; AA207810.
 XX New prodrug activating agent targeted to selected cells or tissues,
 PT particularly hypoxic cells, for treating e.g. tumors or inflammation.
 XX Example 9; Fig 3F; 149pp; English.
 XX The invention provides a new prodrug activating agent that comprises: (i)
 CC a localization domain (LD; other than a tumor-selective antibody) and a
 CC prodrug activating domain (PAD); (ii) at least one nucleic acid encoding
 CC a cytochrome P450 and under control of at least one constitutive or
 CC inducible expression control sequence or (iii) a modified hematopoietic
 CC stem cell (MHC) containing at least one nucleic acid encoding a PAD and
 CC under control of elements as in (ii). The prodrug activating agent or
 CC vectors that express them, are specifically used to treat tumors,
 CC inflammation, atherosclerosis and muscular dystrophy, but may also be
 CC used to treat many other conditions, e.g. cerebral malaria, rheumatoid
 CC arthritis, or conditions associated with hypoxia, hypoglycemia or
 CC ischemia, or to deliver antibiotics, antiviral agents, analgesics,
 CC anesthetics, anti-inflammatories, antineoplastic agents and diagnostic
 CC agents. LD optimize activity of PAD, e.g. by delivering it to selected
 CC locations or by delivering it to neighboring cells (bystander effect),
 CC and allow a reduction in dose of prodrug, and thus of systemic side-
 CC effects. Nucleic acids encoding the agent may be expressed selectively in
 CC hypoxic cells. The present sequence represents the single chain variable
 CC antibody fragment against the tumor antigen 5T4 (5T4 scFv). 5T4 scFv is

CC used in the construction of a fusion protein comprising 5T4 scFv and a
 CC human P450 reductase derivative alp450R
 XX Sequence 243 AA;
 SQ
 Query Match 27.68; Score 972.5; DB 2; Length 243;
 Best Local Similarity 40.1%; Pred. No. 4.3e-50;
 Matches 227; Conservative 3; Mismatches 13; Indels 323; Gaps 5;
 QY 1 EVQLQQSGPDLVKPGASVKISKASGYSTFGYMHVWKQSPGKGLWIGRINPNNGVTLY 60
 Db 1 EVQLQQSGPDLVKPGASVKISKASGYSTFGYMHVWKQSPGKGLWIGRINPNNGVTLY 60
 QY 61 NQKPKDKATITVDKSTTAYMELRLTSEDSAVYCARSTMITNYMDYVWGQSTVTVSS 120
 Db 61 NQKPKDKATITVDKSTTAYMELRLTSEDSAVYCARSTMITNYMDYVWGQSTVTVSS- 119
 QY 121 AKTTPPSVYPLAPGSAAGTNSMTLGLVKGYPEPVTVTWNSGSLSSGVHTTFAVLQSD 180
 Db 120 ----- 119
 QY 181 LYTLSSSVTPSPSTWPTSETVTCNVHPASSTKVDKKIIVPRDSGPPSEKSEINEKDLRKK 240
 Db 120 -----SGG----- 122
 QY 241 SELQGTALGNLKOIYYVNSKAITSSSEKSADQFLNTLLFKGFTGHPWYNDLLVDLGSTA 300
 Db 123 ----- 122
 QY 301 ATSEYEGSSVDLYGAYYGYCAGGTGNKACTACMYGGVTLHDNNLTLBEKKVPINLWIDGKQ 360
 Db 123 -----GGSGGGGT-----GG----- 132
 QY 361 TTVPIDKVKTSKEVTVOELDLQARHYLHGKFLGYNLSDSGGKVGQRLIVPHSSEGSTVS 420
 Db 133 -----GG----- 134
 QY 421 YDLFDAQGYPTLLRIYRDNTTISTSLISLYYTSIVMTQPTSLVAGDRVTIT 480
 Db 135 -----SSIVMTQPTFLVAGDRVTIT 157
 QY 481 CKASQSVNDVAVYQKPGQSKLLISYTSRYAGVDFSGGYGTPTLTISVQAE 540
 Db 158 CKASQSVNDVAVYQKPGQSKLLISYTSRYAGVDFSGGYGTPTLTISVQAE 217
 QY 541 AAVYFCQDYNPPTFGGKTLEIKR 566
 Db 218 LAVYFCQDYNPPTFGGKTLEIKR 243

RESULT 45
 AAB83835
 ID AAB83835 standard; protein; 243 AA.
 XX AC AAB83835;
 XX DT 23-JUL-2001 (first entry)
 XX DE Amino acid sequence of a 5T4 ScFv designated 5T4ScFv.1.
 XX KW Single chain antibody; ScFv; inflammatory disease; arthritis; cancer;
 KW hypersensitivity; autoimmune disease; central nervous system disorder;
 KW Parkinson's disease; periodontal disease; cardiopulmonary disease;
 KW cardiovascular disease; gastrointestinal disorder; infection; diabetes;
 KW Helicobacter-related disease; immune disorder.
 XX OS Synthetic.
 OS Mus sp.
 XX Key Location/Qualifiers
 FT Misc-difference 169
 FT /note= "Ala encoded by GDT"
 XX

PN WO200136486-A2.
 XX PD 25-MAY-2001.
 XX PF 13-NOV-2000; 2000WO-GB004317.
 XX PR 18-NOV-1999; 99WO-GB003859.
 XX PR 15-FEB-2000; 2000GB-00003527.
 XX PR 02-MAR-2000; 2000GB-00005071.
 XX PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 XX PI Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;
 XX PI Myers KA;
 XX DR WPI: 2001-343805/36.
 XX DR N-PSDB; AAF89729.
 XX PT Use of single chain antibody capable of recognizing a disease associated
 PT molecule for manufacturing a medicament for preventing and/or treating a
 PT disease condition associated with disease associated molecule.
 XX PS Claim 3; Fig 1; 118pp; English.
 XX CC The specification describes the use of a single chain antibody (ScFv),
 CC which is capable of recognizing a disease associated molecule in the
 CC manufacture of a medicament for the prevention and treatment of a disease
 CC condition. The ScFv antibody is useful in the manufacture of a
 CC medicament for affecting a disease in vivo, for preparing a
 CC pharmaceutical composition, for in vivo imaging and/or for adjuvant
 CC treatment of a disease. The ScFv antibody is also useful for treating
 CC inflammatory diseases including arthritis, hypersensitivity, autoimmune
 CC diseases, cancers, central nervous system disorders including Parkinson's
 CC disease, pericardial diseases, cardiopulmonary diseases, cardiovascular
 CC diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
 CC related diseases, and other immune disorders. The present sequence
 CC represents a 574 ScFv of the invention. The antibody comprises the VH and
 CC VL regions from murine 574 monoclonal antibody, joined by a linker
 CC sequence
 XX SQ Sequence 243 AA;

Query Match 27.6%; Score 972.5; DB 4; Length 243;
 Best Local Similarity 40.1%; Pred. No. 4.3e-50;
 Matches 227; Conservative 3; Mismatches 13; Indels 323; Gaps 5;
 QY 1 EVQLQQSGPDLVKPGASVKISKASGYSFTGYMHVWVQSPGKLEWIGRINPNNGVTLY 60
 DB 1 EVQLQQSGPDLVKPGASVKISKASGYSFTGYMHVWVQSPGKLEWIGRINPNNGVTLY 60
 QY 61 NQKPKDKATLVDSSTAYMELSLTSEDNAVYVCARSTMTINVMYDYGQTSVTSS 120
 DB 61 NQKPKDKATLVDSSTAYMELSLTSEDNAVYVCARSTMTINVMYDYGQTSVTSS- 119
 QY 121 AKTTPSPVYPLAPGSAAGTNSMTVLGCLVKGYPFPEPTVTWNSGSLSGGVHTFPVLQSD 180
 DB 120 ----- 119
 QY 181 LYTSSSVTPSPSTWSPSTVTCNVNAPASSTKVDKIVPRDSGDPSEKSEINEKLRKK 240
 DB 120 -----SGG----- 122
 QY 241 SELQGTALGNLQKIYYNYSKAITSSKSAQDQFLNTLLFKGFFTGHPWYNDLLVDLGSTA 300
 DB 123 ----- 122
 QY 301 ATSEYEGSSVDLYGAYGYQCAGTTPNKTAQWCGVTLHDNNRLTEKKVPINLWIDGKQ 360
 DB 123 -----GGSGGGGT-----GG----- 132
 QY 361 TTVPIDKVKTSKEVTYQELDLQARHYLHGKFGLYNSDSFGGKVGQGLIVFHSSEGSTVS 420
 DB 133 -----GG----- 134

QY 421 YDLFDAQGOYPTLLRIYRDNNTTISSTLSISLYLTTSIVMTOTPTPTLLYSAGDRVTIT 480
 DB 135 -----SSIVMTOTPTPTLLYSAGDRVTIT 157
 QY 481 CKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDTFTITISVQAE 540
 DB 158 CKASQSVNDVAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDTFTITISVQAE 217
 QY 541 AAVYFCQDYNPPTFGGTTKLEIKR 566
 DB 218 LAVYFCQDYNPPTFGGTTKLEIKR 243
 RESULT 46
 AAY44176
 ID AAY44176 standard; protein; 214 AA.
 XX AC AAY44176;
 XX DT 01-FEB-2000 (first entry)
 XX DE MAb Fab13B5 heavy chain protein sequence.
 XX KW Peptide ligand; affinity; p24; human immune deficiency virus-1; HIV-1;
 KW light chain; heavy chain; Fab; monoclonal antibody; hypervariable region;
 KW infection.
 XX OS Mus sp.
 XX PN FR2777285-A1.
 XX PD 15-OCT-1999.
 XX PF 10-APR-1998; 98FR-00004876.
 XX PR 10-APR-1998; 98FR-00004876.
 XX PA (INMR) BIO MERIEUX.
 XX PI Novelli RA, Monaco S, Piga N, Berthet C, Mallet F, Cusack S;
 PI Chassaing V;
 DR WPI: 1999-593428/51.
 DR N-PSDB; AA228805.
 XX PT New peptide ligand specific for p24 of human immune deficiency virus
 PT contains hypervariable regions of antibody 13B5, used for diagnosing HIV
 PT infection.
 XX PS Claim 2; Page 20-21; 27pp; French.
 XX CC The invention relates to a peptide ligand with specific affinity for the
 CC p24 protein of human immune deficiency virus-1 (HIV-1) comprising at
 CC least one peptide strand corresponding to the N-terminal region of the
 CC light and/or heavy chain of the Fab fragment of monoclonal antibody 13B5
 CC in which: (i) the light chain includes three hypervariable regions (HVR)
 CC at amino acid (aa) positions 24-33, 49-55 and 88-95 of AAY44175; and (ii)
 CC the heavy chain includes three HVR at aa positions 26-35, 49-65 and 99-
 CC 109 of this sequence. The peptide ligands are reagents for detecting p24
 CC (by standard immunoassays) in biological samples, specifically for
 CC diagnosis of HIV-1 infection or can be used to treat HIV-1 infections
 XX SQ Sequence 214 AA;

Query Match 27.5%; Score 970; DB 2; Length 214;
 Best Local Similarity 85.0%; Pred. No. 5.2e-50;
 Matches 182; Conservative 15; Mismatches 17; Indels 0; Gaps 0;
 QY 1 EVQLQQSGPDLVKPGASVKISKASGYSFTGYMHVWVQSPGKLEWIGRINPNNGVTLY 60
 DB 1 EVQLQQSGAELARPASVKMSCKASGYFTTSTWVHWKQRPQGKLEWIGYINPSSGSYNY 60

DE	Amino acid sequence of a B7-1.5T4.1 fusion protein.
XX	
XX	Single chain antibody; SCFv; inflammatory disease; arthritis; cancer;
KW	hypersensitivity; autoimmune disease; central nervous system disorder;
KW	Parkinson's disease; periodontal disease; cardiopulmonary disease;
KW	cardiovascular disease; gastrointestinal disorder; infection; diabetes;
KW	Helicobacter-related disease; immune disorder.
XX	
XX	Synthetic.
OS	Mus sp.
OS	Homo sapiens.
XX	
XX	
PN	WO200136486-A2.
XX	
PD	25-MAY-2001.
XX	
XX	
PF	13-NOV-2000; 2000WO-GB004317.

PR 18-NOV-1999; 99WO-GB003859.
 PR 15-FEB-2000; 2000GB-00003527.
 PR 02-MAR-2000; 2000GB-00005071.
 PA (OXFO-) OXFORD BIOMEDICA UK LTD.
 PA Kingsman A, Kingsman SM, Bebbington CR, Carroll MW, Ellard FM;
 PI Myers KA;
 XX WPI; 2001-343805/36.
 DR N-PSDB; AAF89730.
 XX Use of single chain antibody capable of recognizing a disease associated
 PT molecule for manufacturing a medicament for preventing and/or treating a
 PT disease condition associated with disease associated molecule.
 XX
 PS Claim 3; Fig 2; 118pp; English.
 XX The specification describes the use of a single chain antibody (ScFv),
 CC which is capable of recognizing a disease associated molecule in the
 CC manufacture of a medicament for the prevention and treatment of a disease
 CC condition. The ScFv antibody is useful in the manufacture of a
 CC medicament, for affecting a disease in vivo, for preparing a
 CC pharmaceutical composition, for in vivo imaging and/or for adjuvant
 CC treatment of a disease. The ScFv antibody is also useful for treating
 CC inflammatory diseases including arthritis, hypersensitivity, autoimmune
 CC diseases, cancers, central nervous system disorders including Parkinson's
 CC disease, periodontal diseases, cardiopulmonary diseases, cardiovascular
 CC diseases, gastrointestinal disorders, infections, diabetes, Helicobacter-
 CC related diseases, and other immune disorders. The present sequence
 CC represents a B7-1.574.1 fusion protein. This comprises the N-terminus of
 CC the 574 ScFv is fused after amino acid 215 of human B7-1
 XX
 SQ Sequence 488 AA;
 Query Match 27.5%; Score 967.5; DB 4; Length 488;
 Best Local Similarity 40.0%; Pred. No. 2e-49;
 Matches 226; Conservative 3; Mismatches 13; Indels 323; Gaps 5;
 QY 1 EVOIQSGPDLVKPGASVKISKASGYSFTGYNHWKQSPGKLEWIRPNNGVTLY 60
 DB 247 EVOIQSGPDLVKPGASVKISKASGYSFTGYNHWKQSPGKLEWIRPNNGVTLY 306
 QY 61 NQKFKDKATLVDSSTAYMELSLTSEDSAVYICARSTMTNYVMDYWGQSTVTVS 120
 DB 307 NQKFKDKAILAVDKSSSTAYMELSLTSEDSAVYICARSTMTNYVMDYWGQSTVTVS 365
 QY 121 AKTTPSPVYPLAPGSAAGTNSMTVLGCLVKGYPPEVTVTWNSGLSSGVTTPAVLQSD 180
 DB 366 ----- 365
 QY 181 LYTLSSTVTPSTWSPSETVTCNVAHPASTKVDKIVPRDSGGPSEKSEINEKDLRX 240
 DB 366 -----SGG----- 368
 QY 241 SELQGTALGNLKQIYYNSKAITSEKSAQDQFLNTLLFKGFFTCGHPWYNDLLVLDGSTA 300
 DB 369 ----- 368
 QY 301 ATSEYEGSSVDLYGAYGYQCAGCTPNKTCACMGGVTLHDNNRLTEBKVPINLWIDGKQ 360
 DB 369 -----GGSGGGT----- 378
 QY 361 TTVPIDKVKTSKEVTVQELDLQARHYLHGKFLGYNLSDSPGKQVORGLIVFHSSEGSTVS 420
 DB 379 ----- 380
 QY 421 YDLFDAQSQGPDLLRIYRDNNTTISLSTSLSYLYTTSIVMTQTPSTLLVLSAGDRVTIT 480
 DB 381 -----SSIVMTQTPSTLLVLSAGDRVTIT 403
 QY 481 CKASQSVNDVAVYQQKPGQSPKLLISYTSRYAGVPRFPGSGYGTDTFTTISTLQAE 540

DB 404 CKASQSVNDVAVYQQKPGQSPKLLISYTSRYAGVPRFPGSGYGTDTFTTISTLQAE 463
 QY 541 AAVYFCQQDYNSPPTFGGKLEIK 565
 DB 464 LAVYFCQQDYNSPPTFGGKLEIK 488
 RESULT 49
 ABU07262
 ID ABU07262 standard; protein; 488 AA.
 XX AC
 XX ABU07262;
 XX 29-JAN-2003 (first entry)
 XX Human expressed protein tag (BPT) #1963.
 DE XX
 XX Translational profiling; expressed protein tag; BPT; kinase; phosphatase;
 KW protease; protease inhibitor; transporter; cytoskeletal protein;
 KW receptor; transcription factor; cancer; MHC;
 KW major histocompatibility complex; myeloma; colon cancer; gastric cancer;
 KW adenocarcinoma; sarcoma; melanoma; lymphoma; leukaemia.
 OS Homo sapiens.
 XX WO200278524-A2.
 XX 10-OCT-2002.
 XX 28-MAR-2002; 2002WO-US009671.
 XX 28-MAR-2001; 2001US-0279495P.
 PR 21-MAY-2001; 2001US-0292544P.
 PR 08-AUG-2001; 2001US-0310801P.
 PR 01-OCT-2001; 2001US-0326370P.
 PR 04-DEC-2001; 2001US-0336780P.
 PR 20-FEB-2002; 2002US-0358985P.
 XX (ZYCO-) ZYCOS INC.
 XX Chicx RM, Tomlinson AJ, Urban RG;
 XX WPI; 2003-040607/03.
 DR XX
 XX New polypeptides (e.g. kinases, phosphatases, proteases, transporters,
 PT cytoskeletal proteins, receptors or transcription factors), useful for
 PT treating cancer, e.g. colon cancer, gastric cancer, sarcoma, lymphoma or
 PT leukemia.
 XX
 PS Example 2; SEQ ID NO 1963; 134pp; English.
 XX
 CC The invention describes a purified polypeptide, which comprises a
 CC fragment of a kinase, phosphatase, protease, protease inhibitor,
 CC transporter, cytoskeletal protein, receptor or transcription factor. The
 CC polypeptide is useful as an immunogenic composition for eliciting in a
 CC mammal an immunogenic response directed against any of the purified
 CC polypeptide. The purified polypeptide, or the antibody that binds to this
 CC polypeptide, is useful for treating cancer. The polypeptide is also
 CC useful for identifying compounds that binds to a naturally processed
 CC class I or class II MHC-binding polypeptide. The polypeptides and
 CC polynucleotides are particularly useful for treating or preventing
 CC myeloma, colon cancer, gastric cancer, adenocarcinoma, sarcoma, melanoma,
 CC lymphoma or leukaemia. These are also useful for screening agents for
 CC treating the above mentioned diseases. This sequence represents an
 CC expressed protein tag (BPT) isolated from human tissue for translational
 CC profiling. Note: This sequence does not appear in the printed
 CC specification but was obtained in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 488 AA;
 Query Match 27.5%; Score 967.5; DB 6; Length 488;
 Best Local Similarity 40.0%; Pred. No. 2e-49;

QY 541 AAVYFCQDYNPPTFGGTTKLEIK 565
 DB 464 LAVYFCQDYNPPTFGGTTKLEIK 488

RESULT 51
 ABP96772
 ID ABP96772 standard; protein; 209 AA.

AC ABP96772;
 XX
 DT 05-JUN-2003 (first entry)
 XX
 DE TSH receptor antibody 3C7 heavy chain amino acid sequence.
 KW Thyrotropin receptor; TSH receptor; epitope region; antibody;
 KW autoantibody; autoimmune disease; thyroid tissue; cytostatic;
 KW gene therapy; immune reaction; thyroid cancer.
 XX
 OS Synthetic.
 XX
 PN WO2003018632-A2.
 PD 06-MAR-2003.
 XX
 PF 21-AUG-2002; 2002WO-GB003831.
 XX
 PR 23-AUG-2001; 2001GB-00020649.
 PR 01-JUL-2002; 2002GB-00015212.
 XX
 PA (RSRR-) RSR LTD.
 XX

PI Smith BR, Furmaniak J, Sanders JF;

DR WPI; 2003-290051/28.
 DR N-PSDB; ACC44927.

XX New polypeptide sequence having part or all of the primary structural
 PT conformation of one or more TSH receptor epitopes, useful for treating an
 PT autoimmune disease associated with an immune reaction to a TSH receptor,
 PT e.g. thyroid cancer.
 XX

PS Claim 67; Fig 46; 196pp; English.

CC The present invention describes a polypeptide sequence comprising part or
 CC all of the primary structural conformation of one or more thyrotropin
 CC (TSH) receptor epitopes with which autoantibodies and/or lymphocytes
 CC produced in response to a TSH receptor interact. Also described: (1) one
 CC or more receptor TSH epitopes with which the autoantibodies and/or
 CC lymphocytes interact, as with the polypeptide sequence described above;
 CC (2) a method of screening for autoantibodies or lymphocytes produced in
 CC response to a TSH receptor in a sample of body fluid obtained from a
 CC subject suspected of suffering from, susceptible to, having or recovering
 CC from autoimmune disease associated with an immune reaction to a TSH
 CC receptor; and (4) a combination comprising the binding partner
 CC and one or more further agents capable of stimulating thyroid tissue,
 CC or tissue containing a TSH receptor, for simultaneous, separate or
 CC sequential use in stimulating thyroid tissue, and/or tissue containing a
 CC TSH receptor. A TSH receptor has cytostatic activity and can be used in
 CC gene therapy. The polypeptide, compositions and methods from the present
 CC invention can be used for treating an autoimmune disease associated with
 CC an immune reaction to a TSH receptor. The specific binding partner is
 CC useful for the manufacture of a medicament for stimulating thyroid tissue
 CC or tissue containing a TSH receptor, and for treating thyroid cancer.
 CC ACC44874 to ACC44905 and ABP96719 to ABP96750 represent TSH receptor
 CC sequences, and ACC44910 to ACC44933 encode the TSH receptor antibody VH
 CC and VL domains given in ABP96751 to ABP96778, which are used in the
 CC exemplification of the present invention

SQ Sequence 209 AA;

Query Match 27.4%; Score 966.5; DB 6; Length 209;
 Best Local Similarity 87.4%; Pred. No. 8.2e-50;
 Matches 187; Conservative 9; Mismatches 13; Indels 5; Gaps 1;

QY 1 EVQLQSGPDLVKPGASVKISKASGYSTGYMHVWQSPKGLWIGRINPNNGVTLV 60
 DB 1 DVQLXSGPELVKPGASMKISKASGYSTGYTMWVRQSHGKNDLWIGLINPYNGGTSY 60
 QY 61 NQKFKDKATLTVDKSTTAYMELRSITSEDSAVVYCARSTMTITNVMYDYGQGTSTVSS 120
 DB 61 DQKFKGATLTVDKSSSTAYMELLSITSEDSAVVYCARDGL-----MDYWGQGTSTVSS 115
 QY 121 AKTTPPSVYVPLAPGSAQAQTNSMVTGLGCLVKGYFPEPTVTWNSGSLSSGVHTFPAVLQSD 180
 DB 116 AKTTPPSVYVPLAPGSAQAQTNSMVTGLGCLVKGYFPEPTVTWNSGSLSSGVHTFPAVLQSD 175
 QY 181 LYTLLSSVTPSPSTWPSSETVTCNVAHPASSIKVD 214
 DB 176 LYTLLSSVTPSPSTWPSSETVTCNVAHPASKTKVD 209

RESULT 52

ABP96771
 ID ABP96771 standard; protein; 209 AA.

AC ABP96771;

DT 05-JUN-2003 (first entry)

DE TSH receptor antibody 3C7 heavy chain amino acid sequence.

XX Thyrotropin receptor; TSH receptor; epitope region; antibody;
 KW autoantibody; autoimmune disease; thyroid tissue; cytostatic;
 KW gene therapy; immune reaction; thyroid cancer.
 XX

OS Synthetic.

PN WO2003018632-A2.

PD 06-MAR-2003.

PF 21-AUG-2002; 2002WO-GB003831.

PR 23-AUG-2001; 2001GB-00020649.

PR 01-JUL-2002; 2002GB-00015212.

XX (RSRR-) RSR LTD.

PI Smith BR, Furmaniak J, Sanders JF;

DR WPI; 2003-290051/28.

DR N-PSDB; ACC44926.

XX New polypeptide sequence having part or all of the primary structural
 PT conformation of one or more TSH receptor epitopes, useful for treating an
 PT autoimmune disease associated with an immune reaction to a TSH receptor,
 PT e.g. thyroid cancer.
 XX

PS Claim 71; Fig 45; 196pp; English.

XX The present invention describes a polypeptide sequence comprising part or
 CC all of the primary structural conformation of one or more thyrotropin
 CC (TSH) receptor epitopes with which autoantibodies and/or lymphocytes
 CC produced in response to a TSH receptor interact. Also described: (1) one
 CC or more receptor TSH epitopes with which the autoantibodies and/or
 CC lymphocytes interact, as with the polypeptide sequence described above;
 CC (2) a method of screening for autoantibodies or lymphocytes produced in
 CC response to a TSH receptor in a sample of body fluid obtained from a
 CC subject suspected of suffering from, susceptible to, having or recovering
 CC from autoimmune disease associated with an immune reaction to a TSH
 CC receptor; and (3) a binding partner for a TSH receptor, which is capable of

ID AAR40385 standard; protein, 225 AA.
 AC AAR40385;
 XX
 DT 25-MAR-2003 (revised)
 DT 10-MAR-2003 (revised)
 DT 08-FEB-1994 (first entry)
 XX
 DE Monoclonal antibody M(alpha)2-3 light-chain.
 XX
 KW anti-snake small neurotoxin antibody; kappa; light chain; immunoglobulin;
 KW bispecific bivalent antibody; cell-targeting; cytotoxic agent.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..12
 FT /label= signal_peptide
 FT Region 13..118
 FT /label= variable
 FT Region 119..225
 FT /label= constant
 XX
 XX EP556111-A1.
 PN
 XX
 PD 18-AUG-1993.
 XX
 XX 09-FEB-1993; 93EP-00400323.
 PF
 XX 11-FEB-1992; 92FR-00001505.
 PR
 XX (COMS) COMMISSARIAT ENERGIE ATOMIQUE.
 PA
 XX Boulain J, Ducancel F, Gillet D, Menez A;
 PI
 XX WPI; 1993-260351/33.
 DR
 DR N-PSDB; AAQ48038.
 XX
 XX New immunoglobulin hybrid proteins - with immunoglobulin fragments linked
 FT to dimeric protein, for diagnostic or therapeutic use.
 PT
 XX
 PS Example 1; Fig 3B; 37pp; French.
 XX
 CC A fragment of the heavy chain (VH + CH1) from the anti-snake small
 CC neurotoxin monoclonal antibody M(alpha)2-3 was PCR-amplified from
 CC hybridoma-derived cDNA using primers AAQ48039 and AAQ48040. A light chain
 CC fragment (VL + CL) was amplified from the same source using primers
 CC AAQ48041 and AAQ48042. The two amplified fragments were inserted into the
 CC same vector; the H-chain fragment was inserted (in-frame) between codons
 CC 6-7 of the phoA coding sequence and the L-chain fragment was inserted
 CC into a cassette which contained a phoA S-D sequence, a signal peptide and
 CC the first 6 codons of phoA. The cassette was positioned between the
 CC termination codon and the transcription termination sequence of phoA. The
 CC fusion construct is expected to encode a hybrid protein comprising two
 CC identical Ab-derived units. The invention also covers hybrid proteins
 CC containing two different Ab-derived units (i.e. to produce bispecific
 CC antibodies). When a toxic protein is used in place of phoA, the hybrid
 CC molecules can be used as cell-targeting therapeutic agents. (Updated on
 CC 10-MAR-2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct
 CC PN field.)
 XX
 SQ Sequence-225 AA;
 XX
 Query Match 27.3%; Score 961.5; DB 2; Length 225;
 Best Local Similarity 88.6%; Pred. No. 1.8e-49;
 Matches 194; Conservative 4; Mismatches 8; Indels 13; Gaps 5;
 QY 459 SIVMTQTPTSLVLSAGDRTTTCRASQSVNDVAVYKQKPGQSKLLIS--YTSRYAGV 516
 DB 13 SIVMTQTPTKLLSAGDRTTTCRASQSVNDVAVY--KPGQSKLLIQYIASSRYTG 70
 QY 517 PDRFGSGYGTDFLTLTSSVQAEADAVYFCQDYNSTPFGGKLEIKRADAAPTYSIF 576

DB 71 PDRFTSGYGTDFLTSTVQAEADLAVYFCQDYNSTPFGGKLEIKRADAAPTYSIF 129
 QY 577 PPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLSWTDQDSKDYMSST 636
 DB 130 PPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLSWTDQDSKDYMSST 189
 QY 637 LTLTKDEYERH-----NSYTCATHKTSTSPVKSFNNE 671
 DB 190 LTL-----YERHTKDNSYTCATHKTSTSPVKSFNNE 224
 RESULT 55
 AAW15932
 ID AAW15932 standard; protein, 212 AA.
 XX
 AC AAW15932;
 XX
 DT 09-DEC-1997 (first entry)
 XX
 DE Antibody 7G12 heavy chain variable region.
 XX
 KW catalytic antibody; enantioselective hydrolysis; hybridoma; ZAA7G12;
 KW ZAA3G2; ds.
 XX
 OS Mus.
 XX
 XX WO9629426-A1.
 PN
 XX 26-SEP-1996.
 PD
 XX 17-MAR-1995; 95WO-JP000462.
 PF
 XX 17-MAR-1995; 95WO-JP000462.
 PR
 XX (PROT-) PROTEIN ENG RES INST.
 XX
 XX Fujii I, Tanaka F, Kinoshita K;
 PI
 XX WPI; 1996-443199/44.
 DR
 DR N-PSDB; AAT67815.
 XX
 XX Catalytic antibody for enantioselective hydrolysis of amino acid ester(s)
 FT - also new hybridoma secreting the antibody.
 PT
 XX
 PS Disclosure; Page 31-32; 49pp; Japanese.
 XX
 CC The patent discloses new catalytic antibodies which hydrolyse amino acid
 CC esters enantioselectively. Preferably the esters are 4-nitro- benzyl
 CC esters and the esterified amino acids are amino-protected. Also disclosed
 CC are new hybridomas expressing the catalytic antibodies, especially
 CC ZAA7G12 (FERM BP-4947) and ZAA3G2 (FERM BP-4946). The antibodies are
 CC raised in mice using the compound p-nitrobenzyl [4-carboxy-1-
 CC (benzyloxy-carbonylamino)-butyl]phosphonate as haptens. They are used for
 CC efficient resolution of racemic amino acids with high optical
 CC selectivity, giving optically active amino acids useful for the
 CC production of optically active drugs and chiral separation agents. The
 CC present sequence represents the variable region of the heavy chain of
 CC antibody 7G12, produced by the hybridoma ZAA7G12
 XX
 SQ Sequence 212 AA;
 XX
 Query Match 27.3%; Score 950; DB 2; Length 212;
 Best Local Similarity 84.7%; Pred. No. 2e-49;
 Matches 183; Conservative 11; Mismatches 14; Indels 8; Gaps 1;
 QY 6 QSGPDLVPGASVKISCKASGYFTGYMHVWVKQSPGKLEWIGRINPNNGVTLNQKFK 65
 DB 2 ESGTELAKEGASVKISCKASGYFTSYIHWVKRPGQGLEWIGYINFTDYTEIQKFK 61
 QY 66 DKATLTVDKSSYTAWEIARSLTSDSAYVYCARSTMIINYVDWYGQSTSVSSAKTTP 125
 DB 62 DKATLTADKSSYTAWEIARSLTSDSAYVYCV-----MKDYWGQSTSVSSAKTTP 113

QY 126 PSVYPLAPGSAQTNSMTLGLVKGYPFPPVTVTWNSGSLSSGVHTFPAVLQSDLYTLS 185
 DB 114 PSVYPLAPGSAQTNSMTLGLVKGYPFPPVTVTWNSGSLSSGVHTFPAVLQSDLYTLS 173
 QY 186 SSVTVPSSTWPSSTVTCNVAHPASSTKVDKKIIVPRD 221
 DB 174 SSVTVPSSTWPSSTVTCNVAHPASSTKVDKKIIVPRD 209
 RESULT 56
 AAR13203
 ID AAR13203 standard; protein; 233 AA.
 XX AC AAR13203;
 XX DT 15-OCT-1991 (first entry)
 XX DE Staphylococcal enterotoxin A.
 XX KW SEA; cancer treatment; pyrogen; tumouricide.
 XX OS Staphylococcus aureus.
 XX PN WO9110680-A.
 XX PD 25-JUL-1991.
 XX PF 17-JAN-1990; 90US-00466577.
 XX PR 17-JAN-1990; 90US-00466577.
 XX PA (TERM/) Terman D S.
 XX PI Terman DS;
 XX DR WPI; 1991-237984/32.
 XX PT Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumoricidal activity as
 PT Staphylococcal protein A without potential toxic reactions.
 XX PS Disclosure; Fig 1; 74pp; English.
 XX CC SEA was isolated and purified from S. aureus. It can be used for treating
 CC cancer, activating cytokine mediators and procoagulant systems,
 CC augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be
 CC administered intravenously, optionally with ibuprofen to attenuate toxic
 CC reaction to SEA. Synthetic polypeptides having structural homology to
 CC Staphylococcal exotoxins are claimed, provided the homology includes
 CC statistically significant sequence homology, alignment of Cysteine
 CC residues and similar hydrophathy profiles. See also AAR13204-R13211
 XX Sequence 233 AA;
 Query Match 27.3%; Score 960; DB 2; Length 233;
 Best Local Similarity 77.3%; Pred. No. 2.3e-49;
 Matches 180; Conservative 21; Mismatches 32; Indels 0; Gaps 0;
 QY 226 SESEINEKDLRKKSELOGTALGNLKOIYYNSKAITSEKSADOFNTLLFGFTG 285
 DB 1 SESEINEKDLRKKSELOGTALGNLKOIYYNEKAKTENKESHQDFLQHTLFGFTG 60
 QY 286 HPYNDLLVDLGSATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 345
 DB 61 HSYNDLLVDKSGKDIDVYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 120
 QY 346 EEKVPINLWIDGKQTVTDIKVTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 405
 DB 121 EEKVPINLWIDGKQTVPLETVTKNKNVTVQELDPQARRYLQEKYLYNSDVFQKQV 180
 QY 406 RGLIVPHSSEGSTVSVDLFDACQVPTTLIRYRDNNTTISSTLSLSLYTT 458
 DB 181 RGLIVPHSTEPSVNDLFDACQVNTLLIRYRDNNTINSENMDIYLYTS 233

RESULT 57
 AAR75456
 ID AAR75456 standard; protein; 223 AA.
 XX AC AAR75456;
 XX DT 07-FEB-1996 (first entry)
 XX DE Mouse antibody FB3-2 heavy chain variable region protein sequence.
 XX KW Primer; amplification; PCR; mouse; kappa chain; heavy chain; Fab;
 KW antibody; immunotolerance; animal; variegated display library;
 KW variable region; antigen; immunorecessive; cell surface marker; foetal;
 KW cancer; stem cell; variant; therapy; Alzheimer's disease; hybridoma;
 KW familial hypercholesterolaemia; binding affinity.
 XX OS Mus musculus.
 XX PN WO9515982-A2.
 XX PD 15-JUN-1995.
 XX PF 08-DEC-1994; 94WO-US014106.
 XX PR 08-DEC-1993; 93US-00164022.
 XX PR 06-DEC-1994; 94US-00350400.
 XX PA (GENZ) GENZYME CORP.
 XX PI Barsomian G, Copeland DP, Hillhouse D, Johnson T;
 XX DR WPI; 1995-224291/29.
 XX DR N-PSDB; AAQ92500.
 XX PT Generating new antibodies specific for immunorecessive epitopes - by
 PT selection from variegated V gene library cloned from immunotolerance
 PT derived antibody repertoire, useful in diagnosis, purificn. and therapy,
 PT e.g. of cancer.
 XX PS Disclosure; Page 74-75; 109pp; English.
 XX CC The sequence of the heavy chain variable region from the mouse antibody
 CC FB3-2. This sequence was isolated from a variegated display library (VDL)
 CC of variable regions derived from a repertoire of antibodies from an
 CC immunotolerised animal. The VDL is generated by PCR amplifying the
 CC variable regions from the antibody coding sequences using the primers
 CC AAQ74153-74. The variable regions, esp the complementarity determining
 CC regions (CDR; see AAR75462-93 for examples of CDRs) from the
 CC immunotolerant animals' antibodies are used to construct an antibody
 CC against a immunorecessive antigen e.g. a cell surface marker on a foetal,
 CC cancer or stem cell, which can differentiate between variant or related
 CC forms of the antigen. The antibodies generated can be used in the
 CC diagnosis, e.g. detection of the immunorecessive antigen, or in therapy
 CC e.g. of cancer, Alzheimer's disease or familial hypercholesterolaemia.
 CC The method of production of the antibody allows rapid and sensitive
 CC isolation of antibodies that would be difficult to isolate by standard
 CC methods. The antibodies produced have greater binding affinity than those
 CC produced by combinatorial/hybridoma methods
 XX Sequence 223 AA;
 Query Match 27.1%; Score 953.5; DB 2; Length 223;
 Best Local Similarity 83.0%; Pred. No. 5.3e-49;
 Matches 185; Conservative 12; Mismatches 23; Indels 3; Gaps 2;
 QY 1 EVQLQQSGPDLVKGPGASVKISKASGYSTGYNHWYKQSPGKLEWIGRINPNNGVTLY 60
 DB 1 EVQLQQSGPELMPGASVKISKATGYTLSSYWLWYKQSPGKLEWIGILFGSGSAHY 60
 QY 61 NQKFKDKATLTVDKSSATNWLRLSTSDSAYTYCARSTMITYN---VMDYWGQGTSTVY 118

28-JUN-2001; 2001SE-00002327.
(ACTI-) ACTIVE BIOTECH AB.
Forsberg G, Erlandsson E, Antonsson P, Walse B;
WPI; 2003-201467/19.
Conjugate for therapy, has bacterial superantigen with a region in T-cell receptor and four regions to determine binding to class II major histocompatibility complex, antibody to cancer associated cell surface structure.
Example 3; Fig 3; 102pp; English.
The present sequence is the protein sequence of staphylococcal enterotoxin A (SEA). The invention provides novel conjugates (see ABP58454) for human cancer therapy. These comprise an engineered bacterial superantigen, such as novel SEA/E-120 (see ABP58455), and an antibody moiety, such as tumour reactive antibody 574. Bacterial enterotoxins such as SEA, SEE, SED and SEH were used in the molecular modelling of the engineered superantigens. The superantigens were engineered to reduce seroreactivity whilst maintaining biological activity and production levels. The novel conjugates were designed to target and destroy cancer cells, including cancer of the lung, breast, colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)

Query Match 26.9%; Score 948; DB 6; Length 233;
Best Local Similarity 76.4%; Pred. No. 1.2e-48;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKSDAQFLTNTLLFKGFTG 285
Db 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHQFLQHTLLFKGFTD 60

QY 286 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 345
Db 61 HSWYNDLLVDFSDKIDVKGKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120

QY 346 BEKKVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKVQ 405
Db 121 BEKKVPINLWDGKQNTVPLETVTKNKNVTVOELDLQARRYLOEKYLYNSDVFQKVQ 180

QY 406 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNNTISSTLSISLYLYTT 458
Db 181 RGLIVFHTSTEPSVNYDLFGAQGYNTLLRIYRDNKNTINSENHDIYLYTS 233

RESULT 62
AAU14104
ID AAU14104 standard; peptide; 257 AA.
AC AAU14104;
DT 21-NOV-2001 (first entry)
DE Peptide sequence from Staphylococcus aureus enterotoxin A.
XX Anti-retroviral; DP178-like; DP107-like; enterotoxin A; antifusogenic;
XX antiviral; HIV transmission.
XX Staphylococcus aureus.
XX WC200151673-A2.
XX 19-JUL-2001.
XX 05-JUL-2000; 2000WO-US035727.
XX 09-JUL-1999; 99US-00350841.
XX

(TRIM-) TRIMERIS INC.
Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
WPI; 2001-442157/47.
Identifying a compound that inhibits the formation of or disrupts a DP107/DP178 complex, especially compounds with antifusogenic, antiviral or intracellular modulatory activity, by detecting the formation of a DP107/DP178 complex.
Disclosure; Fig 42; 259pp; English.
The present invention relates to peptides which exhibit anti-retroviral activity. The peptides of the invention (AAU12559-AAU14009) comprise DP178-like and DP107-like peptides. The DP178 peptide corresponds to amino acids 639-673 of the transmembrane protein gp41 from human immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide corresponds to amino acids 558-595 of gp41 from HIV-1 LAI. The invention also relates to a method of identifying compounds that inhibit the formation of or disrupts a DP107/DP178 complex. The method comprises detecting the formation of a DP107/DP178 complex, both in the presence or absence of a test compound, in a reaction mixture containing DP107 and DP178 peptides. The method is useful for identifying compounds, including small molecule compounds, which may themselves exhibit antifusogenic, antiviral or intracellular modulatory activity. The DP178-like/DP107-like peptides are useful to inhibit human and non-human retroviral, particularly HIV, transmission to uninfected cells. The present sequence represents a peptide sequence from Staphylococcus aureus enterotoxin A

Query Match 26.9%; Score 948; DB 4; Length 257;
Best Local Similarity 76.4%; Pred. No. 1.3e-48;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKSDAQFLTNTLLFKGFTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHQFLQHTLLFKGFTD 84

QY 286 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 345
Db 85 HSWYNDLLVDFSDKIDVKGKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 144

QY 346 BEKKVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKVQ 405
Db 145 BEKKVPINLWDGKQNTVPLETVTKNKNVTVOELDLQARRYLOEKYLYNSDVFQKVQ 204

QY 406 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNNTISSTLSISLYLYTT 458
Db 205 RGLIVFHTSTEPSVNYDLFGAQGYNTLLRIYRDNKNTINSENHDIYLYTS 257

RESULT 63
ABO10269
ID ABO10269 standard; protein; 257 AA.
AC ABO10269;
DT 19-AUG-2003 (first entry)
XX S. aureus enterotoxin A.
XX HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;
XX Spstein-Barr virus infection; heptad repeat motif.
XX Staphylococcus aureus.
XX US6518013-B1.
XX 11-FEB-2003.
XX 07-JUN-1995; 95US-00485546.
XX

XX 07-JUN-1993; 93US-00073028.
 PR 07-JUN-1994; 94US-00255208.
 PR 20-DEC-1994; 94US-00360107.
 XX (TRIM-) TRIMERIS INC.
 XX Barney SO, Lambert DM, Petteway SR;
 XX WPI; 2003-465599/44.
 XX Inhibiting transmission of Epstein-Barr virus to a cell, by contacting
 PT the cell with a peptide consisting of a region of Epstein-Barr virus
 PT protein.
 XX Example; Fig 42; 716pp; English.
 XX The invention relates to inhibiting (M) transmission of an Epstein-Barr
 CC virus to a cell, comprising contacting the cell with an effective
 CC concentration of a peptide consisting of a region of 18-39 consecutive
 CC amino acids of an Epstein-Barr virus protein for an effective period of
 CC time, where the region is recognised by one or more of ALLMOT15,
 CC 107x178x4 or PIZIP sequence search motifs, the peptide further comprises
 CC an amino terminal X, and a carboxy terminal Z in which X comprises an
 CC amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic
 CC group or macromolecular carrier group, and Z comprises a carboxyl group,
 CC amido group, hydrophobic group, or macromolecular carrier group, and
 CC fusion of the virus to the cell is inhibited. The peptides were
 CC identified by analysing the structure/motifs present in the HIV-1
 CC glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat
 CC motif containing peptides were used to design the motifs cited above,
 CC which in turn were used to analyse proteins from other pathogenic
 CC organisms and HIV isolates, looking for DP107/178 structural analogues.
 CC The method is useful for inhibiting transmission of Epstein-Barr viruses to
 CC a cell and Epstein-Barr virus infection. The present sequence is a
 CC protein from a pathogenic organism analysed for regions analogous to
 CC DP107 or DP178
 XX
 SQ Sequence 257 AA;

Query Match 26.9%; Score 948; DB 6; Length 257;
 Best Local Similarity 76.4%; Pred. No. 1.3e-48;
 Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
 QY 226 SEKSEINEKDLRKSELOGTALGNLQIYYNKAITSSEKSDQFLNTLLKGFFTG 285
 DB 25 SEKSEINEKDLRKSELOGTALGNLQIYYNKAITSSEKSDQFLNTLLKGFFTG 84
 QY 286 HPWYNDLLVDLGSTAATSVEYSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
 DB 85 HSWYNDLLVDFDSKDIDYKYGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
 QY 346 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVKQ 405
 DB 145 EEKVPINLWIDGKQNTVPLETVTKNKNVTVOELDLQARRYLQEKYKLYNSDSVDFGKVKQ 204
 QY 406 RGLIVFHSSEGSTVSYDLFDAQGQYPTLLRIYRDNNTTISSTLSISLYLYTT 458
 DB 205 RGLIVFHTSTEPSVNYDLFGAQGQYNTLLRIYRDNKNTINSENMHIDIVLYTS 257

RESULT 64
 ADD44368
 ID ADD44368 standard; protein; 257 AA.
 XX
 AC ADD44368;
 XX
 DT 15-JAN-2004 (first entry)
 XX
 DE Staphylococcus aureus enterotoxin A protein.
 XX enterotoxin A; ent A; food poisoning; bacterium; food; milk; fruit juice;
 KW ice cream.

XX Staphylococcus aureus.
 OS WC2003080865-A1.
 XX
 PN 02-OCT-2003.
 PD
 XX 26-MAR-2002; 2002WO-IB001150.
 PF
 XX 26-MAR-2002; 2002WO-IB001150.
 PR
 XX (COUL) COUNCIL SCI & IND RES.
 PA Padmapriya BP, Ramesh A, Chandrashekar A, Varadaraj MC;
 PI WPI; 2003-779273/73.
 XX N-PSDB; ADD44369.
 DR
 XX Novel oligonucleotide primers directed against enterotoxin A gene of
 PT Staphylococcus aureus and heat stable enterotoxin gene of *Yersinia*
 PT enterocolitica, useful for detecting food poisoning causing bacteria.
 XX Example 2; Page 14-15; 34pp; English.
 PS
 XX The invention relates to novel oligonucleotide primers directed against
 CC enterotoxin A gene (ent A) of *Staphylococcus aureus* and heat stable
 CC enterotoxin gene (yest) of *Yersinia enterocolitica*. The novel
 CC oligonucleotide primers are useful for simultaneously detecting food
 CC poisoning bacterial species *Staphylococcus aureus* and/or *Yersinia*
 CC enterocolitica in food systems e.g., milk, fruit juices and ice creams,
 CC without prior enrichment for preventing food poisoning outbreak. The PCR
 CC detection method is useful for detecting the bacteria strains in quantity
 CC as low as one cell. The method can be directly used for detecting
 CC bacterial strains. The oligonucleotide primers allow quick and highly
 CC sensitive detection of the food poisoning bacterial species. This
 CC sequence represents the protein derived from the enterotoxin A gene from
 CC *Staphylococcus aureus* of the invention.
 XX
 SQ Sequence 257 AA;

Query Match 26.9%; Score 948; DB 7; Length 257;
 Best Local Similarity 76.4%; Pred. No. 1.3e-48;
 Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
 QY 226 SEKSEINEKDLRKSELOGTALGNLQIYYNKAITSSEKSDQFLNTLLKGFFTG 285
 DB 25 SEKSEINEKDLRKSELOGTALGNLQIYYNKAITSSEKSDQFLNTLLKGFFTG 84
 QY 286 HPWYNDLLVDLGSTAATSVEYSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
 DB 85 HSWYNDLLVDFDSKDIDYKYGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
 QY 346 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVKQ 405
 DB 145 EEKVPINLWIDGKQNTVPLETVTKNKNVTVOELDLQARRYLQEKYKLYNSDSVDFGKVKQ 204
 QY 406 RGLIVFHSSEGSTVSYDLFDAQGQYPTLLRIYRDNNTTISSTLSISLYLYTT 458
 DB 205 RGLIVFHTSTEPSVNYDLFGAQGQYNTLLRIYRDNKNTINSENMHIDIVLYTS 257

RESULT 65
 AAO29870
 ID AAO29870 standard; protein; 234 AA.
 XX
 AC AAO29870;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE Mouse anti-human DR5 antibody (TRA-8) light chain.
 XX Tumour necrosis factor; TNF-related apoptosis-inducing ligand; allergy;
 KW inflammatory disease; TRAIL receptor; systemic lupus erythematosus; DR4;

KW Hashimoto's disease; rheumatoid arthritis; inflammatory disease; cancer;
KW multiple sclerosis; graft-versus-host disease; arteriosclerosis; asthma;
KW Goodpasture's syndrome; autoimmune disease; glomerular nephritis; DR5;
KW Crohn's disease; diabetes mellitus; antibody; mouse.
XX
OS Mus sp.
XX WO2003037913-A2.
XX PD 08-MAY-2003.
XX PF 01-NOV-2002; 2002WO-US035333.
XX PR 01-NOV-2001; 2001US-0346402P.
XX PA (UABR-) UAB RES FOUND.
XX PI Zhou T, Kimberly RP, Koopman WJ, Lobuglio AF, Buchsbaum DJ;
XX WPI; 2003-441350/41.
XX DR N-PSDB; AAL60478.
XX
XX New purified antibody that specifically binds a TNF-related apoptosis-
PT inducing ligand receptor DR4 or DR5, useful for treating cancer, or
PT inflammatory disease or autoimmune disease in a subject, e.g. asthma or
PT rheumatoid arthritis.
XX
XX Example 16; Page 225-226; 251pp; English.
XX
XX The invention relates to an antibody that specifically binds a tumour
CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
CC DR4 or DR5. Antibodies of the invention are useful for selectively
CC inducing apoptosis in target cells expressing DR4, for inhibiting
CC proliferation of target cells expressing DR4 or for treating cancer,
CC inflammatory disease or autoimmune disease in a subject e.g. systemic
CC lupus erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-
CC versus-host disease, Goodpasture's syndrome, Crohn's disease, multiple
CC sclerosis, diabetes mellitus, allergy, asthma, arteriosclerosis or
CC glomerular nephritis. The present sequence is mouse anti-human DR5
CC antibody (TRA-8) light chain
XX
XX Sequence 234 AA;
XX
Query Match 26.8%; Score 945; DB 6; Length 234;
Best Local Similarity 83.3%; Pred. No. 1.8e-48;
Matches 185; Conservative 12; Mismatches 21; Indels 4; Gaps 2;
QY 453 LYLVT---TSIVMTQPTSLVLSAGDVTITCKASQSVSNDAVYQKQSPKLLISYT 509
DB 13 LFLPAGVEGDIVMTQSHKFMSTSVGDRVSIITCKASQDVGTAVAVYQKQSPKLLIYA 72
QY 510 SRYAGVDRSGSGYGTDFLTITSSVQAEADAVYFCQDYNSPPTGGGTLKLEKADA 569
DB 73 STRHTGVDPDRFTGSGSGTDFLTITSNVQSEDLADYFCQQ-YSSRYTFGGGTLKLEKADA 131
QY 570 APTVSIFFPSSEQLTSGASVVCFLNNFPYKIDVGVKIDGSRQNGVLSNWTQDQSKDS 629
DB 132 APTVSIFFPSSEQLTSGASVVCFLNNFPYKIDVGVKIDGSRQNGVLSNWTQDQSKDS 191
QY 630 TVSMSTLTLDKDEYERHNSYTCATHTKTSTSPIVKSFNRNE 671
DB 192 TVSMSTLTLDKDEYERHNSYTCATHTKTSTSPIVKSFNRNE 233
RESULT 66
ID ABP96752 standard; protein; 209 AA.
XX
XX ABP96752;
XX AC
XX
XX 05-JUN-2003 (first entry)
XX
XX TSH receptor antibody 4D7 heavy chain amino acid sequence.
DE

XX Thyrotropin receptor; TSH receptor; epitope region; antibody;
KW autoantibody; autoimmune disease; thyroid tissue; cytostatic;
KW gene therapy; immune reaction; thyroid cancer.
XX
OS Synthetic.
XX WO2003018632-A2.
XX PD 06-MAR-2003.
XX PF 21-AUG-2002; 2002WO-GB003831.
XX PR 23-AUG-2001; 2001GB-00020649.
XX PR 01-JUL-2002; 2002GB-00015212.
XX PA (RSRR-) RSR LTD.
XX PI Smith BR, Furmaniak J, Sanders JF;
XX WPI; 2003-290051/28.
XX DR N-PSDB; ACC44907.
XX
XX New polypeptide sequence having part or all of the primary structural
PT conformation of one or more TSH receptor epitopes, useful for treating an
PT autoimmune disease associated with an immune reaction to a TSH receptor,
PT e.g. thyroid cancer.
XX
XX Claim 67; Fig 10; 196pp; English.
XX
XX The present invention describes a polypeptide sequence comprising part or
CC all of the primary structural conformation of one or more thyrotropin
CC (TSH) receptor epitopes with which autoantibodies and/or lymphocytes
CC produced in response to a TSH receptor interact. Also described: (1) one
CC or more receptor TSH epitopes with which the autoantibodies and/or
CC lymphocytes interact, as with the polypeptide sequence described above;
CC (2) a method of screening for autoantibodies or lymphocytes produced in
CC response to a TSH receptor in a sample of body fluid obtained from a
CC subject suspected of suffering from, susceptible to, having or recovering
CC from autoimmune disease associated with an immune reaction to a TSH
CC receptor; (3) a binding partner for a TSH receptor, which is capable of
CC binding to a TSH receptor to stimulate the TSH receptor, where the
CC binding partner does not comprise TSH or naturally produced antibodies to
CC the TSH receptor; and (4) a combination comprising the binding partner
CC and one or more further agents capable of stimulating thyroid tissue,
CC and/or tissue containing a TSH receptor, for simultaneous, separate or
CC sequential use in stimulating thyroid tissue, and/or tissue containing a
CC TSH receptor. A TSH receptor has cytostatic activity and can be used in
CC gene therapy. The polypeptide, compositions and methods from the present
CC invention can be used for treating an autoimmune disease associated with
CC an immune reaction to a TSH receptor. The specific binding partner is
CC useful for the manufacture of a medicament for stimulating thyroid tissue
CC or tissue containing a TSH receptor, and for treating thyroid cancer.
CC ACC44874 to ACC44905 and ABP96719 to ABP96750 represent TSH receptor
CC sequences, and ACC44910 to ACC44933 encode the TSH receptor antibody VH
CC and VL domains given in ABP96751 to ABP96778, which are used in the
CC exemplification of the present invention
XX
XX Sequence 209 AA;
XX
Query Match 26.8%; Score 944.5; DB 6; Length 209;
Best Local Similarity 85.5%; Pred. No. 1.7e-48;
Matches 183; Conservative 10; Mismatches 16; Indels 5; Gaps 1;
QY 1 EVOLQSGPDLVKPGASVKISCKASGYSFTGYMHWKQSPGKLEWIGRINPNNGVTLY 60
DB 1 DVQLKHSGLPELVKPGASMKISCKASGYSFTGYTMWVKQSHGKLEWIGLINPYTGTY 60
QY 61 NQKFKDKALITVDKSTTAYMELRLSTSEDSAVYYCARSTMTITNYMDYWGQSTVTVSS 120
DB 61 NQKFKGKALITVDKSSSTAFMELLSTSEDSAVYYCARDGN-----LDYWGQSTVTVSS 115
QY 121 AKTTPPSVYPLAPGSAQTNSMVTGLCLVKGYFPEPTVTWNSGSLSSGVHTFPVAVLQSD 180

DB 116 AKTTPSVYPLAPGSAQAQNSMTGLCLVKGFPEPVTVTNWSSGSLSSGVHTFPAVLQSD 175
QY 181 LYTSSSVTPSSWTPSETVTCNVAHPASSTKVD 214
DB 176 LYTSSSVTPSSWTPSETVTCNVAHPASSTKVD 209
RESULT 67
ID ABP96751 standard; protein; 209 AA.
XX AC ABP96751;
XX DT 05-JUN-2003 (first entry)
XX DE TSH receptor antibody 4D7 heavy chain amino acid sequence.
XX KW Thyrotropin receptor; TSH receptor; epitope region; antibody;
XX KW autoantibody; autoimmune disease; thyroid tissue; cytostatic;
XX KW gene therapy; immune reaction; thyroid cancer.
XX OS Synthetic.
XX PN WO2003018632-A2.
XX PD 06-MAR-2003.
XX PF 21-AUG-2002; 2002WO-GB003831.
XX PR 23-AUG-2001; 2001GB-00020649.
XX PR 01-JUL-2002; 2002GB-00015212.
XX PA (RSRR-) RSR LTD.
XX PI Smith BR, Furmaniak J, Sanders JF;
XX DR WPI; 2003-290051/28.
XX DR N-PSDB; ACC44906.
XX PT New polypeptide sequence having part or all of the primary structural
XX PT conformation of one or more TSH receptor epitopes, useful for treating an
XX PT autoimmune disease associated with an immune reaction to a TSH receptor,
XX PS e.g. thyroid cancer.
XX PS Claim 71; Fig 9; 196pp; English.
XX CC The present invention describes a polypeptide sequence comprising part or
XX CC all of the primary structural conformation of one or more thyrotropin
XX CC (TSH) receptor epitopes with which autoantibodies and/or lymphocytes
XX CC produced in response to a TSH receptor interact. Also described: (1) one
XX CC or more receptor TSH epitopes with which the autoantibodies and/or
XX CC lymphocytes interact, as with the polypeptide sequence described above;
XX CC (2) a method of screening for autoantibodies or lymphocytes produced in
XX CC response to a TSH receptor in a sample of body fluid obtained from a
XX CC subject suspected of suffering from, susceptible to, having or recovering
XX CC from autoimmune disease associated with an immune reaction to a TSH
XX CC receptor; (3) a binding partner for a TSH receptor, which is capable of
XX CC binding to a TSH receptor to stimulate the TSH receptor, where the
XX CC binding partner does not comprise TSH or naturally produced antibodies to
XX CC the TSH receptor; and (4) a combination comprising the binding partner
XX CC and one or more further agents capable of stimulating thyroid tissue,
XX CC and/or tissue containing a TSH receptor, for simultaneous, separate or
XX CC sequential use in stimulating thyroid tissue, and/or tissue containing a
XX CC TSH receptor. A TSH receptor has cytostatic activity and can be used in
XX CC gene therapy. The polypeptide, compositions and methods from the present
XX CC invention can be used for treating an autoimmune disease associated with
XX CC an immune reaction to a TSH receptor. The specific binding partner is
XX CC useful for the manufacture of a medicament for stimulating thyroid tissue
XX CC or tissue containing a TSH receptor, and for treating thyroid cancer.
XX CC ACC44874 to ACC44905 and ABP96719 to ABP96750 represent TSH receptor
XX CC sequences, and ACC44910 to ACC44933 encode the TSH receptor antibody VH
XX CC and VL domains given in ABP96751 to ABP96778, which are used in the

CC exemplification of the present invention
XX SQ Sequence 209 AA;
Query Match 26.8%; Score 944.5; DB 6; Length 209;
Best Local Similarity 85.5%; Pred. No. 1.7e-48;
Matches 183; Conservative 10; Mismatches 16; Indels 5; Gaps 1;
QY 1 EVQLQQSGDPLVKPGASVKISKASGYSFTGYMHVYKQSPGKLEWIGRINPNNGVTLY 60
DB 1 DVQLKHSGPELVKPGASMKISKASGYSFTGYTMNVKQSHGKNLEWIGLINPYTGCTNY 60
QY 61 NQEKDKATLTVDKSTTAYMELRSLTSEDSAVYYCARSTMITNYMDYWGQSTSVTVSS 120
DB 61 NQKFGKRAKLTVDKSSSTAFMELLSLTSSEDSAVYYCARDGN-----LDYWGQGTLLTVSS 115
QY 121 AKTTPSVYPLAPGSAQAQNSMTGLCLVKGFPEPVTVTNWSSGSLSSGVHTFPAVLQSD 180
DB 116 AKTTPSVYPLAPGSAQAQNSMTGLCLVKGFPEPVTVTNWSSGSLSSGVHTFPAVLQSD 175
QY 181 LYTSSSVTPSSWTPSETVTCNVAHPASSTKVD 214
DB 176 LYTSSSVTPSSWTPSETVTCNVAHPASSTKVD 209
RESULT 68
AAR76087
ID AAR76087 standard; protein; 239 AA.
XX AC AAR76087;
XX DT 25-MAR-2003 (revised)
XX DT 21-NOV-1995 (first entry)
XX DE MAB 55.1 light chain.
XX KW Antigen binding structure; complementarity determining region; CDR;
XX KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;
XX KW monoclonal antibody; MAB; immunotherapy; therapy; diagnosis;
XX KW transgenic animal; transgenic plant; antibody engineering;
XX KW humanized antibody; immunotoxin.
XX OS Mus sp.
XX FH Key Location/Qualifiers
XX FT Peptide 1..20 /label= Sig_peptide
XX FT Protein 21..239 /label= Mat_protein
XX FT /note= "claim 3, page 98"
XX WO9515382-A1.
XX PD 08-JUN-1995.
XX PF 29-NOV-1994; 94WO-GB0002610.
XX PR 03-DEC-1993; 93GB-00024819.
XX PR 03-JUN-1994; 94GB-00011089.
XX PA (ZENE) ZENECA LTD.
XX PI Rose MS, Boot C, Copley CG, Paterson DS, Hall SM, Wright AF;
XX PI Blakey DC;
XX DR WPI; 1995-215262/28.
XX DR N-PSDB; AAQ94036.
XX PT Antigen binding structures containing CDR's recognising the CA55.1
XX PT antigen - produced by hybridomas and host cells, for use in the diagnosis
XX PT and therapy of cancer.
XX PS Disclosure; Fig 16; 121pp; English.

CC MAB 55.1 (ECACC 93081901) recognises the colorectal tumor-associated
 CC antigen CA55.1. cDNAs for the heavy (AAQ94037) and light (AAQ94036)
 CC chains of 55.1 were isolated, and F(ab')₂, Fab, Fv, scFv or V-min
 CC humanized 55.1 constructs have been expressed in myeloma cells and E.
 CC coli. (Updated on 25-MAR-2003 to correct FN field.)
 XX
 SQ Sequence 239 AA;

Query Match 26.8%; Score 944.5; DB 2; Length 239;
 Best Local Similarity 78.1%; Pred. No. 2e-48;
 Matches 185; Conservative 22; Mismatches 19; Indels 11; Gaps 3;

QY 445 SSTSLSLSLYIT- ---SIVMTQTPSLVAGDRVTITCKASQSVND-----VAVY 494
 DB 3 SQAQVLLILLVWVSGTCGDIWMSQSPSLVAGSRVMTCKSSQLNSTRKNLAWY 62

QY 495 QKPGQSPKLLISYTSRYAGVDPFRFGSGYGTDTLTISVQAEDAAYVFCQDYNPP 554
 DB 63 QQRFGQSPKLLIYASTRTSGVDPFRFGSGYGTDTLTISVQAEDLAIYCKQSY-TLR 121

QY 555 TFGGKTLEIKRADAAPTIVSIFPPSSQLTSGGASVVCFLNNYPKDIYVKKIDGSEK 614
 DB 122 TFGGKTLEIKRADAAPTIVSIFPPSSQLTSGGASVVCFLNNYPKDIYVKKIDGSEK 181

QY 615 NGVLNMTDQDSKSTYSMSSTLTLTKDEYRHNSTYCEATHSTSPIVKSFNRNE 671
 DB 182 NGVLNMTDQDSKSTYSMSSTLTLTKDEYRHNSTYCEATHSTSPIVKSFNRNE 238

RESULT 69
 AAW06738
 ID AAW06738 standard; protein; 233 AA.
 XX
 AC AAW06738;
 XX
 DT 08-MAR-1997 (first entry)
 XX
 DE Staphylococcus enterotoxin A.
 XX
 KW Enterotoxin A; superantigen; antigen; cytokine; Chemokine; T cell;
 KW lymphocyte; monocyte; natural killer cell; gene therapy; cancer; vaccine;
 KW adjuvant.
 XX
 OS Staphylococcus sp.
 XX
 PN WO9636366-A1.
 XX
 PD 21-NOV-1996.
 XX
 PF 20-MAY-1996; 96WO-US007432.
 XX
 PR 18-MAY-1995; 95US-00446918.
 PR 29-DEC-1995; 95US-00580806.
 XX
 PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
 XX
 PI Dow SW, Elmalie RE, Potter TA;
 XX
 DR WPI; 1997-011857/01.
 DR N-PSDB; AAT45699.
 XX
 PT Recombinant molecule encoding superantigen and opt. cytokine or
 PT chemokine - controls activity of effector cells (T cells, monocytes,
 PT natural killer cells), used for gene therapy of cancer.
 XX
 PS Example 1; Page 98-99; 131pp; English.
 XX
 CC A cDNA clone (AAT45699) codes for staphylococcal enterotoxin A (AAW06738)
 CC superantigen. Nucleic acids encoding superantigens (see also AAW06737,
 CC AAW06739), esp. truncated forms of the superantigen lacking the leader
 CC peptide, can be used in the gene therapy of cancer, infectious diseases
 CC and immunological disorders. The nucleic acid, optionally in combination

CC with cytokine or chemokine nucleic acids, is delivered to an animal using
 CC e.g. liposomes. It acts by controlling the activity of effector cells,
 CC such as T-cells, macrophages, monocytes and/or natural killer cells.
 CC Localised prodn. of an effective but non-toxic amount of encoded proteins
 CC allows safe treatment of the animal
 XX
 SQ Sequence 233 AA;

Query Match 26.8%; Score 944; DB 2; Length 233;
 Best Local Similarity 76.3%; Pred. No. 2e-48;
 Matches 177; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 227 EKSEINEKDLRKSELOGTALGNLKIYYNYSKAITSSSEKSAQDFTNTLLFKGFTGH 286
 DB 2 EKSEINEKDLRKSELOGTALGNLKIYYNYSKAITSSSEKSAQDFTNTLLFKGFTGH 61

QY 287 PWYNDLLVDLSTATSEYEGSSVDLYGAYGYCAGGTPNKTACMYGGVTLHNNELTE 346
 DB 62 SWYNDLLVDFDSKDIVDKYKGGKVDLYGAYGYCAGGTPNKTACMYGGVTLHNNELTE 121

QY 347 EKKYPINLWIDGKOTVPIDKVTSEKVTVOELDLQARHYLHGKFGLYNSDSFGGVQV 406
 DB 122 EKKYPINLWIDGKQNTVPLETVTKNKNVTVOELDLQARRVLOEKYLYNSDVDFGVQV 181

QY 407 GLIVFHSSEGSTVSYDLPDAQGYPTLLRIYRNTTISSTLSISLYLTT 458
 DB 182 GLIVFHTSTEPSVNYDLFGAQQYSNTLLRIYRNDKNTINSENMHIDIYLYTS 233

RESULT 70
 AAR45011
 ID AAR45011 standard; protein; 233 AA.
 XX
 AC AAR45011;
 XX
 DT 25-MAR-2003 (revised)
 DT 08-JUN-1994 (first entry)
 XX
 DE Staphylococcal enterotoxin SEA.
 XX
 KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
 KW autoimmune disease; toxicity; Protein A; perfusion system.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 49 /note= "Given in the specification as O, no further
 FT details given"
 XX
 PN WO9324136-A1.
 XX
 PD 09-DEC-1993.
 XX
 PF 01-JUN-1993; 93WO-US005213.
 XX
 PR 01-JUN-1992; 92US-00891718.
 XX
 PA (TERM/) TERMAN D S.
 PA (STON/) STONE J L.
 XX
 PI Terman DS, Stone JL;
 XX
 DR WPI; 1993-405418/50.
 XX
 PT Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
 PT in a patient or for the treatment of auto-immune diseases.
 XX
 PS Disclosure; Fig 1; 90pp; English.
 XX
 CC The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer in
 CC a patient. These SEs, and homologues of them, can be used as tumouricidal

CC agents for treating cancers and autoimmune disease. They exhibit
CC tumorigenic activity and toxicity identical to that observed for the
CC Protein A perfusion system. They may be administered by i.v. injection.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 233 AA;

Query Match 26.7%; Score 942; DB 2; Length 233;
Best Local Similarity 76.0%; Pred. No. 2.7e-48;
Matches 177; Conservative 21; Mismatches 35; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKQIYYNSKAITSEKSAOFLNNTLLEKGFPTG 285
DB 1 SEKSEINEKDLRKSELOGTALGNLKQIYYNEKAKTENKESHQFLAHTLIFKGFPTD 60
QY 286 HPYNDLLVLDGSTAATSEYSSVDLYGAYTYGQCAGTGNKACMYGGVTLHDNNRLT 345
DB 61 HSWYNDLLVDFDSKIDVYKGGKVDLYGAYTYGQCAGTGNKACMYGGVTLHDNNRLT 120
QY 346 EEKVPINLWIDGKQTVTDKVKTSKSVTVQELDLQARHVLHGKGLYNSDSFGKQVQ 405
DB 121 EEKVPINLWIDGKQTVTDKVKTSKSVTVQELDLQARHVLHGKGLYNSDSFGKQVQ 180
QY 406 RGLIVFHSSEGSTSVSYDLFDAQGYPTDILLRIYRDNNTTSSSTLSLSLYLYTT 458
DB 181 RGLIVFHTSTEPSVNYDLFCAQGYNTLLRIYRDNNTTSENHMDIILYLYTS 233

RESULT 71
ID AAR76086
AC AAR76086 standard; peptide; 219 AA.
XX
AC AAR76086;
XX
DT 25-MAR-2003 (revised)
DT 21-NOV-1995 (first entry)
XX
DE MAb 55.1 light chain.
XX
KW Antigen binding structure; complementarity determining region; CDR;
KW CA55.1; colorectal cancer; tumor-associated antigen; hybridoma;
KW monoclonal antibody; MAb; immunotherapy; therapy; diagnosis;
KW transgenic animal; transgenic plant; antibody engineering;
KW humanized antibody; immunotoxin.
XX
OS Mus sp.
XX
FN WO9515382-A1.
XX
XX 08-JUN-1995.
XX
XX 29-NOV-1994; 94WO-GB002610.
XX
XX 03-DEC-1993; 93GB-00024819.
XX
XX 03-JUN-1994; 94GB-00011089.
XX
XX (ZENE) ZENECA LTD.
XX
XX Rose MS, Boot C, Copley CG, Paterson DS, Hall SM, Wright AF;
PI Blakey DC;
XX
XX WPI; 1995-215262/28.
XX
XX Antigen binding structures containing CDR's recognising the CA55.1
PT antigen - produced by hybridomas and host cells, for use in the diagnosis
PT and therapy of cancer.
XX
XX Claim 3; Page 98; 121pp; English.
XX
CC An antigen binding structure is based on the CDRs (given in AAR76078- 84)
CC of the heavy (AAR76085) and light (AAR76086) chains of Mab 55.1 (EACAC
CC 93081901), which recognises the colorectal tumor-associated antigen
CC CA55.1. It is optionally humanized and in the form F(ab')2, F(ab)', Fab,
CC

CC Fv, scFv or V-min, and is produced in transgenic animals or plants.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 219 AA;

Query Match 26.7%; Score 941.5; DB 2; Length 219;
Best Local Similarity 83.0%; Pred. No. 2.7e-48;
Matches 181; Conservative 19; Mismatches 11; Indels 7; Gaps 2;

QY 460 IVMTQTPTSLIVSAGDRVTITCKASQSVND-----VAVYQQKPGQSPKLLISYTSRY 513
DB 2 IVMSQSPSSLAWSAGEKVTMSCKSQSLNSTRKKNVLAWSYQRPQSPKLLIYASTRT 61
QY 514 AGVDPDRSGSGYGRDFLTITSSVOAEAAVYFCQDYNPSPTFGGTYKLEIKRADAAPT 573
DB 62 SGVDPDRFTGSGSGDFLTITSSVOAEALAIYCKQSY-TLRTFGGTYKLEIKRADAAPT 120
QY 574 SIFPPSEQLTSGGASVGVCFINNFYKIDGSRQGVNSWTQDQSKDSTYSM 633
DB 121 SIFPPSEQLTSGGASVGVCFINNFYKIDGSRQGVNSWTQDQSKDSTYSM 180
QY 634 SSTLTLTAKDEYERNHSYTCBATHKTSTSPIVKSNRNE 671
DB 181 SSTLTLTAKDEYERNHSYTCBATHKTSTSPIVKSNRNE 218

RESULT 72
ID AAW35373
AC AAW35373 standard; peptide; 233 AA.
XX
AC AAW35373;
XX
DT 20-APR-1998 (first entry)
XX
DE Staphylococcus enterotoxin SEA wild-type superantigen.
XX
KW SEE; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment;
KW cancer; infection; autoimmune disease; antibody.
XX
OS Staphylococcus sp.
XX
FN WO9736932-A1.
XX
PD 09-OCT-1997.
XX
XX 26-MAR-1997; 97WO-SE000537.
XX
XX 29-MAR-1996; 96SE-00001245.
XX
XX 12-AUG-1996; 96US-00695692.
XX
XX (PHAA) PHARMACIA & UPJOHN AB.
XX
XX Antonsson P, Hansson J, Bjoerk P, Dohlsten M, Kalland T;
PI Abrahamson L, Forsberg G;
XX
XX WPI; 1997-503052/46.
XX
XX Conjugate of target seeking moiety and modified superantigen - useful for
PT activating the immune system to treat cancer, viral infections, parasitic
PT infestations and autoimmune diseases.
XX
XX Claim 8; Page 36-37; 58pp; English.
XX
XX This is the wild-type Staphylococcus enterotoxin SEA superantigen. This
CC SEA superantigen can be modified to be used in a novel conjugate. The
CC novel conjugate comprises a target seeking moiety and a modified wild
CC type superantigen. The modified superantigen retains its ability to
CC activate a subset of T cells, even though 1 or more wild-type amino acid
CC residues in at least 1 region which functions in determining binding to T
CC cell receptor (TCR) and activation of a subset of T cells has/have been
CC replaced. Such a modified superantigen can optionally be used as part of
CC a conjugate with a target seeking moiety, for activating the immune
CC system to treat a mammalian disease. A pharmaceutical composition can be

CC prepared comprising a modified antibody (preferably a Fab fragment fused
 CC to a peptide moiety providing activation of T cells in vitro specific
 CC manner) in which cysteines providing for interchain cysteine linkages in
 CC the native antibody have been replaced (preferably by serine residues) to
 CC prohibit cysteine formation. The modified wild-type superantigen is used
 CC for treating cancer, viral infections, parasitic infestations and
 CC autoimmune disease. The modified wild type superantigen has a lower
 CC immunogenicity and reactivity with neutralising antibodies and has fewer
 CC side-effects when used as a drug, compared to wild type superantigen
 XX
 SQ Sequence 233 AA;

Query Match 26.7%; Score 941; DB 2; Length 233;
 Best Local Similarity 76.0%; Pred. No. 3.1e-48;
 Matches 177; Conservative 21; Mismatches 35; Indels 0; Gaps 0;
 QY 226 SEKSEINEKDLRKSELOQTALGNLKIYYNYSKAITSEKSDQFLTWLTFKGFPTG 285
 DB 1 SEKSEINEKDLRKSELOQTALGNLKIYYNYSKAITSEKSDQFLTWLTFKGFPTG 60
 QY 286 HPWNLDLLVDSGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
 DB 61 HSWNDLLVDFDSDKIDVYKYGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
 QY 346 BEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKQV 405
 DB 121 BEKVPINLWIDGKQNTVPLETVTNKKNVTVOELDQARHYLHGKFGLYNSDSFGKQV 180
 QY 406 RGLIVFHSSEGSTVSYDLFDAGQGYPTLLRIYRDNTTISTSLISLYLYTT 458
 DB 181 RGLIVFHTSTEPSVNYDLFGAGQYSNTLLRIYRDNTTINSENMHDIYLYTS 233

RESULT 73
 AAB67338
 ID AAB67338 standard; peptide; 233 AA.

XX AC AAB67338;
 XX DT 23-APR-2001 (first entry)
 XX DE Staphylococcus aureus enterotoxin A protein.
 XX KW Tumour; cancer; immune; enterotoxin.
 XX OS Staphylococcus aureus.
 XX PN US6180097-B1.
 XX PD 30-JAN-2001.
 XX PF 30-OCT-1998; 98US-00183437.
 XX PR 03-OCT-1989; 89US-00416530.
 XX PR 17-JAN-1990; 90US-00466577.
 XX PR 17-JAN-1991; 91WO-US000342.
 XX PR 01-JUN-1992; 92US-00891718.
 XX PR 02-MAR-1993; 93US-00025144.
 XX PR 31-JAN-1994; 94US-00189424.
 XX PR 19-JUN-1995; 95US-004931746.
 XX PA (TERM/) TERMAN D S.
 XX PI Terman DS;
 XX DR WPI; 2001-158657/16.

XX Tumor cell capable of stimulating antitumor immune reactivity in vitro or
 PT in vivo comprises exogenous nucleic acids encoding a superantigen and a
 PT costimulatory molecule.
 XX
 PS Disclosure; Fig 2; 16pp; English.
 XX

CC The present invention relates to a tumour cell capable of stimulating
 CC antitumor immune reactivity in vitro or in vivo contains and expresses an
 CC exogenous nucleic acid molecule encoding a superantigen or its active
 CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
 CC molecule that activates T cells in conjunction with an antigenic
 CC stimulus. The invention may be used for cancer therapy by stimulating an
 CC anticancer immune response in vivo or ex vivo
 XX
 SQ Sequence 233 AA;

Query Match 26.7%; Score 941; DB 4; Length 233;
 Best Local Similarity 76.0%; Pred. No. 3.1e-48;
 Matches 177; Conservative 21; Mismatches 35; Indels 0; Gaps 0;
 QY 226 SEKSEINEKDLRKSELOQTALGNLKIYYNYSKAITSEKSDQFLTWLTFKGFPTG 285
 DB 1 SEKSEINEKDLRKSELOQTALGNLKIYYNYSKAITSEKSDQFLTWLTFKGFPTG 60
 QY 286 HPWNLDLLVDSGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
 DB 61 HSWNDLLVDFDSDKIDVYKYGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
 QY 346 BEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKQV 405
 DB 121 BEKVPINLWIDGKQNTVPLETVTNKKNVTVOELDQARHYLHGKFGLYNSDSFGKQV 180
 QY 406 RGLIVFHSSEGSTVSYDLFDAGQGYPTLLRIYRDNTTISTSLISLYLYTT 458
 DB 181 RGLIVFHTSTEPSVNYDLFGAGQYSNTLLRIYRDNTTINSENMHDIYLYTS 233

RESULT 74
 AAU72802
 ID AAU72802 standard; protein; 234 AA.

XX AC AAU72802;
 XX DT 26-FEB-2002 (first entry)
 XX DE TRA-8 light chain.
 XX KW Tumour necrosis factor-related apoptosis-inducing ligand receptor; TRAIL;
 KW TRAIL receptor DR5; cytostatic; apoptosis; cell proliferation;
 KW autoimmune disease; systemic lupus erythematosus; Hashimoto's disease;
 KW rheumatoid arthritis; Sjogren's syndrome; Chron's disease; anaemia;
 KW Addison disease; scleroderma; Goodpasture's syndrome; sterility;
 KW myasthenia gravis; multiple sclerosis; Basedow's disease; diabetes;
 KW allergy; arteriosclerosis; myocarditis; cardiomyopathy;
 KW glomerular nephritis; cancer; antibody; chromosome 8p21-22; TRA-8.
 XX MS musculus.
 XX OS WO200183560-A1.
 XX PN 08-NOV-2001.
 XX PR 02-MAY-2001; 2001WO-US014151.
 XX PR 02-MAY-2000; 2000US-0201344P.
 XX PA (UABR-) UAB RES FOUND.
 XX PI Zhou T, Ichikawa K, Kimberly RP, Koopman WJ;
 XX DR WPI; 2002-049338/06.
 XX DR N-PSDB; AAS97063.

XX Novel antibody specific for tumor necrosis factor-related apoptosis-
 PT inducing ligand, useful for inhibiting cell proliferation in cancer.
 PT
 XX Claim 30; Page 200; 229pp; English.
 XX
 PS The invention describes a novel antibody which recognizes a tumour
 XX
 CC

CC necrosis factor (TNF)-related apoptosis-inducing ligand (TRAIL) receptor
CC DR5 (located on chromosome 8p21-22). The antibody has apoptosis-inducing
CC activity to a cell expressing DR5 in vivo. It is also useful for
CC preparing a therapeutic for selective apoptosis of abnormal or
CC dysregulated cells, and for inhibiting cell proliferation in a cell,
CC preferably a human breast, ovary, colon, haematopoietic, prostate,
CC lymphatic, lung, glioma or liver cancer cell. A therapeutic agent may
CC also be administered e.g. paclitaxel, taxol or cycloheximide. The
CC antibody is used to treat an autoimmune disease, systemic lupus
CC erythematosus, Hashimoto's disease, rheumatoid arthritis, graft-versus-
CC host disease, Sjogren's syndrome, Chron's disease, pernicious anaemia,
CC Addison disease, scleroderma, Goodpasture's syndrome, autoimmune
CC haemolytic anaemia, sterility, myasthenia gravis, multiple sclerosis,
CC Basedow's disease, insulin-dependent diabetes mellitus, allergy, atopic
CC disease, arteriosclerosis, myocarditis, cardiomyopathy, glomerular
CC nephritis, hypoplastic anaemia, rejection after organ transplantation,
CC and numerous malignancies of lung, prostate, liver, ovary, lymphatic or
CC breast tissue. Peptides used to design primers for isolating heavy and
CC light chain cDNA of the mouse TRAIL (AAU72801 and AAU72802), TRA-8 are
CC shown in AAU72799 and AAU72800
XX
SQ Sequence 234 AA;

Query Match 26.5%; Score 938; DB 5; Length 234;
Best Local Similarity 82.9%; Pred. No. 4.7e-48;
Matches 184; Conservative 12; Mismatches 22; Indels 4; Gaps 2;
QY 453 LYLVT---TSIVMTQPTLLVSAGDRVITTCASQSVSNDAVWYQKQPGQSPKLLISVT 509
DB 13 LFLFAGVEGDIWVTQSHKFWISVGDVRSITCKASQDVGTAVWYQKQPGQSPKLLIYWA 72
QY 510 SRYAGVDPDRFGSGYGTDFTLTISVQAEADAATVFCQDDYNSPPTFGGTYKLEIKRADA 569
DB 73 STRHTGVDPDRFTGSGSGTDTLTISNVQSEDLADYFCQ-QYSSYRTFGGTYKLEIKRADA 131
QY 570 APTVSIFFPSSEQLTSGGASVVCFLNNFYPKDNVKKWIDGGERQNGVLSNWTDDQSDS 629
DB 132 APTVSIFFPSSEQLTSGGASVVCFLNNFYPKDNVKKWIDGGERQNGVLSNWTDDQSDS 191
QY 630 TVSMSSTLTITKDEYHRHNSYTCETHKSTSTSPIVKSFNRNE 671
DB 192 TVSMSSTLTITLDEYHRHNSYTCETHKSTSTSPIVKSFNRNE 233

RESULT 75
ABU79068
ID ABU79068 standard; protein; 257 AA.
XX
AC ABU79068;
XX
DT 18-JUN-2003 (first entry)
XX
DE S. aureus SEA (staphylococcus enterotoxin A) protein.
XX
KW Superantigen; SAG; staphylococcal enterotoxin; tumour; cancer; apoptosis;
KW gene therapy; mammalian cell receptor; tumour associated lipid; energy;
KW T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;
KW APC; antitumour.
XX
CS Staphylococcus aureus.
XX
PN US2002177551-A1.
XX
PD 28-NOV-2002.
XX
PF 30-MAY-2001; 2001US-00870759.
XX
PR 31-MAY-2000; 2000US-0208128P.
XX
PA (TERM/) Terman D S.
XX
PI Terman DS;
XX

DR WPI; 2003-361759/34.
DR N-PSDB; ACA64694.
XX
PT A mammalian cell receptor, useful in the treatment of cancer by binding
PT to tumour associated lipids where the binding induces energy or apoptosis
XX in T cells and antigen presenting cells.
PS Disclosure; Page; 167pp; English.
XX
CC The invention relates to a mammalian cell receptor, useful in the
CC treatment of cancer, which binds to tumour associated lipids and induces
CC energy or apoptosis in the T cells and antigen presenting cells (APCs).
CC Also included are a mammalian cell useful in the treatment of cancer
CC where the receptor which binds tumour associated lipids and induces
CC cellular inactivation or death is deleted or functionally deactivated,
CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal
CC (by allowing tumour associated lipids to contact immunocytes in which
CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,
CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
CC deleted), a construct useful in the treatment of cancer comprising a
CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
CC useful in the treatment of cancer (where an adaptor protein which
CC inhibits T cell activation by tumour associated antigens is deleted or
CC functionally deactivated), a composition useful in the treatment of
CC cancer (comprising a lipid raft conjugated to a superantigen), producing
CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
CC allowing tumour associated lipids to contact immunocytes, in which
CC receptors for the lipids are inactivated or deleted to produce a
CC tumouricidal immunocyte population, and administering the tumouricidal APC
CC activated immunocytes to the host), producing (M3) a tumouricidal APC
CC population ex vivo in a mammal (by allowing a tumour associated lipid to
CC contact APCs, in which receptors for the tumour associated lipids are
CC inactivated or deleted to produce a tumouricidally activated population,
CC and administering APCs to the host), producing a tumouricidal T cell
CC population ex vivo in a mammal (by allowing a tumour associated lipids to
CC contact T cells, in which adaptor proteins, which inhibit T cell
CC activation by tumour associated antigens, are deleted or functionally
CC deactivated to produce a tumouricidal population of T cells, and
CC administering the tumouricidally activated T cells to the host, or
CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
CC administering the tumouricidally activated T cells to the host), treating
CC (M5) cancer in a mammal (by administering a lipid binding molecule which
CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
CC a tumouricidal T cell population in vivo in a mammal (by allowing a
CC tumour associated antigen to contact immunocytes in which adaptor
CC proteins which inhibit T cell activation by tumour associated antigens
CC are deleted or functionally deactivated) and producing (M7) a
CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
CC receptors methods and compositions are useful for treating cancers and
CC tumours. Bacterial superantigens are co-administered or administered as
CC fusion constructs with anti-tumour proteins or motifs. The present
CC sequence represents a bacterial superantigen protein (e.g. a
CC staphylococcal enterotoxin). Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format from the US patent office website at
CC "seqdata.uspto.gov/sequence.html?DocID=20020177551"
XX
SQ Sequence 257 AA;

Query Match 26.5%; Score 935; DB 6; Length 257;
Best Local Similarity 75.5%; Pred. No. 7.9e-48;
Matches 176; Conservative 21; Mismatches 36; Indels 0; Gaps 0;
QY 226 SEKSEENEXKDLRKSELOGTALGNLQIYYNKAITSSEKSDADQTLTTLFKGPTG 285
DB 25 SEKSEENEXKDLRKSELOGTALGNLQIYYNKAITSSEKSDADQTLTTLFKGPTG 84
QY 286 HPWYNDLLVLDGTAATSEYGGSSVDLYGAYGQCACAGTGNKTCACMYGGVTLHDNNRLT 345
DB 85 HSWYNDLLVDFDSKDIVDKYKGVLDLYGAYGQCACAGTGNKTCACMYGGVTLHDNNRLT 144

us-09-900-766-1.rag

346	BEKKVPINLWIDGQVTPVDPDKVTSKKEVTQELDLQARHYLHGKFGHYNDSFGGKVQ	405
QY		
Db		
145	BEKKVPINLWJGQNTVPTVTKNKNVTQELDLQARRYLQEKINYINSDVFDGKVQ	204
Db		
406	RGLIVFHSSEGSTVSYDLFDAQGQYPTLLIRYRDNTTISSTLSLSLYTT	458
QY		
205	RGLIVFHTSTERSVNYDLFQAQGNSTLLIRYRDNKTINSENMHIDIVLYTS	257
Db		

Search completed: August 12, 2004, 13:29:58
Job time : 97.4429 secs

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OM protein - protein search, using sw model

Run on: August 12, 2004, 13:32:36 ; Search time 71.4517 Seconds
(without alignments)
2952.472 Million cell updates/sec

Title: US-09-900-766-1

Perfect score: 3522

Sequence: 1 EVQLQQSGFDLVKPGASVKI.....EATHKTSPIVKSFNRNES 672

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1292805 seqs, 313927144 residues

Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA.*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.rep.*
- 2: /cgn2_6/ptodata/2/pubpaa/FCR_NEW_PUB.rep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.rep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.rep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.rep.*
- 6: /cgn2_6/ptodata/2/pubpaa/FCRUS_PUBCOMB.rep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.rep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.rep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.rep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.rep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.rep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.rep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.rep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.rep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.rep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.rep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.rep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.rep.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3522	100.0	672	10	US-09-900-766-1
2	1832.5	52.0	478	16	US-10-679-620-72
3	1832.5	52.0	509	16	US-10-679-620-90
4	1653	46.9	552	16	US-10-679-620-86
5	1257	35.7	669	9	US-09-807-721-2
6	1218	34.6	233	10	US-09-900-766-2
7	1130	32.1	233	10	US-09-900-766-3
8	1107	31.4	233	10	US-09-900-766-7
9	1107	31.4	233	14	US-10-283-838-8
10	1107	31.4	257	12	US-10-267-682-112
11	1107	31.4	257	12	US-10-267-748-112
12	1072	30.4	248	9	US-09-870-759-16
13	1072	30.4	248	10	US-09-751-708A-16
14	1069	30.4	600	16	US-10-334-235-38
15	1028	29.2	597	9	US-09-903-327A-11

16	1025.5	29.1	464	14	US-10-216-484-9	Sequence 9, Appli
17	1025.5	29.1	464	14	US-10-384-933-9	Sequence 9, Appli
18	1024.5	29.1	613	9	US-09-903-327A-14	Sequence 14, Appli
19	1023.5	29.1	456	9	US-09-903-327A-2	Sequence 2, Appli
20	1023.5	29.1	493	9	US-09-903-327A-13	Sequence 13, Appli
21	1023.5	29.1	510	9	US-09-903-327A-12	Sequence 12, Appli
22	1022.5	29.0	438	9	US-09-903-327A-6	Sequence 6, Appli
23	1000	28.4	700	16	US-10-679-620-94	Sequence 94, Appli
24	980.5	27.8	711	14	US-10-071-485-90	Sequence 90, Appli
25	979.5	27.8	223	15	US-10-410-907A-36	Sequence 36, Appli
26	972.5	27.6	243	16	US-10-334-235-37	Sequence 37, Appli
27	967.5	27.5	488	16	US-10-334-233-39	Sequence 39, Appli
28	965.5	27.4	510	16	US-10-679-620-74	Sequence 74, Appli
29	965.5	27.4	510	16	US-10-679-620-92	Sequence 92, Appli
30	958	27.2	214	16	US-10-679-620-84	Sequence 84, Appli
31	957	27.2	468	10	US-09-795-515-7	Sequence 7, Appli
32	957	27.2	468	12	US-10-704-352-7	Sequence 7, Appli
33	957	27.2	468	16	US-10-704-071-7	Sequence 7, Appli
34	952	27.0	222	16	US-10-679-620-82	Sequence 82, Appli
35	948	26.9	233	10	US-09-900-766-4	Sequence 4, Appli
36	948	26.9	233	14	US-10-283-838-7	Sequence 7, Appli
37	948	26.9	257	12	US-10-267-682-113	Sequence 113, App
38	948	26.9	257	12	US-10-267-748-113	Sequence 113, App
39	945	26.8	234	14	US-10-281-479A-24	Sequence 24, Appli
40	945	26.8	234	14	US-10-275-180A-24	Sequence 24, Appli
41	945	26.8	234	14	US-10-286-132A-24	Sequence 24, Appli
42	944	26.8	233	12	US-10-354-948-4	Sequence 4, Appli
43	935	26.5	257	9	US-09-870-759-8	Sequence 8, Appli
44	935	26.5	257	10	US-09-751-708A-8	Sequence 8, Appli
45	926	26.3	451	16	US-10-679-620-118	Sequence 118, App
46	925	26.3	257	14	US-10-002-784A-2	Sequence 2, Appli
47	921	26.1	233	14	US-10-002-784A-4	Sequence 4, Appli
48	915	26.0	238	14	US-10-216-484-11	Sequence 11, Appli
49	915	26.0	238	14	US-10-384-933-11	Sequence 11, Appli
50	912	25.9	238	9	US-09-903-327A-4	Sequence 4, Appli
51	908	25.8	257	8	US-08-882-431-2	Sequence 2, Appli
52	903	25.6	233	8	US-08-882-431-4	Sequence 4, Appli
53	900.5	25.6	462	14	US-10-281-479A-23	Sequence 23, Appli
54	900.5	25.6	462	14	US-10-286-132A-23	Sequence 23, Appli
55	900.5	25.6	464	14	US-10-275-180A-23	Sequence 23, Appli
56	894	25.4	218	16	US-10-679-620-80	Sequence 80, Appli
57	894	25.4	712	16	US-10-679-620-116	Sequence 116, App
58	890.5	25.3	215	16	US-10-679-620-120	Sequence 120, App
59	890.5	25.3	483	16	US-10-679-620-122	Sequence 122, App
60	885	25.1	363	15	US-10-291-265-335	Sequence 335, App
61	884.5	25.1	451	16	US-10-679-620-78	Sequence 78, Appli
62	872	24.8	453	14	US-10-159-006-18	Sequence 18, Appli
63	866.5	24.6	215	15	US-10-410-907A-34	Sequence 34, Appli
64	863.5	24.5	472	14	US-10-159-006-30	Sequence 30, Appli
65	855.5	24.3	473	9	US-09-910-059-131	Sequence 131, App
66	852.5	24.2	235	10	US-09-795-515-5	Sequence 5, Appli
67	852.5	24.2	235	12	US-10-704-352-5	Sequence 5, Appli
68	852.5	24.2	235	16	US-10-704-071-5	Sequence 5, Appli
69	852	24.2	448	16	US-10-467-546-4	Sequence 4, Appli
70	849	24.1	448	15	US-10-378-567-2	Sequence 2, Appli
71	841.5	23.9	384	15	US-10-291-265-804	Sequence 804, App
72	841.5	23.9	384	15	US-10-291-265-805	Sequence 805, App
73	841.5	23.9	384	15	US-10-291-265-806	Sequence 806, App
74	841.5	23.9	384	15	US-10-291-265-807	Sequence 807, App
75	827.5	23.5	470	14	US-10-216-484-143	Sequence 143, App
76	827.5	23.5	470	14	US-10-384-933-143	Sequence 143, App
77	825.5	23.4	470	14	US-10-216-484-145	Sequence 145, App
78	825.5	23.4	470	14	US-10-384-933-145	Sequence 145, App
79	824.5	23.4	470	14	US-10-216-484-117	Sequence 117, App
80	824.5	23.4	470	14	US-10-216-484-147	Sequence 147, App
81	824.5	23.4	470	14	US-10-384-933-117	Sequence 117, App
82	824.5	23.4	470	14	US-10-384-933-147	Sequence 147, App
83	821	23.3	367	15	US-10-291-265-899	Sequence 899, App
84	818.5	23.2	472	14	US-10-159-006-43	Sequence 43, Appli
85	816.5	23.2	470	14	US-10-216-484-89	Sequence 89, Appli
86	816.5	23.2	470	14	US-10-384-933-89	Sequence 89, Appli
87	809.5	23.0	449	16	US-10-318-397-22	Sequence 22, Appli
88	809.5	23.0	449	16	US-10-317-747-22	Sequence 22, Appli

Sequence 6, Appli
Sequence 4, Appli
Sequence 157, App
Sequence 157, App
Sequence 71, Appl
Sequence 208511,
Sequence 46, Appl
Sequence 2, Appli
Sequence 56, Appl
Sequence 56, Appl
Sequence 56, Appl

89 807 22.9 448 9 US-09-917-410-6
90 805.5 22.9 451 15 US-10-423-299-4
91 805.5 22.9 470 14 US-10-216-484-157
92 805.5 22.9 470 14 US-10-384-933-157
93 802 22.8 452 10 US-09-726-258-71
94 797 22.6 471 12 US-10-424-599-208511
95 797 22.6 471 12 US-10-292-088-46
96 796 22.6 614 12 US-10-389-223A-2
97 794.5 22.6 448 12 US-10-411-037-56
98 794.5 22.6 448 12 US-10-411-026-56
99 794.5 22.6 448 16 US-10-410-962-56
100 794.5 22.6 448 16 US-10-411-049-56

ALIGNMENTS

RESULT 1
US-09-900-766-1
; Sequence 1, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALISE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERNANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US;10104199
; CURRENT APPLICATION NUMBER: US/09/900, 766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 672
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(672)
; OTHER INFORMATION: Conjugate protein
US-09-900-766-1

Query Match 100.0%; Score 3522; DB 10; Length 672;
Best Local Similarity 100.0%; Pred. No. 3e-184;
Matches 672; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EVQLQQSGPDLVPCASVKISCKASGYSTFGYMHVKQSPGKLEWIGRINPNNGVTLY 60
DB 1 EVQLQQSGPDLVPCASVKISCKASGYSTFGYMHVKQSPGKLEWIGRINPNNGVTLY 60

QY 61 NQKFKDKATLTVDKSSITAYMELSLTSEDYSAVYCARSTMTINVMYDYGQGTSTVSS 120
DB 61 NQKFKDKATLTVDKSSITAYMELSLTSEDYSAVYCARSTMTINVMYDYGQGTSTVSS 120

QY 121 AKTTPPSVYPLAPGSAQTNSMTVLGCLVKGYFPPEVPTVTWNSGSLSSGVHTFPVQLQSD 180
DB 121 AKTTPPSVYPLAPGSAQTNSMTVLGCLVKGYFPPEVPTVTWNSGSLSSGVHTFPVQLQSD 180

QY 181 LYTSSSVTVPSSTWPSSTETVCNVAHPASSTKVDKKIIVPRDSGSPSEKSEINEKDLRKK 240
DB 181 LYTSSSVTVPSSTWPSSTETVCNVAHPASSTKVDKKIIVPRDSGSPSEKSEINEKDLRKK 240

QY 241 SELQGTALGNLKQIYYNSKAITSSKSAQDQFLNTLLFKGFFTGHPWYNDLLVDLGSTA 300
DB 241 SELQGTALGNLKQIYYNSKAITSSKSAQDQFLNTLLFKGFFTGHPWYNDLLVDLGSTA 300

QY 301 ATSEYEGSVLDLYGAYGYQACAGTGNKTAQWYGVTLHNNRLTEBKYPINLWDGKQ 360
DB 301 ATSEYEGSVLDLYGAYGYQACAGTGNKTAQWYGVTLHNNRLTEBKYPINLWDGKQ 360

QY 361 TTVPIDKVKTSKKEVTVOELDQARHYLHGKFLYNSDSFGKVGQRLIVFHSSEGSTVS 420
DB 361 TTVPIDKVKTSKKEVTVOELDQARHYLHGKFLYNSDSFGKVGQRLIVFHSSEGSTVS 420

QY 421 YDLFDAQOQYPTLLRIYRDNTTSSISLSLYLTTISIVMTQTPTSLVSAQDRVTIT 480
DB 421 YDLFDAQOQYPTLLRIYRDNTTSSISLSLYLTTISIVMTQTPTSLVSAQDRVTIT 480

QY 481 CKASQSVNDVAMVYQKPGQSPKLLISYTSRYAGVDPFRFSGSGYGTDTFTLTSSVQAE 540
DB 481 CKASQSVNDVAMVYQKPGQSPKLLISYTSRYAGVDPFRFSGSGYGTDTFTLTSSVQAE 540

QY 541 AAVYFCQDDYNSPPTFGGKLEIKRAADAPTSTFFPPSSQLTSGGASVVCFLNNFYPK 600
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QY 601 DINVKWKIDGSRQNGVLNSWTDDQSKDSTYSMSSTLTLTDEYERHNSYTCEATHKTST 660
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QY 661 SPIVKSFNRNES 672
DB 661 SPIVKSFNRNES 672

RESULT 2

US-10-679-620-72
; Sequence 72, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reinl, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 72
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pLSBC1740 , see Example 12
US-10-679-620-72

Query Match 52.0%; Score 1832.5; DB 16; Length 478;
Best Local Similarity 56.5%; Pred. No. 3.1e-92;
Matches 379; Conservative 32; Mismatches 65; Indels 195; Gaps 5;

QY 1 EVQLQQSGPDLVPCASVKISCKASGYSTFGYMHVKQSPGKLEWIGRINPNNGVTLY 60
DB 2 QQLQQSGPDLVPCASVKISCKASGYSTFGYMHVKQSPGKLEWIGRINPNNGVTLY 61

QY 61 NQKFKDKATLTVDKSSITAYMELSLTSEDYSAVYCARSTMTINVMYDYGQGTSTVSS 120
DB 62 DPKFDKATITADTSNTAYLQVSRSLTSEDYSAVYCARSGGDPGFYMDYWGQASVTSS 121

QY 121 AKTTPPSVYPLAPGSAQTNSMTVLGCLVKGYFPPEVPTVTWNSGSLSSGVHTFPVQLQSD 180
DB 122 AKTTPPSVYPLAPGSAQTNSMTVLGCLVKGYFPPEVPTVTWNSGSLSSGVHTFPVQLQSD 181

QY 181 LYTSSSVTVPSSTWPSSTETVCNVAHPASSTKVDKKIIVPRDSGSPSEKSEINEKDLRKK 240
DB 182 LYTSSSVTVPSSTWPSSTETVCNVAHPASSTKVDKKIIVPRDCGG-----GK 227

QY 241 SELQGTALGNLKQIYYNSKAITSSKSAQDQFLNTLLFKGFFTGHPWYNDLLVDLGSTA 300
DB 228 RTIQDQA-----TDT-----VDLGAE 244

QY 301 ATSEYEGSVLDLYGAYGYQACAGTGNKTAQWYGVTLHNNRLTEBKYPINLWDGKQ 360
DB 245 HRDDPPPTASDI-----TDT-----VDLGAE 256

QY	361	TTVPIDKVKTSKKEVTVOQLDLQARHYLHGKFGLYNSDSFGGKVQGRGLIVFHSSSEGSTVS	420
DB	257	-----GSRGKRGGD-----	265
QY	421	YDLFDAQQGYPTLLRIYRDNNTTISSTSLISLYLTTISVMTQTPTSLIVSAGDRVIT	480
DB	266	-----IVMTQSHKPMSTSVGDRVST	286
QY	481	CXASQSVNDVAVYQCKPGQSPKLLISVTSRVAGVDPDRFSGSGYGTFDTFLTITSSVQAB	540
DB	287	-----IVMTQSHKPMSTSVGDRVST	346
QY	541	AAVYFCQDYNPPTFFGGTGLEIKRADAAPTTSIFPPSSEQLTSGGASVVCFLNNFYK	600
DB	347	LAVYVCOQHYTTPPTFFGGTGLEIKRADAAPTTSIFPPSSEQLTSGGASVVCFLNNFYK	406
QY	601	DINVKWKIDGSRQNGVLNSWTDQSKDSTYSMSSTLTLTQDEYERHNSYTCEATHKTST	660
DB	407	DINVKWKIDGSRQNGVLNSWTDQSKDSTYSMSSTLTLTQDEYERHNSYTCEATHKTST	466
QY	661	SPIVKSFNRNE	671
DB	467	SPIVKSFNRNE	477

RESULT 3
 US-10-679-620-90
 ; Sequence 90, Application US/10679620
 ; Publication No. US20040110930A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Large Scale Biology
 ; APPLICANT: Reinel, Stephen J.
 ; APPLICANT: Edwards, Patricia C.
 ; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
 ; FILE REFERENCE: 34150-004A
 ; CURRENT APPLICATION NUMBER: US/10/679,620
 ; CURRENT FILING DATE: 2003-10-03
 ; PRIOR APPLICATION NUMBER: 60/415,940
 ; PRIOR FILING DATE: 2002-10-03
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 90
 ; LENGTH: 509
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: PLSSBC1766, see Example 12
 US-10-679-620-90

Query Match 52.0%; Score 1832.5; DB 16; Length 509;
 Best Local Similarity 56.5%; Pred. No. 3.3e-92;
 Matches 379; Conservative 32; Mismatches 65; Indels 195; Gaps

[illegible]

```

QY   301 ATSEYEGSSVDLGYAYVGYOCAGGTPNKTACMYGGVTLDHNNRLTEKKVPINLWIDCKQ 360
      :          :
Db   276 HRDPPPTASDI-----287
      :          :
QY   361 TTVPIDVKTSKKEVTQELDLQARHYLHGKFGLYNDSFGKVQRGLIVFHSSEGSTVS 420
      - - - - -GKRGKGGD- - - - -296
Db   288 -----317
      :          :
QY   421 YDLFDAQQVPDTRLRIYRONTTISLSLSLYTYTSIMVTQTPTSLLSAGDRVIT 480
      :          :
Db   297 -----317
      :          :
QY   481 CKASQSVSNDVAWYQOKFGOSP KLLISYTSRYAGVDPDRFSGGSGYGDFDTLTISSVQAED 540
      :          :
Db   318 CKASQDVNTAVAWYQOKFGSP KLLIYSASFRTYGVDRFTGNRSCTDFTTSSVQAED 377
      :          :
QY   541 AAVFYCQDDXNSPPTFFGGTGKLEIKRADAAPTVSIFFPSSEQLTSGASVVCFLNFPYPK 600
      :          :
Db   378 LAVYCOCHYTTPPTFFGGTGKLEIKRADAAAPT VSIFFPSSEQLTSGGASVVCFLNFPYPK 437
      :          :
QY   601 DINVKWKIDGSRONGVLNWSWTDQSDSKDYSSMSSTLTTLTKDEYERHNSYTCETHKTST 660
      :          :
Db   438 DINVKWKIDGSRONGVLNWSWTDQSDSKDYSSMSSTLT TLTKDEYERHNSYTCETHKTST 497
      :          :
QY   661 SPIVKSFNRNE 671
      :          :
Db   498 SPIVKSFNRNE 508

RESULT 4
US-10-679-620-86
; Sequence 86, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reisl, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patent version 3.2
; SEQ ID NO 86
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pLSBC1736, see Example 15
US-10-679-620-86

```

Query Match	46.9%	Score 1653;	DB 16;	Length 552;
Best Local Similarity	51.5%;	Pred. No. 2.3e-82;		
Matches 351;	Conservative 40;	Mismatches 85;	Indels 206;	Gaps 7
Qy	1	EVQLQQGGPDLVKPGASVKISCKASGYSFTGYMHWVKQSPGKGLIEWIGRINPNNGVLT	60	
Db	65	EVDLVESGGDLVKPGGSLKLSCAASGFTFSHYGMSWVRQTPDKRLWATIGCSRGTYTHY	124	
Qy	61	NQKPKDKATLVTKDSSITATYMWELRSLTSDSNAVYYCARSTMITNY-----VMDYWGQG	113	
Db	125	PSVKYGRFTISRDNDDKALYQMLNSKSEDTAMTYCARRSEFFYYGNTYTYYSAMDYWGQG	184	
Qy	114	TSVTVSAAKTPPSPVYPLAPGSAQTNSMVTLCGLVKGYPEPVTVTWNSGSLSSGVHTF	173	
Db	185	ASVTVSAAKTPPSPVYPLAPGSAQTNSMVTLCGLVKGYPEPVTVTWNSGSLSSGVHTF	244	
Qy	174	PAVLQSDLYTLSSVTVPSSVTWPSETVTCNVAHPASSTKVDKKIIVPRDSGGPSEKSEBIN	233	
Db	245	PAVLQSDLHTLSSVTVPSSVTWPSETVTCNVAHPASSTKVDKKIIVPRDCGG-----	295	

QY 234 EKDLRKSELOQTALGNLKOIYYNSKAITSSSEKADQFLNTLLFKGFTGHPWYNLL 293
 DB 296 -----GKTIQDSA-----TDT----- 307
 QY 294 VDLGSTAATSEYEGSSVDLYGAYGQCAGGTPNKTACMYGGVTLHNNRLTEKKVPIN 353
 DB 308 VDLGAELHRDDPPPTASDI----- 326
 QY 354 LWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFLGYNDSFGKVQORGLIVFHS 413
 DB 327 -----GKGRKGGD----- 335
 QY 414 SEGSTVSYDLFAQGOVPTLLRIYRDNNTTISLSISLYTTSITMTQTFSLVSA 473
 DB 336 -----IVLTQSPASLAVSL 349
 QY 474 GDRVTITCKASQSVN---DVMYQOKPGQSPKLLIYTSSTRYAGVDPDRFSGSGYGTDF 529
 DB 350 QORATISCRASEVDNIGFSFNNWFQKPGPPKLLIYAINRSGVPAFPSSGSGTDF 409
 QY 530 TLTSSVQAEADAAYFCQDYNPPTFGGFKLEIKRADAAPTYSIFPPSSSQLTSGGAS 589
 DB 410 SLNIHPVEEDDPAMYFCQOTKEVPWTFGGTKLEIKRADAAPTYSIFPPSSSQLTSGGAS 469
 QY 590 VVCFLNFPYKIDINVKWKIDGSRQNGVLNSWTDQDSKSTYSMSSTLTITKDEYERHNS 649
 DB 470 VVCFLNFPYKIDINVKWKIDGSRQNGVLNSWTDQDSKSTYSMSSTLTITKDEYERHNS 529
 QY 650 YTCEATHKTSTSPIVKSFNRNE 671
 DB 530 YTCEATHKTSTSPIVKSFNRNE 551
 RESULT 5
 US-09-807-721-2
 ; Sequence 2, Application US/09807721
 ; Patent No. US20020174453A1
 ; GENERAL INFORMATION:
 ; APPLICANT: AUBURN UNIVERSITY
 ; APPLICANT: UNIVERSITY OF CENTRAL FLORIDA
 ; TITLE OF INVENTION: PRODUCTION OF ANTIBODIES IN TRANSGENIC PLASTIDS
 ; FILE REFERENCE: 1463-PCT-US-00
 ; CURRENT APPLICATION NUMBER: US/09/807,721
 ; CURRENT FILING DATE: 2001-12-21
 ; PRIOR APPLICATION NUMBER: PCT/US01/06274
 ; PRIOR FILING DATE: 2001-02-28
 ; NUMBER OF SEQ ID NOS: 6
 ; SOFTWARE: Patent in Ver. 2.1
 ; SEQ ID NO 2
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-807-721-2

Query Match 35.7%; Score 1257; DB 9; Length 669;
 Best Local Similarity 41.6%; Pred. No. 1.1e-60;
 Matches 308; Conservative 87; Mismatches 201; Indels 144; Gaps 23;
 QY 2 VOLQSGDPLVKPASVKISKASGYSTGYTHMHWKOSPKGLEWIGRINPNNGVTLN 61
 DB 3 VOLQSGDPLVKPASVKISKASGYSTGYTHMHWKOSPKGLEWIGRINPNNGVTLN 62
 QY 62 QKFKDKATLTVDKSTTAYMELRLTSEDGSAVYVCARSTMTINVMYDYGQGTSTVSSA 121
 DB 63 QKFKDKATLTVDNSTTAYMELRLTSEDGSAVYVCAT-----YFDYWGQGTTLTVSSA 115
 QY 122 KITPSPVYPLAPGAAQNTSMWTLGCLVKGYFP-EPVTVTWNSGSLSSGVHTFPAY--LQ 178
 DB 116 SPTSPKVPFPLSLDTPQDGNVV-VACLVQGFPPQELSLVTSWESGGQVNTARNPPSQDAS 174
 QY 179 SDLYTLSSVTVPSSTWP-SETVTCNAHPASSTKVDKIVPRDSGGSPSEKSEINEKOL 237

DB 175 GDLYTTSQLTLPATQCPDGKSVTCHVHYNNSSQ-DVTVFCRVPPPP-----PCC 224
 QY 238 RKKSELQGTALGNLKOIYYNSKAITSSSEKADQFLNTLLFKGFTGHPWYNLLVDLG 297
 DB 225 HPLSLHRLPALEDL-----LLGSEAN-----LTCTL-----TG-----LRDASG 258
 QY 298 STAATSEYEGSSV-----DLYGAY-----YG---YQACAGGTPNKTACMYG 334
 DB 259 ATFTWTTPSSGSAVQPPPERDLGCGYSVSVLPGCAQPMNEGFTCTTAHPELKTPLTA 318
 QY 335 GYTLHNNRLTEKKVP-----INLWIDGKQTTVPIDKV 368
 DB 319 NITKSGNTRFPEVHLPPPSBELANLVELTLCLARGSPKDVLRVWLGSSQ-ELPREKY 377
 QY 369 KT--SKKE-----VTVQELDLQARHYLHGKFLGYNDSFGKVQORGLIVFHSSEGST 418
 DB 378 LTWASRQPSQGTTTYAVTSLRVAEDWKKG-----ETF-----SCMVGHEALPLA 424
 QY 419 VSYDLFAQGOVPTLLRIYRDNNTTISLSISLYL-----YTTISVMTQTFSLV 471
 DB 425 FTQKTIIDRIAGKP-----THNVSVVMAEADGTCYRMDIVMTQSPALMSA 469
 QY 472 SAGDRVTITCKASQSVNDAVYQOKPGQSPKLLIYTSSTRYAGVDPDRFSGSGYGTDFTL 531
 DB 470 SPGEKVTITCSASSMVSY-MHWFOQKPGTSPKLMYSTNSLASGVPAFPSSGSGTSYSL 528
 QY 532 TISSVQAEADAAYFCQDYNPPTFGGFKLEIKRADAAPTYSIFPPSSSQLTSGGASV 591
 DB 529 TISRVEADAATYCHQRTSYPTFGGFKLEIKRVAAPSVFIFPPSDEQLKSGTASV 588
 QY 592 CFLNFPYKIDINVKWKIDGSRQNGVLNSWTDQDSKSTYSMSSTLTITKDEYERHNSY 651
 DB 589 CLNFPYKIDINVKWKIDGSRQNGVLNSWTDQDSKSTYSMSSTLTITKDEYERHNSY 648
 QY 652 CEATHKTSTSPIVKSFNRNE 671
 DB 649 CEVTHQGLSPVTKSFNRNE 668
 RESULT 6
 US-09-900-766-2
 ; Sequence 2, Application US/09900766
 ; Publication No. US20030039655A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FORSBERG, GORAN
 ; APPLICANT: ERLANDSSON, EVA
 ; APPLICANT: ANTONSSON, PER
 ; APPLICANT: WALSE, BJORN
 ; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
 ; FILE REFERENCE: P02188US010104199
 ; CURRENT APPLICATION NUMBER: US/09/900,766
 ; CURRENT FILING DATE: 2001-07-06
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: Peptide
 ; LOCATION: (1)..(233)
 ; OTHER INFORMATION: Chimeric Protein
 US-09-900-766-2

Query Match 34.6%; Score 1218; DB 10; Length 233;
 Best Local Similarity 100.0%; Pred. No. 4.7e-59;
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSSSEKADQFLNTLLFKGFTG 285
 DB 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSSSEKADQFLNTLLFKGFTG 60
 QY 286 HPWYNLLVDLGSTAAATSEYEGSSVDLYGAYGQCAGGTPNKTACMYGGVTLHNNRLT 345

Db 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYYGQCAGTTPNKTAQMYGGVTLHNNRLT 120
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 406 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNNTTISSTLSISLYTT 458
Db 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNNTTISSTLSISLYTT 233

RESULT 7
US-09-900-766-3
; Sequence 3, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 233
; TYPE: PRT
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(233)
; OTHER INFORMATION: Chimeric Protein
US-09-900-766-3

Query Match 32.1%; Score 1130; DB 10; Length 233;
Best Local Similarity 91.4%; Pred. No. 3e-54;
Matches 213; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSELOGTALGNLQIYYVNSKAITSEKSAOFLTNTLLFKGFTG 285
Db 1 SEKSEINEKDLRKSELOGTALGNLQIYYVNSKAITSEKSAOFLTNTLLFKGFTG 60
QY 286 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYYGQCAGTTPNKTAQMYGGVTLHNNRLT 345
Db 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGQCAGTTPNKTAQMYGGVTLHNNRLT 120
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 406 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNNTTISSTLSISLYTT 458
Db 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNNTTISSTLSISLYTT 233

RESULT 8
US-09-900-766-7
; Sequence 7, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 7
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-900-766-7
Query Match 31.4%; Score 1107; DB 10; Length 233;
Best Local Similarity 89.7%; Pred. No. 5.4e-53;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSELOGTALGNLQIYYVNSKAITSEKSAOFLTNTLLFKGFTG 285
Db 1 SEKSEINEKDLRKSELOGTALGNLQIYYVNSKAITSEKSAOFLTNTLLFKGFTG 60
QY 286 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYYGQCAGTTPNKTAQMYGGVTLHNNRLT 345
Db 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGQCAGTTPNKTAQMYGGVTLHNNRLT 120
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 406 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNNTTISSTLSISLYTT 458
Db 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNNTTISSTLSISLYTT 233

RESULT 9
US-10-283-838-8
; Sequence 8, Application US/10283838
; Publication No. US20030092894A1
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlstén,
; Johan Hansson, Terje Kalland, Lars
; Abrahamsen and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,838
; FILING DATE: 30-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,692
; FILING DATE: August 12, 1996
; APPLICATION NUMBER: 9601245-5
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 41986/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-10-263-838-8

Query Match 31.4%; Score 1107; DB 14; Length 233;
Best Local Similarity 89.7%; Pred. No. 5.4e-53;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSDADQFLTLLPKGFTG 285
DB 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSDADQFLTLLPKGFTG 60
QY 286 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGQCAGGTPNKTCACMYGGVTLHDNNRLT 345
DB 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGQCAGGTPNKTCACMYGGVTLHDNNRLT 120
QY 346 BEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLOARHYLHGKFGLYNSDSFGGKVQ 405
DB 121 BEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLOARHYLHGKFGLYNSDSFGGKVQ 180
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYLYTT 458
DB 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYLYTT 233

RESULT 10

US-10-267-682-112
; Sequence 112, Application US/10267682
; Publication No. US20040033235A1

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteaway, Stephen R.
Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION

NUMBER OF SEQUENCES: 239

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/267,682

FILING DATE: 08-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/484,223A

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-029

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 112:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: unknown

MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 112:

US-10-267-682-112

Query Match 31.4%; Score 1107; DB 12; Length 257;
Best Local Similarity 89.7%; Pred. No. 6e-53;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSDADQFLTLLPKGFTG 285
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSDADQFLTLLPKGFTG 84
QY 286 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGQCAGGTPNKTCACMYGGVTLHDNNRLT 345
DB 85 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGQCAGGTPNKTCACMYGGVTLHDNNRLT 144
QY 346 BEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLOARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 BEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLOARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYLYTT 458
DB 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYLYTT 257

RESULT 11

US-10-267-748-112

; Sequence 112, Application US/10267748
; Publication No. US20040052820A1

GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteaway, Stephen R.
Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION

NUMBER OF SEQUENCES: 239

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/267,748

FILING DATE: 08-Oct-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/484,223A

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.

REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-029

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864

TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 112:

SEQUENCE CHARACTERISTICS:

LENGTH: 257 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: unknown

```
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-267-748-112

Query Match
Best Local Similarity 31.4%; Score 1107; DB 12; Length 257;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKQIYYNKAITSSEKSADQFLNTLLFKGFPTG 285
DB 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFPTG 84
QY 286 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYYQCAGTTPNKTCMYGGVTLHNNRLT 345
DB 85 HPWYNDLLVLDGSKDATNKYKKVDLYGAYYQCAGTTPNKTCMYGGVTLHNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYLTT 458
DB 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTINSENHLDLYLTT 257

RESULT 12
US-09-870-759-16
/ Sequence 16, Application US/09870759
/ Patent No. US20020177552A1
/ GENERAL INFORMATION:
/ APPLICANT: TERMAN, David S
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
/ FILE REFERENCE: 870759
/ CURRENT APPLICATION NUMBER: US/09/870,759
/ CURRENT FILING DATE: 2002-01-14
/ PRIOR APPLICATION NUMBER: US 60/208,128
/ PRIOR FILING DATE: 2000-05-30
/ NUMBER OF SEQ ID NOS: 166
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 16
/ LENGTH: 248
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
US-09-870-759-16

Query Match
Best Local Similarity 30.4%; Score 1072; DB 9; Length 248;
Matches 202; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKQIYYNKAITSSEKSADQFLNTLLFKGFPTG 285
DB 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFPTG 84
QY 286 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYYQCAGTTPNKTCMYGGVTLHNNRLT 345
DB 85 HPWYNDLLVLDGSKDATNKYKKVDLYGAYYQCAGTTPNKTCMYGGVTLHNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLS 449
DB 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTINSEN 248

RESULT 13
US-09-751-708A-16
/ Sequence 16, Application US/09751708A
/ Publication No. US2003057113A1
/ GENERAL INFORMATION:
/ APPLICANT: TERMAN, David S
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
```

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/ FILE REFERENCE: 751708
/ CURRENT APPLICATION NUMBER: US/09/751.708A
/ CURRENT FILING DATE: 2002-10-15
/ PRIOR APPLICATION NUMBER: US 60/173,371
/ PRIOR FILING DATE: 1999-12-28
/ NUMBER OF SEQ ID NOS: 166
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 16
/ LENGTH: 248
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus
US-09-751-708A-16

Query Match
Best Local Similarity 30.4%; Score 1072; DB 10; Length 248;
Matches 202; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKQIYYNKAITSSEKSADQFLNTLLFKGFPTG 285
DB 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFPTG 84
QY 286 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYYQCAGTTPNKTCMYGGVTLHNNRLT 345
DB 85 HPWYNDLLVLDGSKDATNKYKKVDLYGAYYQCAGTTPNKTCMYGGVTLHNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLS 449
DB 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTINSEN 248

RESULT 14
US-10-334-235-38
/ Sequence 38, Application US/10334235
/ Publication No. US20040131591A1
/ GENERAL INFORMATION:
/ APPLICANT: Oxford Biomedica (UK) Ltd.
/ APPLICANT: Kingsman, Alan
/ APPLICANT: Bebbington, Christopher
/ APPLICANT: Carroll, Miles
/ APPLICANT: Ellard, Fiona
/ APPLICANT: Kingsman, Susan
/ APPLICANT: Myers, Kevin
/ APPLICANT: Lamikandra, Abigail
/ TITLE OF INVENTION: VECTOR SYSTEM
/ FILE REFERENCE: 53268200920
/ CURRENT APPLICATION NUMBER: US/10/334,235
/ CURRENT FILING DATE: 2002-12-30
/ PRIOR APPLICATION NUMBER: US 10/060,585
/ PRIOR FILING DATE: 2002-01-29
/ PRIOR APPLICATION NUMBER: PCT/GB00/04317
/ PRIOR FILING DATE: 2000-11-13
/ PRIOR APPLICATION NUMBER: US 09/445,375
/ PRIOR FILING DATE: 1998-06-04
/ NUMBER OF SEQ ID NOS: 40
/ SOFTWARE: FastSeq for Windows version 4.0
/ SEQ ID NO 38
/ LENGTH: 600
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: peptide of 5T4Sabl
US-10-334-235-38

Query Match
Best Local Similarity 30.4%; Score 1069; DB 16; Length 600;
Matches 254; Conservative 20; Mismatches 60; Indels 336; Gaps 9;

QY 1 EVQLQQSGPDLVKKPGASVKISKASGYFTGYMHWVKQSPGKLEWIGRPNNGVTLY 60
```

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Db      23 EVLQQSGDLVVKPGASVKISKASGYSTFYNNHWKQSHGKSLGWGRINPNNGVTLY 82
Qy      61 NQKFKDKATLLVDKSSSTAYMELSLTSEDASAVYCARSTMITNYVMDYQGQTSVTYSS 120
Db      83 NQKFKDKAILLVDKSSSTAYMELSLTSEDASAVYCARSTMITNYVMDYQGQTSVTYS- 141
Qy     121 AKTTPPSVYPLAPGSAAGTNSMVLGCLVKGYPFPTVTVNSGSLSSGVHTTFAVLQSD 180
Db     142 ----- 141
Qy     181 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKYDKIIVPRDSGGPSEKSEINEKDLRKK 240
Db     142 ----- 144
Qy     241 SELQGTALGNLKQIYYNSKAITSSSEKSAQDQFLNTLLFKGFFTGHPWYNDLLVDLGSTA 300
Db     145 ----- 144
Qy     301 ATSEYEGSSVDLYGAYGYQCAGGTPNKACMYGGVTLHDNNRLTEBKVPINLWIDGKQ 360
Db     145 ----- 154
Qy     361 TTVPIDKVKTSKEVTVQELDLQARHVLHGKFGLYNSDSFGKVQRGVLIVFHSSEGSTVS 420
Db     155 ----- 156
Qy     421 YDLFDAQQYPTLLRIYRDNNTTSSSTSLISLYLTTISVMTQPTSLVSSAGDRVTIT 480
Db     157 ----- 179
Qy     481 CKASQSVNDVAVTQKPGQSPKLLISYTSRYAGVDPDRSGSGYGTDFTLTSSVQAE 540
Db     180 CKASQSVNDVAVTQKPGQSPKLLISYTSRYAGVDPDRSGSGYGTDFTLTSSVQAE 239
Qy     541 AAVTFCQDYNPPTFGGKTKLEIKRADA-APTYSIFPPSEQLTSGASVWCFNNFY 599
Db     240 LAVTFCQDYNPPTFGGKTKLEIKRASKTPSFPPLAPSKSTSGTAALGCLVKDYFP 299
Qy     600 KDINVKWK-----IDGSRQNGVLNSWTDQDSKDSYMSSTLTLDKDEYERHNSYCEAT 655
Db     300 EPTVTVSMNGALTSQVHTFPAVLQS-----SGLYSLSSVTVTPSSSLGT-QTYICNVN 351
Qy     656 HKTSTSPIVK 665
Db     352 HKPSNTKVDK 361

RESULT 15
US-09-903-327A-11
; Sequence 11, Application US/09903327A
; Patent No. US20020164333A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
; TITLE OF INVENTION: GENE
; TITLE OF INVENTION: DELIVERY
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 597
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain
; OTHER INFORMATION: and INF alpha mature peptide
US-09-903-327A-11

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Query Match      29.2%; Score 1028; DB 9; Length 597;
Best Local Similarity 37.2%; Pred No. 3.1e-48;
Matches 253; Conservative 53; Mismatches 115; Indels 260; Gaps 15;

Qy      1 EVLQQSGDLVVKPGASVKISKASGYSTFYNNHWKQSPKGLGWITGRINPNNGVTLY 60
Db      20 EVLQQSGDLVVKPGASVKISKASGYSTFYNNHWKQSHGKSLGWITGYIYPKGGTGY 79
Qy      61 NQKFKDKATLLVDKSSSTAYMELSLTSEDASAVYCARSTMITNYVMDYQGQTSVTYSS 120
Db      80 NQKFKDKATLLVDKSSSTAYMELSLTSEDASAVYCARSTMITNYVMDYQGQTSVTYSS 132
Qy     121 AKTTPPSVYPLAPGSAAGTNSMVLGCLVKGYPFPTVTVNSGSLSSGVHTTFAVLQSD 180
Db     133 AKTTPPSVYPLAPGSAAGTNSMVLGCLVKGYPFPTVTVNSGSLSSGVHTTFAVLQSD 192
Qy     181 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKYDKIIVPRDSGGPSEKSEINEKDLRKK 240
Db     193 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKYDKIIVPRDCG----- 235
Qy     241 SELQGTALGNLKQIYYNSKAITSSSEKSAQDQFLNTLLFKGFFTGHPWYNDLLVDLGSTA 300
Db     236 CKPCICTVPEVSSVIFPPK-----PKDVLITL----- 264
Qy     301 ATSEYEGSSVDLYGAYGYQCAGGTPNKACMYGGVTLHDNNRLTEBKVPINLWIDGKQ 360
Db     265 -----TP-KVTCVVDIIS-----KDDPEVQFSMFVD--- 289
Qy     361 TTVPIDKVKTSKEV-----TVQELDLQARHVLHGK-FGL-YNSDSFGKVQRGVLIVF 411
Db     290 -DVEVHTAQTPREOFNSTFRSSELPIMQDNLNGKEFKCRVNSAFAPIEK----- 343
Qy     412 HSSEGSTVSYDLFDAQQYPTLLRIYRDNNTTSSSTSLISLYLTTISVMTQPTSLV 471
Db     344 -----TISKT----- 348
Qy     472 SAGDRVTITCKASQSVNDVAVTQKPGQSPKLLISYTSRYAGVDPDRSGSGYGTDFTL 531
Db     349 ----- 348
Qy     532 TISSVQAEADAAYFCQDYNPPTFGGKTKLEIKRADAAPTYSIFPPSEQLTSGGASV 591
Db     349 -----XGRPKAPQVYTIPTPPKQMAKDKVSLT 375
Qy     592 CFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDSYMSSTLTLDKDEYERHNSY 651
Db     376 CMITDFFPDITVEQWNGQPAEN-YKNTQFIMDT-DGSYFYVSKLVQKSNWEAGNTFI 433
Qy     652 CEATHKTSPIVKSFRNES 672
Db     434 CSVLHE-----FVRSSTRTPS 449

RESULT 16
US-10-216-484-9
; Sequence 9, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Pas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 9

```


FILE REFERENCE: 22908-1228
CURRENT APPLICATION NUMBER: US/09/903,327A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 09/613,017
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 14
LENGTH: 613
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain
OTHER INFORMATION: and SCF mature peptide
US-09-903-327A-14

Query Match 29.1%; Score 1024.5; DB 9; Length 613;
Best Local Similarity 37.3%; Pred. No. 5e-48;
Matches 250; Conservative 51; Mismatches 115; Indels 255; Gaps 14;
QY 1 EVQLQDSGPDLVKPGASVKISCKASGYFTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
DB 20 EVQLQDSGPELVKPGASVKISCKASGYFTDYNHWHVQSHGKSLWIGYIYPKGGTGY 79
QY 61 NQKFKDKATLTVDKSSITAYMELRSLTSDSAVYCARSTMTINVMYDYGQGTSTVSS 120
DB 80 NQKFKSKATLTDDSSNTAYMELRSLTSDSAVYCARSTMTINVMYDYGQGTSTVSS 132
QY 121 AKTTPPSVYPLAPGSAQTNSMTLGLVKGYPPEPTVTWNSGSLSSGVHTFPVAVLQSD 180
DB 133 AKTTPPSVYPLAPGSAQTNSMTLGLVKGYPPEPTVTWNSGSLSSGVHTFPVAVLQSD 192
QY 181 LYTSSSVTPSPSTWPTETVCNVAHPASSTKVDKVIIPRDSGGSPSEKSEINEKDLRKK 240
DB 193 LYTSSSVTPSPSTWPTETVCNVAHPASSTKVDKVIIPRDSGGSPSEKSEINEKDLRKK 235
QY 241 SELQGTALGNLQKIIYYNKSIAITSEKSAADQFLNTLLFKGFFTGHPWYNDLLVDLGSTA 300
DB 236 CKPCTCTVPEVSSVFIFFPK-----PKDVLITL----- 264
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPTNKTACMGVGTLDHNNRLTEKKVPINLWIDGKQ 360
DB 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFDV--- 289
QY 361 TTVPIDKVKTSKEV-----TVQELDLOARHYLHGK-FGL-VNSDSFGKVGQVGLIVF 411
DB 290 -DVEHTAQTPREBQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAPPAPIEK----- 343
QY 412 HSEGSTVSYDLFDAQGGYPTDLLRIYRDNNTTISSTLSISLSLYLTTTSIVMTQPTSLLV 471
DB 344 -----TISKT----- 348
QY 472 SAGDRVTITCKASQSVSNDVAVYQKPGQSKLLISYTSRYAGVDPFRFSGSGYGTDTFL 531
DB 349 ----- 348
QY 532 TISSVQAEADAAYVFCQDYNSPPTFGGKTKLEIKRADAAPTYSIFPPSSSEQLTSGGASV 591
DB 349 -----KGRPKAPQVYTIPTPKQMAKDKVSLT 375
QY 592 CFLNNFYKIDINVKWKIDSERQNGVLSWTDQSKDSTYSMSSTLTITKDEYERHNSYT 651
DB 376 CMITDFPEDITVEQWNGQPAEN-YKNTQPTIMDT-DGSYFYVSKLVNQRKNSWEAGNTFI 433
QY 652 CEATHKSTSP 662
DB 434 CSQLHEFCRYP 444

RESULT 19

US-09-903-327A-2
Sequence 2, Application US/09903327A
Patent No. US2002016433A1

GENERAL INFORMATION:
APPLICANT: Nemerow, Glen R.
TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGETED
TITLE OF INVENTION: GENE
TITLE OF INVENTION: DELIVERY
FILE REFERENCE: 22908-1228
CURRENT APPLICATION NUMBER: US/09/903,327A
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 09/613,017
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 456
TYPE: PRT
ORGANISM: Mouse
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (0)...(0)
OTHER INFORMATION: DAV-1 heavy chain, penton base monoclonal antibody
US-09-903-327A-2

Query Match 29.1%; Score 1023.5; DB 9; Length 456;
Best Local Similarity 37.4%; Pred. No. 4.1e-48;
Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;
QY 1 EVQLQDSGPDLVKPGASVKISCKASGYFTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
DB 20 EVQLQDSGPELVKPGASVKISCKASGYFTDYNHWHVQSHGKSLWIGYIYPKGGTGY 79
QY 61 NQKFKDKATLTVDKSSITAYMELRSLTSDSAVYCARSTMTINVMYDYGQGTSTVSS 120
DB 80 NQKFKSKATLTDDSSNTAYMELRSLTSDSAVYCARSTMTINVMYDYGQGTSTVSS 132
QY 121 AKTTPPSVYPLAPGSAQTNSMTLGLVKGYPPEPTVTWNSGSLSSGVHTFPVAVLQSD 180
DB 133 AKTTPPSVYPLAPGSAQTNSMTLGLVKGYPPEPTVTWNSGSLSSGVHTFPVAVLQSD 192
QY 181 LYTSSSVTPSPSTWPTETVCNVAHPASSTKVDKVIIPRDSGGSPSEKSEINEKDLRKK 240
DB 193 LYTSSSVTPSPSTWPTETVCNVAHPASSTKVDKVIIPRDSGGSPSEKSEINEKDLRKK 235
QY 241 SELQGTALGNLQKIIYYNKSIAITSEKSAADQFLNTLLFKGFFTGHPWYNDLLVDLGSTA 300
DB 236 CKPCTCTVPEVSSVFIFFPK-----PKDVLITL----- 264
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPTNKTACMGVGTLDHNNRLTEKKVPINLWIDGKQ 360
DB 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFDV--- 289
QY 361 TTVPIDKVKTSKEV-----TVQELDLOARHYLHGK-FGL-VNSDSFGKVGQVGLIVF 411
DB 290 -DVEHTAQTPREBQFNSTFRSVSELPIMHQDWLNGKEFKCRVNSAAPPAPIEK----- 343
QY 412 HSEGSTVSYDLFDAQGGYPTDLLRIYRDNNTTISSTLSISLSLYLTTTSIVMTQPTSLLV 471
DB 344 -----TISKT----- 348
QY 472 SAGDRVTITCKASQSVSNDVAVYQKPGQSKLLISYTSRYAGVDPFRFSGSGYGTDTFL 531
DB 349 ----- 348
QY 532 TISSVQAEADAAYVFCQDYNSPPTFGGKTKLEIKRADAAPTYSIFPPSSSEQLTSGGASV 591
DB 349 -----KGRPKAPQVYTIPTPKQMAKDKVSLT 375
QY 592 CFLNNFYKIDINVKWKIDSERQNGVLSWTDQSKDSTYSMSSTLTITKDEYERHNSYT 651
DB 376 CMITDFPEDITVEQWNGQPAEN-YKNTQPTIMDT-DGSYFYVSKLVNQRKNSWEAGNTFI 433
QY 652 CEATHK 657

Db 434 CSVLHE 439

RESULT 20

US-09-903-327A-13

; Sequence 13, Application US/09903327A

; Patent No. US20020164333A1

; GENERAL INFORMATION:

; APPLICANT: Nemerow, Glen R.

; APPLICANT: Li, Erluang

; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET

; TITLE OF INVENTION: GENE

; TITLE OF INVENTION: DELIVERY

; FILE REFERENCE: 22908-1228

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: US/09/903,327A

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13

; LENGTH: 493

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain

; OTHER INFORMATION: and EGF mature peptide

US-09-903-327A-13

Query Match 29.1%; Score 1023.5; DB 9; Length 493;

Best Local Similarity 37.4%; Pred. No. 4.4e-48;

Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;

QY 1 EVLOQSGPDLVKGASVKISCKASGYFTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60

DB 20 EVLOQSGPDLVKGASVKISCKASGYFTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 79

QY 61 NQKFKDKATLTVDKSSTAYMELRSLTSDSAVYICARSTMTINVMYDYGQGTSTVSS 120

DB 80 NQKFKSKATLTDDSSNTAYMELRSLTSDSAVYICARG-----IAYWGQGLTVTVA 132

QY 121 AKTTTPSVYPLAPGSAQTNSMTVLCGLVKGYPPEPVTVTNWSSLSGSHVHTFPVAVLQSD 180

DB 133 AKTTTPSVYPLAPGSAQTNSMTVLCGLVKGYPPEPVTVTNWSSLSGSHVHTFPVAVLQSD 192

QY 181 LYTLSSSVTPSSTWSPSETVTCNVAHPASSTKVYDKKIVPRDGGSPSEKSEINEKDLRKK 240

DB 193 LYTLSSSVTPSSTWSPSETVTCNVAHPASSTKVYDKKIVPRDCG-----235

QY 241 SELOGTALGNLKIYYNNSKAITSEKSAQDLTNTLLFKGFTGHPWYNDLLVGLSTA 300

DB 236 CKPCICTVPEVSSVFIFPPK-----PKDVLTTITL-----264

QY 301 ATSEVEGSSVDLYGAYGYQCAGTGNKTCMVGVTLDHNNRLTEKKVPINLWIDGKQ 360

DB 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFDV---289

QY 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKRVQGLIVF 411

DB 290 -DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLNKGKFKCRVNSAAPPAIEK-----343

QY 412 HSESGSTVSDLDFAQQGYPDTLIRYDRNTTISSTLSISLYLTTISIVMTQTFTSLV 471

DB 344 -----TISK-----348

QY 472 SAGDRVTITCKASQSVSDNVAMVYQKPGQSKLLISYTSRVRAGVDRFSGSGYGTDFTL 531

DB 349 -----348

QY 532 TISSVQAEAAVYFCQDYNSTPTGGGKLEIKRADAAPTIVSIPPPSEQLTSGASV 591

DB 349 -----KGRKPAQVYTIPTPPKEQMAKDKVSLT 375

QY 592 CFLANFPKIDINVKWKIDGSRQGVLSNWTQDQSKDSTYSMSSTLTTLTKDEYERHNSYT 651

DB 376 CMITDFPEPITVEQWNGQPAEN-YKNTQPIMDT-DGSYFYVSKLVNQRSNWEAGNTFI 433

QY 652 CEATHK 657

DB 434 CSVLHE 439

RESULT 21

US-09-903-327A-12

; Sequence 12, Application US/09903327A

; Patent No. US20020164333A1

; GENERAL INFORMATION:

; APPLICANT: Nemerow, Glen R.

; APPLICANT: Li, Erluang

; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET

; TITLE OF INVENTION: GENE

; TITLE OF INVENTION: DELIVERY

; FILE REFERENCE: 22908-1228

; CURRENT APPLICATION NUMBER: US/09/903,327A

; CURRENT FILING DATE: 2001-07-10

; PRIOR APPLICATION NUMBER: 09/613,017

; PRIOR FILING DATE: 2000-07-10

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12

; LENGTH: 510

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Fusion protein with N-terminal portion of DAV-1 heavy chain

; OTHER INFORMATION: and IGF-1 mature peptide

US-09-903-327A-12

Query Match 29.1%; Score 1023.5; DB 9; Length 510;

Best Local Similarity 37.4%; Pred. No. 4.6e-48;

Matches 249; Conservative 51; Mismatches 111; Indels 255; Gaps 14;

QY 1 EVLOQSGPDLVKGASVKISCKASGYFTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60

DB 20 EVLOQSGPDLVKGASVKISCKASGYFTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 79

QY 61 NQKFKDKATLTVDKSSTAYMELRSLTSDSAVYICARSTMTINVMYDYGQGTSTVSS 120

DB 80 NQKFKSKATLTDDSSNTAYMELRSLTSDSAVYICARG-----IAYWGQGLTVTVA 132

QY 121 AKTTTPSVYPLAPGSAQTNSMTVLCGLVKGYPPEPVTVTNWSSLSGSHVHTFPVAVLQSD 180

DB 133 AKTTTPSVYPLAPGSAQTNSMTVLCGLVKGYPPEPVTVTNWSSLSGSHVHTFPVAVLQSD 192

QY 181 LYTLSSSVTPSSTWSPSETVTCNVAHPASSTKVYDKKIVPRDGGSPSEKSEINEKDLRKK 240

DB 193 LYTLSSSVTPSSTWSPSETVTCNVAHPASSTKVYDKKIVPRDCG-----235

QY 241 SELOGTALGNLKIYYNNSKAITSEKSAQDLTNTLLFKGFTGHPWYNDLLVGLSTA 300

DB 236 CKPCICTVPEVSSVFIFPPK-----PKDVLTTITL-----264

QY 301 ATSEVEGSSVDLYGAYGYQCAGTGNKTCMVGVTLDHNNRLTEKKVPINLWIDGKQ 360

DB 265 -----TP-KVTCVVVDIS-----KDDPEVQFSWFDV---289

QY 361 TTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKRVQGLIVF 411

DB 290 -DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLNKGKFKCRVNSAAPPAIEK-----343

QY 412 HSESGSTVSDLDFAQQGYPDTLIRYDRNTTISSTLSISLYLTTISIVMTQTFTSLV 471

DB 344 -----TISK-----348

QY 472 SAGDRVTITCKASQSVSDNVAMVYQKPGQSKLLISYTSRVRAGVDRFSGSGYGTDFTL 531

Db 484 ICTVPEVSSVFIF-----PPK-----PKDVLITLITPKV 512
 QY 361 TTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDFGKVGQVQGLVIFHSSSEGSTVS 420
 Db 513 TCWVD-----ISKDDPEVQ-----FS 529
 QY 421 YLDFDAQGVDPDLLRIYRDNTTISSTISLSLYLVTTSIVMTQTPTSLLVAGDRVIT 480
 Db 530 WFVDDVEVHTAQTPREEQFNSTFRSVS-----ELPIHQD-----565
 QY 481 CKASQSVNDVAVYQKPGSPKLLISYSSRYAGVPDRFSGSGYGTDFTLTSSVQABD 540
 Db 566 -----WLNKDFKC-----RVNSAAPPAPIEKTIIS-----590
 QY 541 AAVYFCQDYNSTPTFGGKTLEIKRADAAPTYSIFPPSSSEOLTSGASVWCFLLNFPYK 600
 Db 591 -----KTKGRPKAPQVYTIPTPPKEQWAKDKVSLTCAITDFPPE 628
 QY 601 DINVKKIDGSRONGVNSWTDQSDKSTYSNSSTLTITKBEYRHNSYTCETHK 657
 Db 629 DITVEQWNGQPAEN-YKNTQPIMDT-DGSYFYSKLVQKNWEAGNTFTCSVLHE 683

RESULT 24

US-10-071-485-90
 ; Sequence 90, Application US/10071485
 ; Publication No. US20030099648A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Buysse, Marie-Ange
 ; APPLICANT: Sablon, Erwin
 ; TITLE OF INVENTION: INTERFERON-gamma-BINDING MOLECULES FOR TREATING SEPTIC
 ; TITLE OF INVENTION: SHOCK
 ; TITLE OF INVENTION: CACHEXIA, IMMUNE DISEASES AND SKIN DISORDERS
 ; FILE REFERENCE: INNS:015
 ; CURRENT APPLICATION NUMBER: US/10/071,485
 ; CURRENT FILING DATE: 2002-02-07
 ; PRIOR FILING DATE: 2002-02-07
 ; PRIOR FILING DATE: 2000-02-14
 ; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
 ; PRIOR FILING DATE: 1998-08-14
 ; PRIOR APPLICATION NUMBER: EPO 98870139.7
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: EPO 97870122.5
 ; PRIOR FILING DATE: 1997-08-18
 ; NUMBER OF SEQ ID NOS: 104
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 90
 ; LENGTH: 711
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: SYNTHETIC
 US-10-071-485-90

Query Match 27.8%; Score 980.5; DB 14; Length 711;
 Best Local Similarity 35.3%; Pred. No. 1.5e-45;
 Matches 254; Conservative 103; Mismatches 180; Indels 183; Gaps 23;
 QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYMHWVKOSPGKLEWIGRIINPNNGVTLY 60
 Db 21 QVQLVSGSELKPKGASVKISKASGYTFTDYGMMWVKQAPQGLKWMGWINTYTGESTY 80
 QY 61 NQKFKDKATLTVDKSSSTAYMELRLSITSDSAVYICARSTMITNYYMDYWGQTSVTYSS 120
 Db 81 VDDFKGRFVFLDTSVSAAYLIQISLKAEDTATYFCARGF---YAMDYWGQTTVTYSS 137
 QY 121 AKTTPSVVPLAPGSAQAQNSMTVLCGLVKGFPEPVTVTWNSGSLSSGVHTFPVAVLQSD 180
 Db 138 ASTKGSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVMNSGALTSGVHTFPAVLQSS 197
 QY 181 -LYLTSSVTVPSSSTWPSSTVTCNVAHPASSTKVDKKIVPRDS-----GG 224
 Db 198 GLYSLSVTVTPSSSLGCTGYICNVNPKSNIKVDKRVKPSCKDTHCTPCPAPELLGG 257

QY 225 PS-----EKSEBI-----NEKDLRKSELOGTALGNLK---QIYYN 258
 Db 258 PSVFLPPKPKDITLMISRTPEVTCVVVDVSHEDDEVKFNWYVDGVFNNAKTKPREQYN 317
 QY 259 S-----KATTS-EK-----SADQ 271
 Db 318 STYRVSVLTVLHQDWLNGKEYCKCKSVNKALPASIEKTIKAKGQPREPQVYVITLPPSREE 377
 QY 272 FLTN-----TLLFKGFFTCHPWYNDLLVLDLGSTA--ATSEYEGSS--VDLYGAYGYQCAGG 324
 Db 378 MTKQVSLTCLVKGFY-----SDIAVESNGQPEPNYKITPPVLDSDGSFFLYSKL-- 430
 QY 325 TPNTACMGGV-----TLHD--NNRLTEEK-----KVPINLWIDGKQITTVPIDKY 368
 Db 431 TVDKSRWQQGNVFCSCVMHEALHNHYTKLSLSLSPGKLGGSQVQLVCSGSELKPKGASV 490
 QY 369 KTSKKEVTVQELDLQARHYLHGKFGLYNSDFGKVGQVQGLVIFHSSSEGSTVSIDLFAQG 428
 Db 491 KISCK-----ASGYTFTDYGMMWVKQAPQGLKWMGWINTYTGESTYVD--DFKG 538
 QY 429 QYPDTLLRIYRDNTTISSTLSIS-----LYLYT-----457
 Db 539 RF-----VFSLDTSVSAAYLIQISLKAEDTATYFCARGFYAMDYWGQTTVTVSSGGG 592
 QY 458 -----TSIVMTQTPTSLLVSGDRVTITCKASQSVNDVAVYQKPGSPKLLI 506
 Db 593 GSGGSGSGGSDIVLTQSPATMSAASPCERVTLTCSASSISY-MFWYHORPGQSPRLLI 651
 QY 507 SYTSRRVAGVDPDRFSGSGYGTDFLTITSSVQAEADAAYVFCQDYNSTPTFGGKTKLEIKR 566
 Db 552 YDTSNLAGVPAERFSGSGSTYSYSLTISRMEPEDFATYFCHQSSSYFTFGQGTKEIKR 711
 RESULT 25
 US-10-410-907A-36
 ; Sequence 36, Application US/10410907A
 ; Publication No. US20030215880A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dennis R. Burton
 ; APPLICANT: R. Anthony Williamson
 ; APPLICANT: Gianluca Moroncini
 ; TITLE OF INVENTION: MOTIF-GRAFTED HYBRID POLYPEPTIDES AND
 ; TITLE OF INVENTION: USES THEREOF
 ; FILE REFERENCE: 22908-1229
 ; CURRENT APPLICATION NUMBER: US/10/410,907A
 ; CURRENT FILING DATE: 2003-04-08
 ; PRIOR APPLICATION NUMBER: 60/371,610
 ; PRIOR FILING DATE: 2002-04-09
 ; NUMBER OF SEQ ID NOS: 36
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 36
 ; LENGTH: 223
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: D18 Heavy Chain
 US-10-410-907A-36

Query Match 27.8%; Score 979.5; DB 15; Length 223;
 Best Local Similarity 87.4%; Pred. No. 4.6e-46;
 Matches 194; Conservative 7; Mismatches 16; Indels 5; Gaps 2;
 QY 1 EVQLQSGDPLVKPGASVKISKASGYSTGYMHWVKOSPGKLEWIGRIINPNNGVTLY 59
 Db 3 EVQLLESGSELKPKGASVKISKASRYTFTDYMWMVKOSHGRLEWIGIYIPNTGVG 62
 QY 60 YNQKFKDKATLTVDKSSSTAYMELRLSITSDSAVYICARSTMITNYYMDYWGQTSVTYS 119
 Db 63 YNQKFKDKATLTVDKSSSTAYMELRLSITSDSAVYICAG----FYGMDYWGQTSVTYS 118
 QY 120 SAKTTPSVVPLAPGSAQAQNSMTVLCGLVKGFPEPVTVTWNSGSLSSGVHTFPVAVLQ 179

Db 119 SAKTTPSVYPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTVNSGSLISGVHTFPAVLQY 178
 QY 180 DLYTLSSSVTPSSVTPSEVTCNVVAHPASSTKVDKKIVPRD 221
 Db 179 DLYTMSSSVTPSSVTPSEVTCNVVAHPASSTKVDKKIVPRD 220

RESULT 26
 US-10-334-235-37
 ; Sequence 37, Application US/10334235
 ; Publication No. US20040131591A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Oxford Biomedica (UK) Ltd.
 ; APPLICANT: Kingsman, Alan
 ; APPLICANT: Bebbington, Christopher
 ; APPLICANT: Carroll, Miles
 ; APPLICANT: Ellard, Fiona
 ; APPLICANT: Kingsman, Susan
 ; APPLICANT: Myers, Kevin
 ; APPLICANT: Lamikandra, Abigail
 ; TITLE OF INVENTION: VECTOR SYSTEM
 ; FILE REFERENCE: 532682000920
 ; CURRENT APPLICATION NUMBER: US/10/334,235
 ; CURRENT FILING DATE: 2002-12-30
 ; PRIOR APPLICATION NUMBER: US 10/060,585
 ; PRIOR FILING DATE: 2002-01-29
 ; PRIOR APPLICATION NUMBER: PCT/GB00/04317
 ; PRIOR FILING DATE: 2000-11-13
 ; PRIOR APPLICATION NUMBER: US 09/445,375
 ; PRIOR FILING DATE: 1998-06-04
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 37
 ; LENGTH: 243
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: mature secreted protein of 574 scFv, designated
 ; OTHER INFORMATION: 574scfv.1
 US-10-334-235-37

Query Match 27.6%; Score 972.5; DB 16; Length 243;
 Best Local Similarity 40.1%; Pred. No. 1.2e-45;
 Matches 227; Conservative 3; Mismatches 13; Indels 323; Gaps 5;

QY 1 EVQLQSGPDLVKPGASVKISKASGYSTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
 Db 1 EVQLQSGPDLVKPGASVKISKASGYSTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
 QY 61 NQKFKDKATLTVDKSSITAYMELRSLTSEDSAVYVCARSTMTINYVDYWGQGSVTSS 120
 Db 61 NQKFKDKATLTVDKSSITAYMELRSLTSEDSAVYVCARSTMTINYVDYWGQGSVTSS 119
 QY 121 AKTTPSVYPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTVNSGSLSSGVHTFPAVLQSD 180
 Db 120 ----- 119
 QY 181 LYTLLSSVTPSSVTPSEVTCNVVAHPASSTKVDKKIVPRDGGPSEKSEINEKDLRKK 240
 Db 120 ----- 122
 QY 241 SELOQTALGNLKIYYNKAITSSEKSADQFLNTLLFKGFFTGHPWYNDLLVDLGSTA 300
 Db 123 ----- 122
 QY 301 ATSEYEGSSVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
 Db 123 ----- 132
 QY 361 TTVPIDKVKTSKEVTVQELDLQARHVLHGKFLYNSDSFGKVGQVGLIVFHSSEGSTVS 420
 Db 133 ----- 134

QY 421 YDLFDAQQYPTDLLRIYRDNTTISSTLSLSLYLYTTSIVMTQTPTPTSLLSVAGDRVTIT 480
 Db 135 ----- 157
 QY 481 CKASQSVNDVAVYQOKPGQSPKLLISYTSRYAGVDPDRSGSGVGTDTFTLTISVQAE 540
 Db 158 CKASQSVNDVAVYQOKPGQSPKLLISYTSRYAGVDPDRFIGSGYGTDTFTLTISLQAE 217
 QY 541 AAVYFCQDYNPPTFGGTTKLEIKR 566
 Db 218 LAVYFCQDYNPPTFGGTTKLEIKR 243

RESULT 27
 US-10-334-235-39
 ; Sequence 39, Application US/10334235
 ; Publication No. US20040131591A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Oxford Biomedica (UK) Ltd.
 ; APPLICANT: Kingsman, Alan
 ; APPLICANT: Bebbington, Christopher
 ; APPLICANT: Carroll, Miles
 ; APPLICANT: Ellard, Fiona
 ; APPLICANT: Kingsman, Susan
 ; APPLICANT: Myers, Kevin
 ; APPLICANT: Lamikandra, Abigail
 ; TITLE OF INVENTION: VECTOR SYSTEM
 ; FILE REFERENCE: 532682000920
 ; CURRENT APPLICATION NUMBER: US/10/334,235
 ; CURRENT FILING DATE: 2002-12-30
 ; PRIOR APPLICATION NUMBER: US 10/060,585
 ; PRIOR FILING DATE: 2002-01-29
 ; PRIOR APPLICATION NUMBER: PCT/GB00/04317
 ; PRIOR FILING DATE: 2000-11-13
 ; PRIOR APPLICATION NUMBER: US 09/445,375
 ; PRIOR FILING DATE: 1998-06-04
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 39
 ; LENGTH: 488
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: peptide of B7-1.5T4.1
 US-10-334-235-39

Query Match 27.5%; Score 967.5; DB 16; Length 488;
 Best Local Similarity 40.0%; Pred. No. 5e-45; 13; Indels 323; Gaps 5;
 Matches 226; Conservative 3; Mismatches 13; Indels 323; Gaps 5;

QY 1 EVQLQSGPDLVKPGASVKISKASGYSTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
 Db 247 EVQLQSGPDLVKPGASVKISKASGYSTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 306
 QY 61 NQKFKDKATLTVDKSSITAYMELRSLTSEDSAVYVCARSTMTINYVDYWGQGSVTSS 120
 Db 307 NQKFKDKATLTVDKSSITAYMELRSLTSEDSAVYVCARSTMTINYVDYWGQGSVTSS 365
 QY 121 AKTTPSVYPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTVNSGSLSSGVHTFPAVLQSD 180
 Db 366 ----- 365
 QY 181 LYTLLSSVTPSSVTPSEVTCNVVAHPASSTKVDKKIVPRDGGPSEKSEINEKDLRKK 240
 Db 366 ----- 368
 QY 241 SELOQTALGNLKIYYNKAITSSEKSADQFLNTLLFKGFFTGHPWYNDLLVDLGSTA 300
 Db 369 ----- 368
 QY 301 ATSEYEGSSVDLYGAYGYQCAGGTGPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
 Db 369 ----- 378

Db 2 IVMTQSHKFMSTVGDVRSITCKASQDNTAVAWYQKPGHSPKLLIYSASFRYTGUPDR 61
QY 520 FSGSGYGTDFTLTSSVQAEDAAVYFCQDYNPPPTFGGTTKLEIKRADAAPTVSIFPPS 579
Db 62 FTGNRSQDFTTSSVQAEDAAVYFCQHYTTPPTFGGTTKLEIKRADAAPTVSIFPPS 121
QY 580 SEQLTSGASVVCFLNFPKDNVKKWIDGSRQNGVLSWTDQSDKSTYSMSSTLTL 639
Db 122 SEQLTSGASVVCFLNFPKDNVKKWIDGSRQNGVLSWTDQSDKSTYSMSSTLTL 181
QY 640 TKDEYERHNSYTCEATHKTSPIVKSFRNRE 671
Db 182 TKDEYERHNSYTCEATHKTSPIVKSFRNRE 213
RESULT 31
US-09-795-515-7
; Sequence 7, Application US/09795515
; Publication No. US20030039645A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yatko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-795-515-7
Query Match 27.2%; Score 957; DB 10; Length 468;
Best Local Similarity 34.7%; Pred. No. 1.8e-44;
Matches 240; Conservative 56; Mismatches 127; Indels 268; Gaps 14;
QY 1 EVQLQSGDPLVKGPGASVKISKASGYSFTGYHHWKQSPGKLEWIGRINPNNGVTLY 60
Db 20 QVQLQSGAEELARPQASVKMSKASGYTFTYTHVWKQRPQGLEWIGYINPSRGYTN 79
QY 61 NQKPKDKATLTVDKSTTAYMELSLTSEDSAVYVCARSTMITNVMYDYGQGSTVTVSS 120
Db 80 NQKPKDKATLTVDKSTTAYMELSLTSEDSAVYVCARSTMITNVMYDYGQGSTVTVSS 138
QY 121 AKTTPPSVYPLAPGSAAGTNSMTVLGCLVKGYPFPPVTLTWNSSGLSGVHTFPVQLQSD 180

Db 139 AKTTPPSVYPLAPVCGDITGSSVTLGCLVKGYPFPPVTLTWNSSGLSGVHTFPVQLQSD 198
QY 181 LYTLSSSVTVSSWTPSTVTCNVAHPASSTKYDKKIVPRDSGGPSPKSEBEINEKDLRKK 240
Db 199 LYTLSSSVTVSSWTPSQSITCNVAHPASSTKYDKKIEPR---GPTIKPCP----- 246
QY 241 SELQGTALGNLKQIYYVNSKAITSEKSADQFLNTLLFKGFTGHPWYNLLVDLGSTA 300
Db 247 ----- 246
QY 301 ATSEYEGSSVDLYGAYGYQACAGTPNKATCMYGGVTLHDNNRLTEKKVPINLWIDCKQ 360
Db 247 -----PCKCPAPN-----LLGGPSVF----- 262
QY 361 TTVPIDKVKTSKKEVTVQELDLQARHYLHGKFLYNSDSFGKVGQGLIVFHSSEGSTVS 420
Db 263 -----IFPPKIKDVLMI---SLSPITV 281
QY 421 YDLFDAQCGYDPTLLRIYRDNTTISSTLSISLYLYTTSIYMTQTPSLLVSGDRVTIT 480
Db 282 CVVVDVSEDDPD-----VOISWFWNVVHTAQTOT----- 312
QY 481 CKASQSVSNDVANYQOKPGQSPKLLISYTSRYAGVPRFSGSGYGTDFTLTSSVQAED 540
Db 313 -----HREDYNSTLRV----- 324
QY 541 AAVYFCQDYNPPPTFGGTTKLEIKRAD-----AAPTVSIFPPSSQLT 584
Db 325 SALPIQHQQDWSGKEF-----KCKYNNKDLPAPIERTISKPGSVRAPQVYVLPPEEEMT 380
QY 585 SGGASVVCFLNFPKDNVKKWIDGSRQNGVLSWTDQSDKSTYSMSSTLTL 639
Db 381 KQVTLTCVMTDFMPEDIYVETNNKTELNYKTEPVLDS-----DGSYFYMSKLURV 433
QY 640 TKDEYERHNSYTCEATHK-TSTSPIVKSFRN 669
Db 434 EKKNWERNISYSCSVVHGLNHNHTTKSFR 464
RESULT 32
US-10-704-352-7
; Sequence 7, Application US/10704352
; Publication No. US20040071693A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/704,352
; FILING DATE: 07-Nov-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE: 28-FEB-2001
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yatko
; REGISTRATION NUMBER: 35,719

[illegible]

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RESULT 33
US-10-704-071-7
; Sequence 7, Application US/10704071
; Publication No. US20040076627A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; Athwal, Diljeet S.
;

```

Entage, John S.
TITLE OF INVENTION: Humanized Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/704,071
FILING DATE: 07-Nov-2003
CLASSIFICATION: (D)
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,658
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yatko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 488 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-704-071-7

Query Match	27.2%	Score 957	DB 16	Length 468
Best Local Similarity	34.7%	Pred. No. 1.8e-44		
Matches	240	Conservative	56	Mismatches 127; Indels 268; Gaps 14;
Qy	1	EVQLQSGSPDLVFGASVKISCKASGYSTFGYYMHVWKQSPGKLEWIGRINPNNGVTLY	60	
Db	20	QVQLQSGAELRPGASVKMSCKASGYTFTRYTMHWVKRPGQGLEWIGYINPSRGYTNY	79	
Qy	61	NQPFKQKATLTVDKSTTAYMELRLTSEDSAYVYCARSTMIINYVDYWGQGTSTVVS	120	
Db	80	NQPFKQKATLTVDKSTTAYMQLSSTSEDSAYVYCAR-YDDHYCLDYWGQGTTLTVSS	138	
Qy	121	AKTTPPSVYPLAPGSAQAQTNMTGLCLVKGYFPEPVTVTVNSGSLSSGHHPTFPAVLQSD	180	
Db	139	AKTTPPSVYPLAPVCGDGTTCSSVTGLCLVKGTPEPVTLTVNSGSLSSGHHPTFPAVLQSD	198	
Qy	181	LYTLSSSVTVPSSTWSEETVCNVAHPASCTKYDKKIIVPRDSGSPSEKSEINEKDLRKK	240	
Db	199	LYTLSSSVTVPSSTWSPQSICTCNVAHPASCTKYDKKIEPR---GPTIKPCP-----	246	
Qy	241	SELQGTALGNLKQIYYNNSKAITSSSEKSAQDLTNTLLFFGFTGHWPYNDLLVDLGSTA	300	
Db	247	-----	246	
Qy	301	ATSEYSGSSVDLYGAYGYOCAGTGNKTACMYGGVTLHDNNRLTEKKYPINLWIDGKQ	360	
Db	247	-----PCKPAPN-----LLGGPSVF-----	262	
Qy	361	TTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVKQGLIIVFHSEGSTVS	420	
Db	263	-----	281	
Qy	421	YDLFDAGQGVDPDLLRIYRDNTTISSTLSISLYLTTSITVMTQTPTSLVSAAGDRVIT	480	

Db 282 CVVVDSEDDP-----VOISWFVNNVHTACTQT----- 312
 QY 481 CKASQSVNDVAVYQOKPGOSPKLLISYTSRYAGVDFRSGSGYGTDFLTITSSVQOAE 540
 Db 313 -----HREDYNSTLRVV----- 324
 QY 541 AAVTFCQDYNPPTFGGTHLEIKRAD-----AAPTVSIFPPSEOLT 584
 Db 325 SALPIQHODMWSGKEF-----KCYNNKDLPAPIERTISKPGSVRAPQVYVLPPEEEMT 380
 QY 585 SGGASVVCFLNFPKDIINVKWKIDGSEKQ-----GVLSNWTDDQSKDSTYSMSSTLTL 639
 Db 381 KKQVTLTCMVDNPDIEDIYVNTNGKTELNYKNTPEVLDS-----DGSYFWSKLRV 433
 QY 640 TKDEYERHNSVTCATHK-TSTSPIVKSFN 669
 Db 434 EKKWVERNSYSCSVVHGLEHHTTKSFSR 464

RESULT 34
 US-10-679-620-82
 ; Sequence 82, Application US/10679620
 ; Publication No. US20040110930A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Large Scale Biology
 ; APPLICANT: Reinl, Stephen J.
 ; APPLICANT: Edwards, Patricia C.
 ; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
 ; FILE REFERENCE: 34150-004A
 ; CURRENT APPLICATION NUMBER: US/10/679,620
 ; CURRENT FILING DATE: 2003-10-03
 ; PRIOR APPLICATION NUMBER: 60/415,940
 ; PRIOR FILING DATE: 2002-10-03
 ; NUMBER OF SEQ ID NOS: 122
 ; SOFTWARE: Patent in version 3.2
 ; SEQ ID NO 82
 ; LENGTH: 222
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: p4DSHy-TOPO, see Exampl 11
 US-10-679-620-82

Query Match 27.0%; Score 952; DB 16; Length 222;
 Best Local Similarity 81.4%; Pred. No. 1.5e-44;
 Matches 180; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

QY 1 EVQLQQSGPDLVKPGASVKISKASGYSFTGYHHWYKQSPGKLEWIGRIINPNNGVTLY 60
 Db 1 QVQLQQSGPELVKPGASLKLCTASGFIKDTYTHWVKRPEQGLEWIGRIYPTNGYTRY 60
 QY 61 NQKFDKATLVDSSTTAYMELSLTSEDSAVYICARSTMTITNYMDYMGQGTSTVSS 120
 Db 61 DPKFDKATITADTSNTAYLQVSLTSEDATVYICRWGGDGYNDYMGQASVTVSS 120
 QY 121 AKTTPPSVYPLAPGAAATNSNVTGLGVKGYFPPEVTVTNWSSGLSSGVTTPPAVLQSD 180
 Db 121 AKTTPPSVYPLAPGAAATNSNVTGLGVKGYFPPEVTVTNWSSGLSSGVTTPPAVLQSD 180
 QY 181 LYTLLSSSVTPSPWSPSTVTCNVAHPASSTKVDKIVPRD 221
 Db 181 LYTLLSSSVTPSPWSPSTVTCNVAHPASSTKVDKIVPRD 221

RESULT 35
 US-09-900-766-4
 ; Sequence 4, Application US/09900766
 ; Publication No. US20030039655A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FORSBERG, GORAN
 ; APPLICANT: ERLANDSSON, EVA
 ; APPLICANT: ANTONSSON, PER
 ; APPLICANT: WALSE, BJORN

; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
 ; FILE REFERENCE: P021800/10104199
 ; CURRENT APPLICATION NUMBER: US/09/900,766
 ; CURRENT FILING DATE: 2001-07-06
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus sp.
 ; US-09-900-766-4

Query Match 26.9%; Score 948; DB 10; Length 233;
 Best Local Similarity 76.4%; Pred. No. 2.5e-44;
 Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSDAQFLNTLLPKGPTG 285
 Db 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESHQDQLQHTILKGFETD 60
 QY 286 HPWYNDLLVGLGTAATSEYSGSSVDLYGAYGYOCAGTGNKTACMYGGVTLHDNNRLT 345
 Db 61 HSWYNDLLVDFDKDIVDKYKGVKVDLYGAYGYOCAGTGNKTACMYGGVTLHDNNRLT 120
 QY 346 EEKVPINLWIDGKQTPIDVKVTSKXEVTVQELDLQARHLYHGKFGLYNSDSFGGKVQ 405
 Db 121 EEKVPINLWLDGKQNTVPLETVTKNKXNTVQELDLQARRYLOBKYNLYNSDVDFGKVQ 180
 QY 406 RGLIVFHSSEGSTVSVDLFDAGQYDPTLLRIYRDNNTTISSTLSISLYLTT 458
 Db 181 RGLIVFHTSTEPSVNYDLFGAQGYSTNLLRIYRDNNTINSENHMDIYLYTS 233

RESULT 36
 US-10-283-838-7
 ; Sequence 7, Application US/10283838
 ; Publication No. US2003002894A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
 ; Johan Hansson, Terje Kalland, Lars
 ; Abrahamson and Goran Forsberg
 ; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
 ; AND THEIR USE
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
 ; STREET: 1177 West Loop South, 10th Floor
 ; CITY: Houston
 ; STATE: TX
 ; COUNTRY: USA
 ; ZIP: 77027-9095
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA: US/10/283,838
 ; FILING DATE: 30-Oct-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/695,692
 ; FILING DATE: August 12, 1996
 ; APPLICATION NUMBER: 9601245-5
 ; FILING DATE: March 29, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Krieger, Paul E.
 ; REGISTRATION NUMBER: 25,886
 ; REFERENCE/DOCKET NUMBER: 41986/1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 713-850-0909
 ; TELEFAX: 713-850-0165
 ; INFORMATION FOR SEQ ID NO: 7:

```
/
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 233 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-283-838-7

Query Match          26.9%; Score 948; DB 14; Length 233;
Best Local Similarity 76.4%; Pred. No. 2.5e-44;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLQIYYNSKAITSEKSAQDFLNTLLFKGFPTG 285
Db 1 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHDFLQHTILFKGFPTD 60
QY 286 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCACMYGGVTLHNNRLT 345
Db 61 HSWYNDLLVDFSKDIDVKYKGVLDLYGAYGYQCAGGTPNKTCACMYGGVTLHNNRLT 120
QY 346 EEKVPINLWIDGKQTTVPIDKVTSKKEVTYQELDLQARHYLHGKFLYNSDSFGKQV 405
Db 121 EEKVPINLWLDGKQNTVPLETVKTNKXNTVQELDLQARRYLQEKYLYNSDSVFDGKQV 180
QY 406 RGLIVHSSEGSTVSYDLFDAQQYPTLLRIYRDNTTISSTLSISLYTT 458
Db 181 RGLIVFTSTEPSVNYDLFGAQQYSNTLLRIYRDNKTINSENMHIDIYLYTS 233

RESULT 37
US-10-267-682-113
/ Sequence 113, Application US/10267682
/ Publication No. US2004003235A1
/ GENERAL INFORMATION:
/ APPLICANT: Bolognesi, Dani P.
/ Matthews, Thomas J.
/ Wild, Carl T.
/ Barney, Shawn O.
/ Lambert, Dennis M.
/ Petteway, Stephen R.
/ Langlois, Alphonse J.
/ TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
/ TRANSMISSION
/ NUMBER OF SEQUENCES: 239
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/267,682
/ FILING DATE: 08-Oct-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/484,223A
/ FILING DATE: 07-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7872-029
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ INFORMATION FOR SEQ ID NO: 113:
```

```
/
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 257 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-267-682-113

Query Match          26.9%; Score 948; DB 12; Length 257;
Best Local Similarity 76.4%; Pred. No. 2.8e-44;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLQIYYNSKAITSEKSAQDFLNTLLFKGFPTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHDFLQHTILFKGFPTD 84
QY 286 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCACMYGGVTLHNNRLT 345
Db 85 HSWYNDLLVDFSKDIDVKYKGVLDLYGAYGYQCAGGTPNKTCACMYGGVTLHNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVTSKKEVTYQELDLQARHYLHGKFLYNSDSFGKQV 405
Db 145 EEKVPINLWLDGKQNTVPLETVKTNKXNTVQELDLQARRYLQEKYLYNSDSVFDGKQV 204
QY 406 RGLIVHSSEGSTVSYDLFDAQQYPTLLRIYRDNTTISSTLSISLYTT 458
Db 205 RGLIVFTSTEPSVNYDLFGAQQYSNTLLRIYRDNKTINSENMHIDIYLYTS 257

RESULT 38
US-10-267-748-113
/ Sequence 113, Application US/10267748
/ Publication No. US20040052820A1
/ GENERAL INFORMATION:
/ APPLICANT: Bolognesi, Dani P.
/ Matthews, Thomas J.
/ Wild, Carl T.
/ Barney, Shawn O.
/ Lambert, Dennis M.
/ Petteway, Stephen R.
/ Langlois, Alphonse J.
/ TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
/ MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
/ TRANSMISSION
/ NUMBER OF SEQUENCES: 239
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/267,748
/ FILING DATE: 08-Oct-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/484,223A
/ FILING DATE: 07-JUN-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7872-029
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ INFORMATION FOR SEQ ID NO: 113:
```

INFORMATION FOR SEQ ID NO: 113:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 257 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 113:
 US-10-267-748-113

Query Match 26.9%; Score 948; DB 12; Length 257;
 Best Local Similarity 76.4%; Pred. No. 2.8e-44;
 Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
 QY 226 SEKSEINEKDLRKKSELOQTALGNLQIYYINSKAITSESSEKADQFLNTLLFKGFFTG 285
 DB 25 SEKSEINEKDLRKKSELOQTALGNLQIYYINEKANTENKESHQFLQHTILFKGFFTD 84
 QY 286 HPWNLLVLDLSTAAISEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 345
 DB 85 HSWYNDLLVDFDSDKIDVKYKGGKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 144
 QY 346 EEKVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHKGFLYNSDSFGKVKQ 405
 DB 145 EEKVPINLWDGKQNTVPLETVKTNKQNTVQELDLQARRYLOEKYLNYSNDSVDFGKVKQ 204
 QY 406 RGLIVFHSSEGSTVSYDLFDAGQGYPTLRIYRDNTTISTLSISLYLYTT 458
 DB 205 RGLIVFHTSTSPSYNDLFGAGQGYVNTLLRIYRDNTKNTINSENHIDIYLYTS 257

RESULT 39
 US-10-281-479A-24
 ; Sequence 24, Application US/10281479A
 ; Publication No. US20030133932A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The UAB Research Foundation
 ; APPLICANT: Zhou, Tong
 ; APPLICANT: Ichikawa, Kimihisa
 ; APPLICANT: Kimberli, Robert P.
 ; APPLICANT: Koopman, William J.
 ; APPLICANT: Oshumi, Jun
 ; APPLICANT: LoBuglio, Albert S.
 ; APPLICANT: Buchsbaum, Donald J.
 ; TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
 ; TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THERE

FILE REFERENCE: 21085.0029U6
 CURRENT FILING DATE: 2003-01-28
 PRIOR FILING DATE: 2003-01-28
 PRIOR FILING DATE: 2002-06-24
 PRIOR FILING DATE: 2002-06-24
 PRIOR FILING DATE: 2001-11-01
 PRIOR FILING DATE: 2001-11-01
 PRIOR FILING DATE: 2001-05-02
 PRIOR FILING DATE: 2001-05-02
 PRIOR FILING DATE: 2000-05-02
 PRIOR FILING DATE: 2000-05-02
 NUMBER OF SEQ ID NOS: 102
 SOFTWARE: PatentIn version 3.0
 SEQ ID NO 24
 LENGTH: 234
 TYPE: PRT
 ORGANISM: artificial sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence./No. US20030133932A1e = Synthetic
 US-10-281-479A-24

Query Match 26.8%; Score 945; DB 14; Length 234;
 Best Local Similarity 83.3%; Pred. No. 3.7e-44;
 Matches 185; Conservative 12; Mismatches 21; Indels 4; Gaps 2;
 QY 453 LLYLT---TSIVMTQPTSLVSGDRVTITCKASQSVNDVAVYQQKPGSPKLLISYT 509

DB 13 LFLFAGVEGDIVMTQSHKFMSTSVGDRVSIITCKASQSDVGTAVAVYQQKPGSPKLLIYWA 72
 QY 510 SSRVAGVDPFRFSGSGYGTDFLTITSSVQAEADAAYVFCQDDYNSPPTFGGKLEIKRADA 569
 DB 73 STRHTGVDPFRFSGSGGTDFLTITSNVQSEDLADYFCQY--YSSYRTFGGKLEIKRADA 131
 QY 570 APTVSIFPPSSSEQLTSGGASVVCFLNNFPYKIDINVKWIDGSRONGVLSNWTQDQSKDS 629
 DB 132 APTVSIFPPSSSEQLTSGGASVVCFLNNFPYKIDINVKWIDGSRONGVLSNWTQDQSKDS 191
 QY 630 TVSMSTLTLTCKDEVERINSYTCETHTKTSTSPVKSFNRE 671
 DB 192 TVSMSTLTLTCKDEVERINSYTCETHTKTSTSPVKSFNRE 233

RESULT 40
 US-10-275-180A-24
 ; Sequence 24, Application US/10275180A
 ; Publication No. US20030190687A1
 ; GENERAL INFORMATION:
 ; APPLICANT: The UAB Research Foundation
 ; APPLICANT: Zhou, Tong
 ; APPLICANT: Ichikawa, Kimihisa
 ; APPLICANT: Kimberli, Robert P.
 ; APPLICANT: Koopman, William J.
 ; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOSIS
 ; TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF
 ; FILE REFERENCE: 21085.0029U5
 ; CURRENT FILING DATE: 2002-10-31
 ; CURRENT FILING DATE: 2002-10-31
 ; NUMBER OF SEQ ID NOS: 102
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 24
 ; LENGTH: 234
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence./No. US20030190687A1e =
 ; OTHER INFORMATION: Synthetic Construct
 US-10-275-180A-24

Query Match 26.8%; Score 945; DB 14; Length 234;
 Best Local Similarity 83.3%; Pred. No. 3.7e-44;
 Matches 185; Conservative 12; Mismatches 21; Indels 4; Gaps 2;
 QY 453 LLYLT---TSIVMTQPTSLVSGDRVTITCKASQSVNDVAVYQQKPGSPKLLISYT 509
 DB 13 LFLFAGVEGDIVMTQSHKFMSTSVGDRVSIITCKASQSDVGTAVAVYQQKPGSPKLLIYWA 72
 QY 510 SSRVAGVDPFRFSGSGYGTDFLTITSSVQAEADAAYVFCQDDYNSPPTFGGKLEIKRADA 569
 DB 73 STRHTGVDPFRFSGSGGTDFLTITSNVQSEDLADYFCQY--YSSYRTFGGKLEIKRADA 131
 QY 570 APTVSIFPPSSSEQLTSGGASVVCFLNNFPYKIDINVKWIDGSRONGVLSNWTQDQSKDS 629
 DB 132 APTVSIFPPSSSEQLTSGGASVVCFLNNFPYKIDINVKWIDGSRONGVLSNWTQDQSKDS 191
 QY 630 TVSMSTLTLTCKDEVERINSYTCETHTKTSTSPVKSFNRE 671
 DB 192 TVSMSTLTLTCKDEVERINSYTCETHTKTSTSPVKSFNRE 233

RESULT 41
 US-10-286-132A-24
 ; Sequence 24, Application US/10286132A
 ; Publication No. US20030198637A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Zhou, Tong
 ; APPLICANT: Kimberli, Robert P.
 ; APPLICANT: Koopman, William J.
 ; APPLICANT: LoBuglio, Albert S.
 ; APPLICANT: Buchsbaum, Donald J.

```
; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED
; FILE REFERENCE: 21085.002907
; CURRENT APPLICATION NUMBER: US/10/286,132A
; PRIOR FILING DATE: 2003-01-22
; PRIOR APPLICATION NUMBER: US 60/346,402
; PRIOR FILING DATE: 2001-11-01
; PRIOR APPLICATION NUMBER: PCT/US01/14151
; PRIOR FILING DATE: 2001-05-02
; PRIOR APPLICATION NUMBER: US 60/201,344
; PRIOR FILING DATE: 2000-05-02
; NUMBER OF SEQ ID NOS: 102
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 24
; LENGTH: 234
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence://No. US20030198637A1e = Synthe
US-10-286-132A-24

Query Match      26.8%; Score 945; DB 14; Length 234;
Best Local Similarity 83.3%; Pred. No. 3.7e-44;
Matches 185; Conservative 12; Mismatches 21; Indels 4; Gaps 2;

QY 453 LYLVT---TSIVMTQPTSLLVASAGDRVTITCKASQSVSNDAVYQQKFGSPKLLISYT 509
Db 13 LFLFAGVEGDIVMTQSHKFMSTSVGRVSITCKASQDVGTAVAWYQQKFGSPKLLIYWA 72

QY 510 SSRVAGVDFRFSGGVGTDTLTITSSVOAEDAAYFCQDYNSPPTFGGKLEIKRADA 569
Db 73 STRHTGVDFRFTSGSGGTDTLTITSNVQSEDADYFCQQ--YSSYRTFGGKLEIKRADA 131

QY 570 APTVSIFFPSSEQLTSGGASVVCFLNNFYPKQINVKWKIDGSRQNGVLSNWTDDSDKS 629
Db 132 APTVSIFFPSSEQLTSGGASVVCFLNNFYPKQINVKWKIDGSRQNGVLSNWTDDSDKS 191

QY 630 TYSMSSTLTITKDEYRHRNSYTCATHKTSTSPVKSFRNE 671
Db 192 TYSMSSTLTITKDEYRHRNSYTCATHKTSTSPVKSFRNE 233

RESULT 42
US-10-354-948-4
; Sequence 4, Application US/10354948
; Publication No. US20030202962A1
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; Elmalie, Robyn E.
; Potter, Terence A.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/354,948
; FILING DATE: 29-Jan-2003
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,806
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
```

```
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-29-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-354-948-4
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```
Query Match      26.8%; Score 944; DB 12; Length 233;
Best Local Similarity 76.3%; Pred. No. 4.2e-44;
Matches 177; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 227 EKSEINEKDLRKSELSQGTALGNLKOIYYVNSKAITSSSEKSAQDQTLNTLLFKGFFTG 286
Db 2 EKSEINEKDLRKSELSQGTALGNLKOIYYVNSKAITSSSEKSHDQFLQHTILFKGFFTDH 61

QY 287 PWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYOCAGTGNKTKACMYGGVTLHNNRLTE 346
Db 62 SWYNDLLVDFDSKQIDVKYKGKVDLYGAYGYOCAGTGNKTKACMYGGVTLHNNRLTE 121

QY 347 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQR 406
Db 122 EKKVPINLWIDGKQNTVPLETVTKNKNTVOELDLQARHYLHGKFGLYNSDSFGKVQR 181

QY 407 GLIVFHSSEGSTVSYDLFDAQQGYPTLLRIYRDNNTTISTSLISLYYTT 458
Db 182 GLIVFHTSTPSVNYDLFGAQQYSNLLRIYRDNKTINSNMHDIYLYTS 233
```

```
RESULT 43
US-09-870-759-8
; Sequence 8, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: Terman, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-8
```

```
Query Match      26.5%; Score 935; DB 9; Length 257;
Best Local Similarity 75.5%; Pred. No. 1.4e-43;
Matches 176; Conservative 21; Mismatches 36; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELSQGTALGNLKOIYYVNSKAITSSSEKSAQDQTLNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELSQGTALGNLKOIYYVNSKAITSSSEKSHDQFLQHTILFKGFFTN 84

QY 286 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYOCAGTGNKTKACMYGGVTLHNNRLT 345
Db 85 HSWYNDLLVDFDSKQIDVKYKGKVDLYGAYGYOCAGTGNKTKACMYGGVTLHNNRLT 144

QY 346 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 405
Db 145 BEKKVPINLWIDGKQNTVPLETVTKNKNTVOELDLQARHYLHGKFGLYNSDSFGKVQ 204

QY 406 RGLIVFHSSEGSTVSYDLFDAQQGYPTLLRIYRDNNTTISTSLISLYYTT 458
Db 182 RGLIVFHTSTPSVNYDLFGAQQYSNLLRIYRDNKTINSNMHDIYLYTS 233
```

Db 205 RGLIVFHTSTPESVNYDLFGAQQGNSNTLLRIYRDNKTINSENHDIYLYTS 257

RESULT 44

US-09-751-708A-8

; Sequence 8, Application US/09751708A

; Publication No. US20030157113A1

; GENERAL INFORMATION:

; APPLICANT: TERMAN, David S

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE

; FILE REFERENCE: 751708

; CURRENT APPLICATION NUMBER: US/09/751,708A

; CURRENT FILING DATE: 2002-10-15

; PRIOR APPLICATION NUMBER: US 60/173,371

; PRIOR FILING DATE: 1999-12-28

; NUMBER OF SEQ ID NOS: 166

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 257

; TYPE: PRT

; ORGANISM: Staphylococcus aureus

US-09-751-708A-8

Query Match 26.5%; Score 935; DB 10; Length 257;

Best Local Similarity 75.5%; Pred. No. 1.4e-43;

Matches 176; Conservative 21; Mismatches 36; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSDAQDLTWLTLFKGFTG 285

Db 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSDAQDLTWLTLFKGFTN 84

QY 286 HPWYNDLAVDLGSAATSEYEGSSVDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLT 345

Db 85 HSWYNDLAVDFDSKDIDVYKGVKVDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLT 144

QY 346 BEKVPINLWIDGQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 405

Db 145 EEKVPINLWIDGQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204

QY 406 RGLIVFHTSTPESVNYDLFGAQQGNSNTLLRIYRDNKTINSENHDIYLYTT 458

Db 205 RGLIVFHTSTPESVNYDLFGAQQGNSNTLLRIYRDNKTINSENHDIYLYTS 257

RESULT 45

US-10-679-620-118

; Sequence 118, Application US/10679620

; Publication No. US20040110930A1

; GENERAL INFORMATION:

; APPLICANT: Large Scale Biology

; APPLICANT: Reinal, Stephen J.

; APPLICANT: Edwards, Patricia C.

; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING

; FILE REFERENCE: 34150-004A

; CURRENT APPLICATION NUMBER: US/10/679,620

; CURRENT FILING DATE: 2003-10-03

; PRIOR APPLICATION NUMBER: 60/415,940

; PRIOR FILING DATE: 2002-10-03

; NUMBER OF SEQ ID NOS: 122

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 118

; LENGTH: 451

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: pLSBC2523 , see Example 6

US-10-679-620-118

Query Match 26.3%; Score 926; DB 16; Length 451;

Best Local Similarity 34.0%; Pred. No. 8.4e-43;

Matches 236; Conservative 59; Mismatches 129; Indels 270; Gaps 15;

QY 1 EVQLQSGPDLVKPGASVKISKASGYFTTHVLRHWKQRPQGLEWIGFISPGNGDIRY 60

Db 1 EVKLEQSGAELVKPGASVKISKASGYFTTHVLRHWKQRPQGLEWIGFISPGNGDIRY 60

QY 61 NQKFKDKATLTVDKSSSTTAYMELASLTSEDGAVYYCARSTMI--TNYVMDYWGQSTVTV 118

Db 61 NEKFKDKATLTADKSSSTAYMQLNSLTSEDGAVYFCKESFYVYDDNY--GDYWGQGTTLTV 119

QY 119 SSAKTPPSVYPLAPGSAQAQNSMTWLTCLVKGYPPEPVTVTWNSGSLSSGVHFFPAVLQ 178

Db 120 SSAKTAPSVYPLAPVCGDTSSTVTLGCLVKGYPPEPVTVTWNSGSLSSGVHFFPAVLQ 179

QY 179 SDLYTLSSSVTPSPSTWPSSTVTCNVAHPASSTKVDKKIVPRDSGGPSEKSEINEKDLR 238

Db 180 SDLYTLSSSVTVSTWPSQSITCNVAHPASSTKVDKKIEPR---GPTIKPCP----- 229

QY 239 KKSSELOGTALGNLKOIYYNKAITSSEKSDAQDLTWLTLFKGFTGHPWYNDLVDLGS 298

Db 230 ----- 229

QY 299 TAATSEYEGSSVDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLTEKKVPINLWIDG 358

Db 230 -----PCKCAPN-----LLGGPSVF----- 245

QY 359 KQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQGLVHFSSEGST 418

Db 246 -----IFPPKIKDVLMI---SLSPI 262

QY 419 VSYDLPAQGGVPTDLLRIYRDNKTISSTLSISLYLTTIVMTQTPTSLVLSAGDRV 478

Db 263 VTCVVVDVSEDDPD-----VOISFWVNVNVEVHTAQOT----- 295

QY 479 ITCKASQSVNDVAVYQKQSGPKLLISYTSRYAGVPDRFSGSGYGTDTFTLTISYQA 538

Db 296 -----HREDYNSLTLEV-- 307

QY 539 EDAAVYFQQDYNSTPTGGGTYLKEIKAD-----AAPTYSIIPPSESEQ 582

Db 308 --SALPIQHQQDWMVSGKEF---KCKVNNKDLFAPERTISKPKGSRVAPQVYVLPPEEE 361

QY 583 LTSGGASVVCFLNNFYPKDINVKKIDGSEQN-----GVLSNMTDQDSKDSYTSMSSTL 637

Db 362 MTYKQVTLTCMTVDMPEDIVYEWNTNNGKTELYNKTETPVLDS-----DGSIFMYSKL 414

QY 638 TLTKDEYERHNSYTCETHK--TSTSPIVKSNRN 670

Db 415 RVEKKNNWERNYSYSCSVVHGLEHNNHHTTKSFSSHS 448

RESULT 46

US-10-002-784A-2

; Sequence 2, Application US/10002784A

; Publication No. US20030036644A1

; GENERAL INFORMATION:

; /33

; APPLICANT: Ulrich, Robert G.

; TITLE OF INVENTION: Bacterial Superantigen Vaccines

; FILE REFERENCE: 003/233/SAP

; CURRENT APPLICATION NUMBER: US/10/002,784A

; CURRENT FILING DATE: 2001-11-26

; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776

; PRIOR FILING DATE: 97-06-25; 98-09-01

; NUMBER OF SEQ ID NOS: 40

; SOFTWARE: Apple Macintosh Microsoft Word 6.0

; SEQ ID NO 2

; LENGTH: 257

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: mutant staphylococcal enterotoxin A periplasmic

US-10-002-784A-2

Query Match 26.3%; Score 925; DB 14; Length 257;

Best Local Similarity 75.1%; Pred. No. 5.1e-43;

```

Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKKSELOQTALGNLQIYYNSKAITSEKSADOFNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKKSELOQTALGNLQIYYNEKAKTENKESHDQPROHTILFKGFFTD 84
QY 286 HPYNLDLVLGSLTAATSEYEGSSVDLYGAYGYOCAGGTPNKTCMYGGVTLHDNNRLT 345
Db 85 HSWYNDLLVRFDSKDIDVKYKGGKVDLYGAYAGYOCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKVQ 405
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKVQ 204
QY 406 RGLIVFHSSGTSVSYDLFPAQOQYPTLLRIYRDNTTISSTLSLSLYTT 458
Db 205 RGLIVFHSTEPSVNYDLFGAQOQYNTLLRIYRDNTINSENWHDIDLYTS 257

RESULT 47
US-10-002-784A-4
; Sequence 4, Application US/10002784A
; Publication No. US20030036644A
; GENERAL INFORMATION:
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/982,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 4
; LENGTH: 233
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin A cytoplasmic
US-10-002-784A-4

Query Match 26.1%; Score 921; DB 14; Length 233;
Best Local Similarity 75.0%; Pred. No. 7.5e-43;
Matches 174; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
QY 227 EKSEINEKDLRKKSELOQTALGNLQIYYNSKAITSEKSADOFNTLLFKGFFTG 286
Db 2 EKSEINEKDLRKKSELOQTALGNLQIYYNEKAKTENKESHDQPROHTILFKGFFTD 61
QY 287 PWYNDLLVLGSLTAATSEYEGSSVDLYGAYGYOCAGGTPNKTCMYGGVTLHDNNRLTE 346
Db 62 SWYNDLLVRFDSKDIDVKYKGGKVDLYGAYAGYOCAGGTPNKTCMYGGVTLHDNNRLTE 121
QY 347 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKVQ 406
Db 122 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKVQ 181
QY 407 RGLIVFHSSGTSVSYDLFPAQOQYPTLLRIYRDNTTISSTLSLSLYTT 458
Db 182 RGLIVFHSTEPSVNYDLFGAQOQYNTLLRIYRDNTINSENWHDIDLYTS 233

RESULT 48
US-10-216-484-11
; Sequence 11, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru

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; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 11
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-216-484-11

Query Match 26.0%; Score 915; DB 14; Length 238;
Best Local Similarity 81.3%; Pred. No. 1.6e-42;
Matches 178; Conservative 9; Mismatches 28; Indels 4; Gaps 1;
QY 457 TTSIVMTQTPTSLVLSAGDRVTITCKASQSVND----VAVYQKPGQSPKLLISYTSR 512
Db 19 TGDIVLTQSPASLAVSLGQRATISCKASQSVYDGDSDYMNWYQKPGQPKLLIYAASNL 78
QY 513 YAGVDFRFGSGGYGTDFTLTITSSVQAEDAAVYFCQDYNSPPTFGGKTKLEIKRADAAPT 572
Db 79 ESGIPARFSGSGGTDFTLNIHPVEEEDAATYYCQSNEDPRTFGGKTKLEIKRADAAPT 138
QY 573 VSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKSTYS 632
Db 139 VSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKSTYS 198
QY 633 MSTLTITKDEYERHNSYTCETHKTSPIVKSFNENE 671
Db 199 MSTLTITKDEYERHNSYTCETHKTSPIVKSFNENE 237

RESULT 49
US-10-384-933-11
; Sequence 11, Application US/10384933
; Publication No. US20030170817A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030170817A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/384,933
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 11
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-384-933-11

Query Match 26.0%; Score 915; DB 14; Length 238;
Best Local Similarity 81.3%; Pred. No. 1.6e-42;
Matches 178; Conservative 9; Mismatches 28; Indels 4; Gaps 1;
QY 457 TTSIVMTQTPTSLVLSAGDRVTITCKASQSVND----VAVYQKPGQSPKLLISYTSR 512
Db 19 TGDIVLTQSPASLAVSLGQRATISCKASQSVYDGDSDYMNWYQKPGQPKLLIYAASNL 78
QY 513 YAGVDFRFGSGGYGTDFTLTITSSVQAEDAAVYFCQDYNSPPTFGGKTKLEIKRADAAPT 572
Db 79 ESGIPARFSGSGGTDFTLNIHPVEEEDAATYYCQSNEDPRTFGGKTKLEIKRADAAPT 138

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QY 573 VSIFFPSSEQLTSGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDYTS 632
Db 139 VSIFFPSSEQLTSGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDYTS 198
QY 633 MSSTLTITKDEYERHNSYTCETHKTSPIVKSFNNE 671
Db 199 MSSTLTITKDEYERHNSYTCETHKTSPIVKSFNNE 237

RESULT 50

US-09-903-327A-4
; Sequence 4, Application US/09903327A
; Patent No. US2002016433A1
; GENERAL INFORMATION:
; APPLICANT: Nemerow, Glen R.
; APPLICANT: Li, Ekguang
; TITLE OF INVENTION: BIFUNCTIONAL MOLECULES AND VECTORS COMPLEXED THEREWITH FOR TARGET
; TITLE OF INVENTION: GENE
; TITLE OF INVENTION: DELIVERY
; FILE REFERENCE: 22908-1228
; CURRENT APPLICATION NUMBER: US/09/903,327A
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 09/613,017
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (0)...(0)
; OTHER INFORMATION: DAV-1 light chain, penton base monoclonal antibody
US-09-903-327A-4

Query Match 25.9%; Score 912; DB 9; Length 238;
Best Local Similarity 81.3%; Pred. No. 2.4e-42;
Matches 178; Conservative 9; Mismatches 28; Indels 4; Gaps 1;
QY 457 TTSIVMTQTPTSLVSAAGRVITTCASQSVSNP-----VAWYQKPGSQKLIISYTSR 512
Db 19 TGDIVLTQSPASLAVSLQRATISCKASQSDYDGDSDVMWYQKPGQPKLLIYAASNL 78
QY 513 YAGVDPDRSGSGYGTDFLTITSSVQAEADAATYFCQDYNSPPTFGGTGKLEIKRADAAPT 572
Db 79 ESGIPAREFGSGSGYGTDFLTINHPVEEADAATYCCQTNEDPWTGFGGTGKLEIKRADAAPT 138
QY 573 VSIFFPSSEQLTSGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDYTS 632
Db 139 VSIFFPSSEQLTSGASVVCFLNNFYPKDINVKWKIDGSRQNGVLNSWTDQDSKDYTS 198
QY 633 MSSTLTITKDEYERHNSYTCETHKTSPIVKSFNNE 671
Db 199 MSSTLTITKDEYERHNSYTCETHKTSPIVKSFNNE 237

RESULT 51

US-08-882-431-2
; Sequence 2, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army NRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND

COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 257
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431-2
Query Match 25.8%; Score 908; DB 8; Length 257;
Best Local Similarity 74.2%; Pred. No. 4.3e-42;
Matches 173; Conservative 21; Mismatches 39; Indels 0; Gaps 0;
QY 226 SKSEINEKDLRKSEKQGTALGNLKIYYNEKAKTENKESHDPQHTILFKGFTD 285
Db 25 SKSEINEKDLRKSEKQGTALGNLKIYYNEKAKTENKESHDPQHTILFKGFTD 84
QY 286 HPWYNDLLVLDLSTAATSEYEGSSVDLYGAVYGYCAGGTGPKTACMYGGVTLHDNNRLT 345
Db 85 HSWYNDLLVRFDSKDIVDKYKKGKVDLYGAVGYCAGGTGPKTACMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDKQTTVPIDKVTSKKEVTVEQLDLQARHYLHGKFLGYNDSDFGKQV 405
Db 145 EEKVPINLWIDKQNTVPELTGKTKNKNVTVEQLDLQARHYLHGKFLGYNDSDFGKQV 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNNTTISSTLSLSISLYLTT 458
Db 205 RGLIVFHTSTEPSVNYDLFGAQGYNTLLRIYRDNNTTISSTLSLSISLYLTT 257

RESULT 52

US-08-882-431-4
; Sequence 4, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army NRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5

SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 233
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431-4

Query Match 25.6%; Score 903; DB 8; Length 233;
Best Local Similarity 73.7%; Pred. No. 7.2e-42;
Matches 171; Conservative 21; Mismatches 40; Indels 0; Gaps 0;
QY 227 EKSEINEKDLRKKSBLQGTALGNLQIYYVNSKAITSEKSDAQPLTNTLLFKGFFTH 286
DB 2 EKSEINEKDLRKKSBLQGTALGNLQIYYVNSKAITSEKSDAQPLTNTLLFKGFFTH 61
QY 287 PWNTDLDVLGSAATSEVSGSDVLYGAYGYQCAGGTPNKTACMYGGVTHDNNRLTE 346
DB 62 SWNTDLDVFPDSKDIYDKYKGVVLYGAYGYQCAGGTPNKTACMYGGVTHDNNRLTE 121
QY 347 EKKVPINLMDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVOR 406
DB 122 EKKVPINLMDGKQNTVPLETKNKNVTVQELDKQARYLQCKYNLYNSDVFDGKVAR 181
QY 407 GLIVFHSSGSGTVSYDLFDAQGGYPTLLRIYRDNNTTISLSLSLYLTT 458
DB 182 GLIVFHTSTPSVNYDLFQAQGGYNTLLRIYRDNNTTISLSLSLYLTT 233

RESULT 53
US-10-281-479A-23
Sequence 23, Application US/10281479A
Publication No. US2003013932A1
GENERAL INFORMATION:
APPLICANT: The UAB Research Foundation
APPLICANT: Zhou, Tong
APPLICANT: Ichikawa, Kimihisa
APPLICANT: Kimberly, Robert P.
APPLICANT: Koopman, William J.
APPLICANT: Oshumi, Jun
APPLICANT: LeBuglio, Albert S.
APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: COMBINATIONS OF ANTIBODIES SELECTIVE FOR A TUMOR NECROSIS
TITLE OF INVENTION: FACTOR-RELATED APOPTOSIS-INDUCING LIGAND RECEPTOR AND OTHER THERE
TITLE OF INVENTION: AGENTS
FILE REFERENCE: 21085.002906
CURRENT APPLICATION NUMBER: US/10/281,479A
CURRENT FILING DATE: 2003-01-28
PRIOR APPLICATION NUMBER: 60/391,478
PRIOR FILING DATE: 2002-06-24
PRIOR APPLICATION NUMBER: 60/346,402
PRIOR FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: PCT/US01/14151
PRIOR FILING DATE: 2001-05-02
PRIOR APPLICATION NUMBER: 60/201,344
PRIOR FILING DATE: 2000-05-02
NUMBER OF SEQ ID NOS: 102

SOFTWARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 462
TYPE: PRT
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence./No. US2003013932A1e = Synthe
US-10-281-479A-23

Query Match 25.6%; Score 900.5; DB 14; Length 462;
Best Local Similarity 33.1%; Pred. No. 2.1e-41;
Matches 221; Conservative 68; Mismatches 126; Indels 253; Gaps 15;
QY 1 EVOLQQSGDLVFKPCASVKISKASGYSTGYVMHWKQSPKGLWIGRINPNNGVTLY 60
DB 20 EVMLVESGGGLVFKPGSLKSCAASGTFSSYVMSVRQTPKEKLEWVATISSGGSYTY 79
QY 61 NQKFKDKATLLVDKSSITAYMELSLTSEDSAVVYCAR--STMITNVMYDYGOGTSVTV 118
DB 80 PDSVKGRFTIISRDNAKNTLYLQMSLSRSEDYAMYCARSGDSMITT---DYWGOGTTLTV 136
QY 119 SSAKTTTPSVYPLAPGSAATQNSMVTLCGLVKGYFPEPVTVMNSGSLSSGVHFFPAVLQ 178
DB 137 SSAKTTTPSVYPLAPGSAATQNSMVTLCGLVKGYFPEPVTVMNSGSLSSGVHFFPAVLQ 196
QY 179 SLDYTLSSSVTPSPSTPSETVTCNVAHPASSTKVDKVIIPRDSGGPSEKSEINEKDLR 238
DB 197 SLDYTLSSSVTPSPSTPSETVTCNVAHPASSTKVDKVIIPRDCG----- 241
QY 239 KXSELQGTALGNLQIYYVNSKAITSEKSDAQPLTNTLLFKGFFTHDNNRLTE 298
DB 242 --KPCICTVPEVSVFIFPK-----PKDVLTLTL----- 270
QY 299 TAATSEVSGSDVLYGAYGYQCAGGTPNKTACMYGGVTHDNNRLTEKKVPIINLWIDG 358
DB 271 -----TP-KVTCVVVDIS-----KDDPEVQSFVFD- 295
QY 359 KQTTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGKVKVQGLI 409
DB 296 ---DVEVHTAQTPREQFNSFTFRSVELPFIHQDNLGKBEFKCRVNSAFAFPPIEX--- 349
QY 410 VFHSSGSGTVSYDLFDAQGGYPTLLRIYRDNNTTISLSLSLYLTTISVMTQTPTSL 469
DB 350 -----TISKT----- 354
QY 470 LVSAGDRVITCKASQSVSNDVAMVQKPGSPKLLISYTSRVSAGVDPFRFSGSGYGTDF 529
DB 355 ----- 354
QY 530 TLTISVQAEDAAYVFCQDYNSPPTFGGKLEIKRADAAPTYSIFPPSSEQLTSGAS 589
DB 355 -----KGRKAPQVYTIPTTPKEQNAKDKVS 379
QY 590 VVCFANFYKPDINVWKIDGSEKQNGVNSWTDQDSKDYSTYSMSSTLTITKDEYERHNS 649
DB 380 LTCMITDFFPEDITVEQWNGQPAEN-YKNTQPTMDT-DGSYFVYKLNQKNSWEAGNT 437
QY 650 YTCETHK 657
DB 438 FTSVLHE 445

RESULT 54
US-10-286-132A-23
Sequence 23, Application US/10286132A
Publication No. US20030198637A1
GENERAL INFORMATION:
APPLICANT: Zhou, Tong
APPLICANT: Kimberly, Robert P.
APPLICANT: Koopman, William J.
APPLICANT: LeBuglio, Albert S.
APPLICANT: Buchsbaum, Donald J.
TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED

;; TITLE OF INVENTION: APOPTOSIS-INDUCING LIGAND RECEPTOR AND USES THEREOF
;; FILE REFERENCE: 21085.0029U7
;; CURRENT APPLICATION NUMBER: US/10/286,132A
;; PRIOR FILING DATE: 2003-01-22
;; PRIOR APPLICATION NUMBER: US 60/346,402
;; PRIOR FILING DATE: 2001-11-01
;; PRIOR APPLICATION NUMBER: PCT/US01/14151
;; PRIOR FILING DATE: 2001-05-02
;; PRIOR APPLICATION NUMBER: US 60/201,344
;; PRIOR FILING DATE: 2000-05-02
;; NUMBER OF SEQ ID NOS: 102
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 23
;; LENGTH: 462
;; TYPE: PRT
;; ORGANISM: artificial sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: /No. US20030198637A1e = Synthe
US-10-286-132A-23

Query Match 25.6%; Score 900.5; DB 14; Length 462;
Best Local Similarity 33.1%; Pred. No. 2.le-41;
Matches 221; Conservative 68; Mismatches 126; Indels 253; Gaps 15;

QY 1 EVQLQQSGDILVKPGASVKISKASGYSFTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
DB 20 EVMLVESGGGLVKPGSLKLSCAASGFTFSYVMSVWVQTPEKLEWVATISSGGSYTY 79
QY 61 NQKFKDKATLVDSKSTTAYMELSLTSEDSAVYYCAR--STMITNYVMDYWGQTSVTV 118
DB 80 PDSVKGRTTISRDNKNTLYLQMSLSRSEDATMYCARRGDSMITT---DYWGQGITLV 136
QY 119 SSAKTPPSVYPLAPGSAQTNSMTVLGCLVKGYPEPPTVWNSGSLSSGVHTFPAVLQ 178
DB 137 SSAKTPPSVYPLAPGSAQTNSMTVLGCLVKGYPEPPTVWNSGSLSSGVHTFPAVLQ 196
QY 179 SDLYTLSSSVTPSPSEVTCNVAHPASSTKVDKIVPRDGGSGSEKSEINEKDLR 238
DB 197 SDLYTLSSSVTPSPSEVTCNVAHPASSTKVDKIVPRDCG-----241
QY 239 KKSELQGTALGNLKIYYNSKAITSSSEKSDAQFLNTLLFKGFTGHPWYNDLLVDLGS 298
DB 242 --CKPCICTVPEVSVFIFPPK-----PKDVLITIL-----270
QY 359 KQTTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVGQGLI 409
DB 296 ---DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLWNGKEFKCRVNSAAPPAPIEK---349
QY 410 VFHSSEGSTVSVDLPDAQGQVPTLLRIYRNTTISSTLSISLYLYTTSIWMQTPTSL 469
DB 350 -----TISK-----354
QY 470 LVSAGDRVITTCASQSVSNDAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDF 529
DB 355 -----354
QY 530 TLTISVQAEDAAYFCQQDYNSPPTFGGKTKLEIKRADAAPTIVSIIPPSSEQLTSGAS 589
DB 355 -----KGRPKAPQVVTIPPPKEQMAKDKVS 379
QY 590 VVCFLNFPKDIINVKKIDGERQNGVLNSWTDDSKDSTYSMSSTLTLTKDEYERHNS 649
DB 380 LTCMITDFFPEDITVEWQNGQPAEN-YKNTQPIMDT-DGSFYVYSKLVQKSNWEAGNT 437
QY 650 YTCEATHK 657
DB 438 FTCSVLHE 445

RESULT 55
US-10-275-180A-23
;; Sequence 23, Application US/10275180A
;; Publication No. US20030190687A1
;; GENERAL INFORMATION:
;; APPLICANT: The UAB Research Foundation
;; APPLICANT: Zhou, Tong
;; APPLICANT: Ichikawa, Kimihisa
;; APPLICANT: Kimberly, Robert P.
;; APPLICANT: Koopman, William J.
;; TITLE OF INVENTION: AN ANTIBODY SELECTIVE FOR A TUMOR NECROSIS FACTOR-RELATED APOPTOSIS
;; TITLE OF INVENTION: INDUCING LIGAND RECEPTOR AND USES THEREOF
;; FILE REFERENCE: 21085.0029U5
;; CURRENT APPLICATION NUMBER: US/10/275,180A
;; CURRENT FILING DATE: 2002-10-31
;; NUMBER OF SEQ ID NOS: 102
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 23
;; LENGTH: 464
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: /No. US20030190687A1e =
US-10-275-180A-23

Query Match 25.6%; Score 900.5; DB 14; Length 464;
Best Local Similarity 33.1%; Pred. No. 2.le-41;
Matches 221; Conservative 68; Mismatches 126; Indels 253; Gaps 15;

QY 1 EVQLQQSGDILVKPGASVKISKASGYSFTGYMHVWVKQSPGKLEWIGRINPNNGVTLY 60
DB 20 EVMLVESGGGLVKPGSLKLSCAASGFTFSYVMSVWVQTPEKLEWVATISSGGSYTY 79
QY 61 NQKFKDKATLVDSKSTTAYMELSLTSEDSAVYYCAR--STMITNYVMDYWGQTSVTV 118
DB 80 PDSVKGRTTISRDNKNTLYLQMSLSRSEDATMYCARRGDSMITT---DYWGQGITLV 136
QY 119 SSAKTPPSVYPLAPGSAQTNSMTVLGCLVKGYPEPPTVWNSGSLSSGVHTFPAVLQ 178
DB 137 SSAKTPPSVYPLAPGSAQTNSMTVLGCLVKGYPEPPTVWNSGSLSSGVHTFPAVLQ 196
QY 179 SDLYTLSSSVTPSPSEVTCNVAHPASSTKVDKIVPRDGGSGSEKSEINEKDLR 238
DB 197 SDLYTLSSSVTPSPSEVTCNVAHPASSTKVDKIVPRDCG-----241
QY 239 KKSELQGTALGNLKIYYNSKAITSSSEKSDAQFLNTLLFKGFTGHPWYNDLLVDLGS 298
DB 242 --CKPCICTVPEVSVFIFPPK-----PKDVLITIL-----270
QY 299 TAATSEYEGSSVDLYGAYGYQCAGGTGPNKTAACMYGGVTLDHNNRLTBEKKVPIINLWIDG 358
DB 271 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD-295
QY 359 KQTTVPIDKVKTSKEV-----TVQELDLQARHYLHGK-FGL-YNSDSFGGKVGQGLI 409
DB 296 ---DVEVHTAQTPREEQFNSTFRSVSELPIMHQDLWNGKEFKCRVNSAAPPAPIEK---349
QY 410 VFHSSEGSTVSVDLPDAQGQVPTLLRIYRNTTISSTLSISLYLYTTSIWMQTPTSL 469
DB 350 -----TISK-----354
QY 470 LVSAGDRVITTCASQSVSNDAVYQKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDF 529
DB 355 -----354
QY 530 TLTISVQAEDAAYFCQQDYNSPPTFGGKTKLEIKRADAAPTIVSIIPPSSEQLTSGAS 589
DB 355 -----KGRPKAPQVVTIPPPKEQMAKDKVS 379
QY 590 VVCFLNFPKDIINVKKIDGERQNGVLNSWTDDSKDSTYSMSSTLTLTKDEYERHNS 649
DB 380 LTCMITDFFPEDITVEWQNGQPAEN-YKNTQPIMDT-DGSFYVYSKLVQKSNWEAGNT 437

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QY 650 YTCETHK 657
Db 438 FTCVLHE 445

RESULT 56
US-10-679-620-80
; Sequence 80, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reini, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 80
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Murine [p9E10LT-TOPO, see Example 3]
US-10-679-620-80

Query Match 25.4%; Score 894; DB 16; Length 218;
Best Local Similarity 80.6%; Pred. No. 2.1e-41;
Matches 174; Conservative 13; Mismatches 25; Indels 4; Gaps 1;

QY 460 IVMTQTPTSLVSGADRVITITCKASQSVN---DVAWYQKPGQSPKLLISYTSRYAG 515
Db 2 IVLTQSPASLAVSLGORATISCRASEVDNFGFMMWFQKQPPKLLIYAIISNRSG 61

QY 516 VPDPRFSGSGYGTDFLTITSSVQAEADAAVYFCQDYNPPTFGGKLEIKRADAAPTYSI 575
Db 62 VPARFSGSGGTDFSLNIHPVEEDDPAMYFCQQTKEVPWTFGGTKLEIKRADAAPTYSI 121

QY 576 FPSSSEQLTSGASVVCFLNNFYPKIDINVKWKIDGSRQNGVLNSWTDQDSKDYSSMS 635
Db 122 FPSSSEQLTSGASVVCFLNNFYPKIDINVKWKIDGSRQNGVLNSWTDQDSKDYSSMS 181

QY 636 TLTLTKDEYERHNSYTCETHTKTSTSPVKSFNNE 671
Db 182 TLTLTKDEYERHNSYTCETHTKTSTSPVKSFNNE 217

RESULT 57
US-10-679-620-116
; Sequence 116, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reini, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 116
; LENGTH: 712
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pLSBCL799, see Example 5
US-10-679-620-116

Query Match 25.4%; Score 894; DB 16; Length 712;
Best Local Similarity 80.6%; Pred. No. 7.7e-41;
Matches 174; Conservative 13; Mismatches 25; Indels 4; Gaps 1;

QY 460 IVMTQTPTSLVSGADRVITITCKASQSVN---DVAWYQKPGQSPKLLISYTSRYAG 515
Db 4 IVLTQSPASLAVSLGORATISCRASEVDNFGFMMWFQKQPPKLLIYAIISNRSG 63

QY 516 VPDPRFSGSGYGTDFLTITSSVQAEADAAVYFCQDYNPPTFGGKLEIKRADAAPTYSI 575
Db 64 VPARFSGSGGTDFSLNIHPVEEDDPAMYFCQQTKEVPWTFGGTKLEIKRADAAPTYSI 123

QY 576 FPSSSEQLTSGASVVCFLNNFYPKIDINVKWKIDGSRQNGVLNSWTDQDSKDYSSMS 635
Db 124 FPSSSEQLTSGASVVCFLNNFYPKIDINVKWKIDGSRQNGVLNSWTDQDSKDYSSMS 183

QY 636 TLTLTKDEYERHNSYTCETHTKTSTSPVKSFNNE 671
Db 184 TLTLTKDEYERHNSYTCETHTKTSTSPVKSFNNE 219

RESULT 58
US-10-679-620-120
; Sequence 120, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reini, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; PRIOR FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 120
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pLSBCL757, see Example 6
US-10-679-620-120

Query Match 25.3%; Score 890.5; DB 16; Length 215;
Best Local Similarity 80.8%; Pred. No. 3.2e-41;
Matches 172; Conservative 15; Mismatches 25; Indels 1; Gaps 1;

QY 460 IVMTQTPTSLVSGADRVITITCKASQSVN---DVAWYQKPGQSPKLLISYTSRYAGVDP 518
Db 2 IVLTQSPAINASLGERVTMTCTASSSVSSSYFHWYQKPGSSPKLWIYTTNLSAGVPA 61

QY 519 RFGSGYGTDFLTITSSVQAEADAAVYFCQDYNPPTFGGKLEIKRADAAPTYSIFPP 578
Db 62 RFGSGSGGTYSLSLTSSMEADAAATYCHQYHRSPLTFGAGTKLEIKRADAAPTYSIFPP 121

QY 579 SSEQLTSGASVVCFLNNFYPKIDINVKWKIDGSRQNGVLNSWTDQDSKDYSSMSSTLT 638
Db 122 SSEQLTSGASVVCFLNNFYPKIDINVKWKIDGSRQNGVLNSWTDQDSKDYSSMSSTLT 181

QY 639 LTKDEYERHNSYTCETHTKTSTSPVKSFNNE 671
Db 182 LTKDEYERHNSYTCETHTKTSTSPVKSFNNE 214

RESULT 59
US-10-679-620-122
; Sequence 122, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reini, Stephen J.
```

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; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 122
; LENGTH: 483
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pLSBCL1792, see Example 6
US-10-679-620-122

Query Match      25.3%; Score 890.5; DB 16; Length 483;
Best Local Similarity 80.8%; Pred. No. 7.8e-41;
Matches 172; Conservative 15; Mismatches 25; Indels 1; Gaps 1;

QY 460 IWTQTPTSLVLSAGDRTITCKASQSVSND-VAWYQKQKQSPKLLISYTSRYAGVDPD 518
DB 2 IVLTQSPALMSASLGERVTMTCTASSVSSSYFHWYQKQKQSPKLLIYTTNLSAGVPA 61

QY 519 RFSGSGYGTDTFTLTISSVQAEADAAYVFCQDYNPPPTFGGKLEIKRADAAPTYSIFPP 578
DB 62 RFSGSGGTSYSLTISSWEADAATYCHQVRSPLTFGAGTKLEKRAADAAPTYSIFPP 121

QY 579 SSEQLTSGGASVVCFLNNFPKIDGSRQNGVLSWTDQSKDSTYSMSSTLT 638
DB 122 SSEQLTSGGASVVCFLNNFPKIDGSRQNGVLSWTDQSKDSTYSMSSTLT 181

QY 639 LTKDEYERHNSYTCETHKTSPIVKSFNRE 671
DB 182 LTKDEYERHNSYTCETHKTSPIVKSFNRE 214

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RESULT 60
US-10-291-265-335
; Sequence 335, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 335
; LENGTH: 363
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-335

Query Match      25.1%; Score 885; DB 15; Length 363;
Best Local Similarity 30.6%; Pred. No. 1.1e-40;
Matches 205; Conservative 56; Mismatches 82; Indels 328; Gaps 5;

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QY 1 EVOLQSGDPIVKGASVKISKASGYSTGYMHWKQSPKGLWIGRINPNNGVTLY 60
DB 20 EVQLLESGGGLVQPGGSLRLSCAASGFTFSFSMSWRQAPKGLWVSSISGSGTYY 79

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QY 61 NOKFKDKATLTVDKSTTAYMELRSLTSDSAVYVCARSTMITNKVMDYWGQSGTSTVSS 120
DB 80 ADSVAGRTTIISRDNSKNTLYIQMNSLRAEDTAVYCAKPPF-----YFDYWGQGLTVIVSS 135
QY 121 AKTTPPSVYPLAPGSAQAQNSMVTLGCLVKGYFPEPVTVTWNSGSLSSGVHTTFFAVLQSD 180
DB 136 G----- 136
QY 181 LYTLLSSVTVPSSSTWPSSETVTCNVAHPASSTKVDKIVPRDSGGPSEKSEBINEKDLKK 240
DB 137 ----- 136
QY 241 SELOGTALGNLKIYYVNSKAITSEKSAQOFLTNLLFKGFFTHGHPWYNDLLVDLQSTA 300
DB 137 ----- 136
QY 301 ATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQ 360
DB 137 -----DGG----- 143
QY 361 TTVPIDKVTSKKVTVOELDLQARHVLHGKFLYNSDSFGKVGQGLIVFHSSEGSTVS 420
DB 144 -----VTVSSSDIQ----- 152
QY 421 YDLFAQOQYPTLRIYRDNTTISSTLSLSLYLYTTSIVMTQTPTSLIYSAGDRTIT 480
DB 153 -----MTQSPSTLSASVGDRTIT 171
QY 481 CKASQSVNDVAWYQKQKQSPKLLISYTSRYAGVDPDFSGSGYGTDTFTLTISSVQAE 540
DB 172 CRASQISGLAWYQKQKQKAPKLLIYKASLESQVPSRFSGSGSGTDFTLTISLQPD 231
QY 541 AAVYFCQDYNPPPTFGGKLEIKRADAAPTYSIFPPSSQLTSGGASVVCFLNNFPK 600
DB 232 FATYICQYVYVPLTFGGGKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPR 291
QY 601 DINVKWKIDGSRQNGVLSWTDQSKDSTYSMSSTLTLTDEYERHNSYTCETHKTS 660
DB 292 EAKVQKVDNALQSGNSQESVTEQDSKDSYLSLTSLTSLKADIEKKHLYACEVTHQGLS 351

QY 661 SPIVKSFNRE 671
DB 352 SPVTKSFNRE 362

RESULT 61
US-10-679-620-78
; Sequence 78, Application US/10679620
; Publication No. US20040110930A1
; GENERAL INFORMATION:
; APPLICANT: Large Scale Biology
; APPLICANT: Reini, Stephen J.
; APPLICANT: Edwards, Patricia C.
; TITLE OF INVENTION: MULTIMERIC PROTEIN ENGINEERING
; FILE REFERENCE: 34150-004A
; CURRENT APPLICATION NUMBER: US/10/679,620
; CURRENT FILING DATE: 2003-10-03
; PRIOR APPLICATION NUMBER: 60/415,940
; PRIOR FILING DATE: 2002-10-03
; NUMBER OF SEQ ID NOS: 122
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 78
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Murine [p9E10Hy-TOPO, see Example 3]
US-10-679-620-78

Query Match      25.1%; Score 884.5; DB 16; Length 451;
Best Local Similarity 33.6%; Pred. No. 1.5e-40;
Matches 223; Conservative 57; Mismatches 147; Indels 237; Gaps 12;
QY 1 EVOLQSGDPIVKGASVKISKASGYSTGYMHWKQSPKGLWIGRINPNNGVTLY 60

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Db 1 EVDLVEGDLVKGKGLKLSAAGTFTSHYGMVWVROTDPKRLWVATIGSRGTYTH 60
QY 61 NOXFKDKATLTVDKSTTAYMELRSITSEDSAVVYCARSTMTINY-----VMDYWGOG 113
Db 61 PDSVKGRFTLSRDNKXALYQMSLKSEDTAMYCCARSEFYFYGNTYYGAMDYWGOG 120
QY 114 TSVTVSSAKTTPSPVYPLAPGSAQAQNSMWTGLCLVKGYFPEPVTVMNSGSLSSGVHTF 173
Db 121 ASVTVSSAKTTPSPVYPLAPGSAQAQNSMWTGLCLVKGYFPEPVTVMNSGSLSSGVHTF 180
QY 174 PAVLQSDLTLSSTVTPSPSTWSEVTCNVAPASSTKVDKIVPRDGGGSEKSEBEIN 233
Db 181 PAVLQSDLTLSSTVTPSPSTWSEVTCNVAPASSTKVDKIVPRDGGGSEKSEBEIN 230
QY 234 EKDLRKKSELGQALGNLQIYYNSKAITSEKSAQDLTNTLLPKGFTHGHPWINDLL 293
Db 231 ----- 230
QY 294 VDLGTAATSEYEGSSVDLYGAYGYOCAGGTPNKTACMYGVTLDHNNRLTEKKVPIN 353
Db 231 ---CKPCICTVPEVSSVFIP-----PPK-----PKDVL 256
QY 354 LWIDGQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKGQVGLVPHS 413
Db 257 IILTPKVTCTVVD-----ISKDDPEVQ----- 278
QY 414 SEGSTVSYDLFDAQGOYPTLLRIYRDNTTISTSLISLYLYTTSIVMTQFTSLLSVA 473
Db 279 -----PSWFVDDVEVHTAQTPREQFNSFRSVS-----ELPIH 314
QY 474 GRVTTICKASQSVNDVAVYQKQKQPKLLISYTSRYAGVDRPFGSGGVTFTLTI 533
Db 315 QD-----WLNKDFKC-----RVNSAAPPAPPIKTI 340
QY 534 SSVQAEADAAYFCQDYNPPFTGGGKLEIKRADAPTYSIIPPSSEOLTSGGASVVC 593
Db 341 S-----KTKGRKAPQVYIIPPKQKQKADKVSLLTCM 372
QY 594 LNFYPKDINVKWIDGSRQNLNSWTDQSKDSTYSMSLTLLTKDEYERHNSYTC 653
Db 373 ITDFEPDITVEMQWNGQPAEN-YKNTQPIMDT-DGSYFVYKLNQVNSWAGNTFTCS 430
QY 654 ATHK 657
Db 431 VLHE 434

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RESULT 62

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US-10-159-006-18
; Sequence 18, Application US/10159006
; Publication No. US20030143229A1
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saldanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: Para-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890002
; CURRENT APPLICATION NUMBER: US/10/159,006
; PRIOR FILING DATE: 2002-06-03
; PRIOR FILING DATE: 1999-04-29
; PRIOR FILING DATE: 1999-04-29
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: US 60/086,049
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 18
; LENGTH: 453
; TYPE: PRT

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; ORGANISM: Homo sapiens
US-10-159-006-18
Query Match 24.8%; Score 872; DB 14; Length 453;
Best Local Similarity 34.1%; Pred. No. 7.4e-40;
Matches 227; Conservative 56; Mismatches 143; Indels 240; Gaps 17;
QY 2 VOLQSGPDLVKGASVKISCKASGYSTGYMHWKQSGKGLWIGRINPNNGVTLYN 61
Db 1 VOLQSGPELVKPGASVAMSKTSRYTFETTHHWVQSHGKSLWIGGINPNNGINPN 60
QY 62 QKFKDKATLTVDKSTTAYMELRSITSEDSAVVYCARSTMTINY-----VMDYWGOGTSVT 117
Db 61 QKFKGRATLTVGKSSSTAYMELRSITSEDSAVVYCARRIAYGYDEGHAMDYWGOGTSVT 120
QY 118 VSSAKTTPSPVYPLAPGSAQAQNSMWTGLCLVKGYFPEPVTVMNSGSLSSGVHTFPAVL 177
Db 121 VSSASTKGPSVFLAPGSKSTGTAALGCLVXDYFPEPVTVMNSGALTSGVHTFPAVL 180
QY 178 QSD-LYTLSSSVTPSPSTWSEVTCNVAPASSTKVDKIVPRDGGGSEKSEBEINEKD 236
Db 181 QSSGLYSLSVVTPSSSLGTQTVICNVNHPKSNKVDKVEPKSC----- 226
QY 237 LRKSELQGTALGNLQIYYNSKAITSEKSAQDLTNTLLPKGFTHGHPWINDLLVLD 296
Db 227 -----DKHTCTCPPAPELIGGPSVF--LFPKP--KDTLM-- 258
QY 297 GSTAATSEYEGSSVDLYGAYGYOCAGGTPNKTACMYGVTLDHNNRLTEKKVPINLWI 356
Db 259 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYV 285
QY 357 DGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKGQVGLVPHSSEG 416
Db 286 DG-----VEVHNAKTKPREQ-----YNSTY--RVSVLTVLHQDWL 320
QY 417 STVSYDLFDAQGOYPTLLRIYRDNTTISTSLISLYLYTTSIVMTQFTSLLSVAGDR 476
Db 321 NGKEY----- 325
QY 477 VTITCKASQSVNDVAVYQKQKQPKLLISYTSRYAGVDRPFGSGGYGDTFTLTISV 536
Db 326 ---CKKVS-----NKALPAP--TEKTSKAKGP----- 349
QY 537 QAEDAAYFCQDYNPPFTGGGKLEIKRADAPTYSIIPPSSEOLTSGASVVCFLNN 596
Db 350 -----REPQVYTLPPSREEMTKNQVSLTCLVKG 377
QY 597 FYPKDINVKWIDGSRQNLNSWTDQSKDSTYSMSLTLLTKDEYERHNSYT 651
Db 378 FYPSDIAVWESNGQPENNYKTPPVLDG-----DGSFFLYSKLIVDKSRWQCGNVFS 430
QY 652 CEATHK 657
Db 431 CSVMHE 436

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RESULT 63

```

US-10-410-907A-34
; Sequence 34, Application US/10410907A
; Publication No. US20030215880A1
; GENERAL INFORMATION:
; APPLICANT: Dennis R. Burton
; APPLICANT: R. Anthony Williamson
; APPLICANT: Gianluca Moroncini
; TITLE OF INVENTION: MOTIF-GRAFTED HYBRID POLYPEPTIDES AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 22908-1229
; CURRENT APPLICATION NUMBER: US/10/410,907A
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/371,610
; PRIOR FILING DATE: 2002-04-09
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: FastSeq for Windows Version 4.0

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; SEQ ID NO 34
; LENGTH: 215
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D18 Light Chain
US-10-410-907A-34

Query Match          24.6%; Score 866.5; DB 15; Length 215;
Best Local Similarity 79.2%; Pred. No. 6.5e-40;
Matches 168; Conservative 17; Mismatches 26; Indels 1; Gaps 1;

QY 460 IVMQTPTSLVSGADRVTTICKASQSVNDVAVYQKPGQSPKLLISYTSRRYAGVDPDR 519
DB 4 LVLTQSPAFMSASPEKVTMTCSASSV-NYMHVYQKSGTSPKRWIYDTSKLASGVPAR 62

QY 520 FSGSGYGTDFLTITSSVQAEAAVYFCQDYNSPPTFGGGTKLEIKADAAAPTYSIFPPS 579
DB 63 FSGSGGTYSYSLTSSMEADAATYVYQWSSNPTFTGGGKLEIKADAAAPTYSIFPPS 122

QY 580 SEQLTSGASVVCFLNFPKIDINVKKIDGSRQNGVLSWTDQDSKSTYSMSSTLT 639
DB 123 SEQLTSGASVVCFLNFPKIDINVKKIDGSRQNGVLSWTDQDSKSTYSMSSTLT 182

QY 640 TKDEYERHNSYTCRATHKTSPIVKSFRNE 671
DB 183 TEDEYERHNSYTCRATHKTSPIVKSFRNE 214

RESULT 64
US-10-159-006-30
; Sequence 30, Application US/10159006
; Publication No. US20030143229A1
; GENERAL INFORMATION:
; APPLICANT: Park, John E.
; APPLICANT: Garin-Chesa, Pilar
; APPLICANT: Bamberger, Uwe
; APPLICANT: Leger, Olivier
; APPLICANT: Saidanha, Jose W.
; APPLICANT: Rettig, Wolfgang J.
; TITLE OF INVENTION: FAPA-specific Antibody with Improved Producibility
; FILE REFERENCE: 0652.1890002
; CURRENT APPLICATION NUMBER: US/10/159,006
; CURRENT FILING DATE: 2002-06-03
; PRIOR APPLICATION NUMBER: US 09/301,593
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: EP 98107925.4
; PRIOR FILING DATE: 1998-04-30
; PRIOR APPLICATION NUMBER: US 60/086,049
; PRIOR FILING DATE: 1998-05-18
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 30
; LENGTH: 472
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-159-006-30

Query Match          24.5%; Score 863.5; DB 14; Length 472;
Best Local Similarity 34.0%; Pred. No. 2.3e-39;
Matches 227; Conservative 57; Mismatches 142; Indels 241; Gaps 18;

QY 1 EVQLQSGDPLVKGASVKISKASGYSFTGYMHWKQSPGKLEWIGRINPNNGVTLY 60
DB 20 EVQLQSGDPLVKGASVKMSCKTSRYTFTYTHHWKQSHGKSLWIGGINPNNGIPNY 79

QY 61 NQKFKDKATLVKDSSTTAYMELSLTSEDSAVYVCARSTMTINY----VMDYNGQCTSV 116
DB 80 NQKFKGRATLVKGSSTTAYMELSLTSEDSAVYFCARRRAYGYDEGHANDYNGQCTSV 139

QY 117 TVSSAKTTPPSVYPLAPGSAQAQTSNMTGLVKRGYFPEPVTVTWNSGSLSSGVHTFPV 176
DB 140 TVSSSS-TKGPSVYPLAPSSKSTSGGTAALGCLVKDYPPEPVTVSWNSGALTSGVHTFPV 198

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QY 177 IQSD-LYTLSSSVTPSPSTWSETVTCNVAHPASTKVDKIVPRDGGSPSEKSEINEK 235
DB 199 LQSSGLYSLSSVTPSPSSLTGTQYICNVNHPKNTKVDKKEPKSC-----245
QY 236 DLKKSEIQGTALGNLKOIYYNNSKAITSEKSDAQFLNTLLFKGFTGHPWYNDLLVD 295
DB 246 -----DKTHCTPCPAPPELLGGPSVF--LPPKP--KDTLM--277
QY 296 LGSTAATSEYEGSSVDLYGAYYQCAGTGNKTAQMYGGVTLHNNRLTEKKVPLNLW 355
DB 278 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWY 303
QY 356 IDGKOTTPIDKVKTSKEVTVQELDLQARHVLHGKFGLYNSDSFGGKVQGLIVEHSE 415
DB 304 VDG-----VEVHNATKPREEQ-----YNSTY---RVSVLTVLHQDW 338
QY 416 GSTSYDLDFAQGGVPTLLRIYRDNTTISSTLSISLYLYTTSIVMTQTPTSLLSAGD 475
DB 339 LMGKEY-----344
QY 476 RVTTICKASQSVNDVAVYQKPGQSPKLLISYTSRRYAGVDPDRFSGSGYGTDFLTLS 535
DB 345 -----KCKVS-----NKALPAP---TEKTSKAKGP-----368
QY 536 VQAEADAAYVFCQDYNSPPTFGGGTKLEIKRADAAPTYSIFPPSSEQLTSGASVVCFLN 595
DB 369 -----REPOVYTLPPSREEMTKNQVSLTCLVK 395
QY 596 NFYPKIDINVKKIDGSRQNGVLSWTDQDSKSTYSMSSTLTTLTKDEYERHNSY 650
DB 396 GFYPSDIAVWEWSNGQPNNTKTPPVLDSD-----DGSFFLYSLKLTVDKSRWQGVNF 448
QY 651 TCEATHK 657
DB 449 SCSVMHE 455

RESULT 65
US-09-910-059-131
; Sequence 131, Application US/09910059
; Patent No. US20020142359A1
; GENERAL INFORMATION:
; APPLICANT: Copley, Clive G
; APPLICANT: Edge, Michael Derek
; APPLICANT: Emery, Stephen Charles
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody, a
; TITLE OF INVENTION: Their Therapeutic use in an Adept System
; FILE REFERENCE: 1991-209
; CURRENT APPLICATION NUMBER: US/09/910,059
; CURRENT FILING DATE: 2001-07-23
; PRIOR APPLICATION NUMBER: US 09/171,945
; PRIOR FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; PRIOR APPLICATION NUMBER: GB 9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 131
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: full-length human B7.1-murine ASB7 Fd fusion
US-09-910-059-131

Query Match          24.3%; Score 855.5; DB 9; Length 473;
Best Local Similarity 72.9%; Pred. No. 6.2e-39;
Matches 164; Conservative 24; Mismatches 34; Indels 3; Gaps 3;

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QY 1 EYVLOQSGEDLVKPGASVKSASGYSTGYMHVWVQSPGKGLIEWIGRI-NPNNGVTL 59
Db 243 EYKLVESGGLVQPGGSLRLSCATSGFTFTDYMMWVRQPPGKALEWLGFIGNKANGYTT 302
QY 60 -YNQFKDKATLVTKSSSTAYMELRSLTSEDSAVYCARSTMITNYVMYKGGQTSVTV 118
Db 303 EYASVKGFTISRDKSQSILYLQMTLRAEDSATYYCTRDRLFPY-FDWGQQTITV 361
QY 119 SSAKTTTPSVYPLAPGSAQOTSMVTLGCLVKGYPEPVTVTWNSGSLSSGVHTFPVAVLQ 178
Db 362 SSAKTTTPSVYPLAPGSAQOTSMVTLGCLVKGYPEPVTVTWNSGSLSSGVHTFPVAVLQ 421
QY 179 SLYTLSSSVTVPPSSWPSETVTCNVAHPASSTKVDKIVPRDSG 223
Db 422 SLYTLSSSVTVPPSSWPSETVTCNVAHPASSTKVDKIVPRDCG 466

RESULT 66
US-09-795-515-5
; Sequence 5, Application US/09795515
; Publication No. US20030039645A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Entage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. US20030039645A1ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-795-515-5

Query Match 24.2%; Score 852.5; DB 10; Length 235;
Best Local Similarity 74.9%; Pred. No. 4.2e-39;
Matches 167; Conservative 18; Mismatches 37; Indels 1; Gaps 1;
QY 449 LSISLYLYTTSIVMTQTPTSLVSGADRVITTCASQSVNDVAVYQKPGQSPKLLISY 508
Db 13 ISASVIRSGQVILVTSQPAIMASPGKVTMTCSASSSVY-MNMYQKSGTSPKRWYD 71
QY 509 TSSRYAGVDPFRSGSGYGTDFTLTSSVQAEAAVYFCQDYNSPPTFGGTTKLEIKRAD 568
Db 72 TSKLASGVPAHFRGSGSGTSYSLTISGMEAEADATYYCQWSSNPFTFGSGTKLEINRAD 131
QY 569 AAPTIVSIFPSSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLSNWTDDQSKD 628
Db 72 TSKLASGVPAHFRGSGSGTSYSLTISGMEAEADATYYCQWSSNPFTFGSGTKLEINRAD 131

QY 569 AAPTIVSIFPSSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLSNWTDDQSKD 628
Db 132 TAPTIVSIFPSSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLSNWTDDQSKD 191
QY 629 STYSMSSTLTLTKDEYERHNSYTCETHKTSTSPIVKSFNRE 671
Db 192 STYSMSSTLTLTKDEYERHNSYTCETHKTSTSPIVKSFNRE 234
RESULT 67
US-10-704-352-5
; Sequence 5, Application US/10704352
; Publication No. US20040071693A1
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/704,352
; FILING DATE: 07-Nov-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE: 28-FEB-2001
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
; US-10-704-352-5

Query Match 24.2%; Score 852.5; DB 12; Length 235;
Best Local Similarity 74.9%; Pred. No. 4.2e-39;
Matches 167; Conservative 18; Mismatches 37; Indels 1; Gaps 1;
QY 449 LSISLYLYTTSIVMTQTPTSLVSGADRVITTCASQSVNDVAVYQKPGQSPKLLISY 508
Db 13 ISASVIRSGQVILVTSQPAIMASPGKVTMTCSASSSVY-MNMYQKSGTSPKRWYD 71
QY 509 TSSRYAGVDPFRSGSGYGTDFTLTSSVQAEAAVYFCQDYNSPPTFGGTTKLEIKRAD 568
Db 72 TSKLASGVPAHFRGSGSGTSYSLTISGMEAEADATYYCQWSSNPFTFGSGTKLEINRAD 131
QY 569 AAPTIVSIFPSSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLSNWTDDQSKD 628
Db 132 TAPTIVSIFPSSSQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLSNWTDDQSKD 191
QY 629 STYSMSSTLTLTKDEYERHNSYTCETHKTSTSPIVKSFNRE 671

Db 192 STYMSSTLTITKDEYERHNSYTCETHKTKSTPIVKSFRNE 234

RESULT 68

US-10-704-071-5
Sequence 5, Application US/10704071
Publication No. US2004007662A1
GENERAL INFORMATION:
APPLICANT: Adair, John R.
Athwal, Diljeet S.
Emtage, John S.
TITLE OF INVENTION: Humanised Antibodies
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10704,071
FILING DATE: 07-Nov-2003
CLASSIFICATION: (D)

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/846,658
FILING DATE: 01-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Irujillo, Doreen Yatkio
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CARP-0057
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 235 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 5:

US-10-704-071-5
Query Match 24.2%; Score 852.5; DB 16; Length 235;
Best Local Similarity 74.9%; Pred. No. 4.2e-39;
Matches 167; Conservative 18; Mismatches 37; Indels 1; Gaps 1;
QY 449 LSISLYLTTSIVTQPTSLVSGADRVITTCASQSVNDVAVYQCKPGQPKLLISY 508
Db 13 ISASVIRSGQIVITQSPAINASPGKEVNTWCASSSVY-MNMYQCKSGTSPKRWYD 71
QY 509 TSSRYAGVPDFSGGYGTDTLTITSSVQAEADAAVYFCQDDYNSPPFTGGGTKEIKRAD- 568
Db 72 TSKLASGVPAHFRGSGGTSYSLTISGWEADAATYVCQWSSNPFFTGSGTKLEINRAD 131
QY 569 AAPTYSIEPPSSEQLTSGASVQCFNNFYKDTINVKWIDGSRQGVNSWTDQDSKD 628
Db 132 TAPTYSIEPPSSEQLTSGASVQCFNNFYKDTINVKWIDGSRQGVNSWTDQDSKD 191
QY 629 STYMSSTLTITKDEYERHNSYTCETHKTKSTPIVKSFRNE 671
Db 192 STYMSSTLTITKDEYERHNSYTCETHKTKSTPIVKSFRNE 234

RESULT 69

US-10-467-546-4

Sequence 4, Application US/10467546
Publication No. US20040096901A1
GENERAL INFORMATION:
APPLICANT: Gregorio Aversa
APPLICANT: Frank Kolbinger
APPLICANT: Jose M. Carballido Herrera
APPLICANT: Andras Aszodi
APPLICANT: Jose W. Saldaña
APPLICANT: Bruce M. Hall
TITLE OF INVENTION: Therapeutic binding molecules
FILE REFERENCE: PCI/EP02/01420
CURRENT APPLICATION NUMBER: US/10/467,546
CURRENT FILING DATE: 2003-08-08
NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn version 3.1
SEQ ID NO 4
LENGTH: 448
TYPE: PRT
ORGANISM: Artificial
FEATURE:
NAME/KEY: MISC FEATURE
OTHER INFORMATION: Amino acid sequence of chimeric heavy chain
US-10-467-546-4

Query Match 24.2%; Score 852; DB 16; Length 448;
Best Local Similarity 33.5%; Pred. No. 9e-39;
Matches 222; Conservative 58; Mismatches 145; Indels 238; Gaps 17;

QY 1 EVLOQSGPDLVKPGASVKISKASGYSTGYVMHWKQSPGKLGLEWIGRINPNNGVTLY 60
Db 1 EVLOQSGPELVKPGASVKMSCKASGYFTTYIIHWKQEPGQGLEWIGYENPNHGTY 60
QY 61 NQKFKDKATLTVDKSSTTAYMELSLTSEDGAVYCARSTMTIYVMDYWCQGSITVSS 120
Db 61 NEKFKGRATLTADKSSNTAYMDLSLTSEDGAVYCARSGPYAWF--DTWQGGTIVTVSS 118
QY 121 AKTTPSVYVPLAPGSAAGTNSMTVLGCLVKGYPPEPTVTWNSSGLSSGVHTFPFAVLQSD 180
Db 119 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 178
QY 181 -LYTLSSSVTVPSSTWPTSETVTCNVHPASTKVDKXIVPRDSGGPSEKSEINEKDLRK 239
Db 179 GLYSLSVVTVPSSSLGTQTVICNVHKNPSNTKVDKRVPEKSC----- 221
QY 240 KSELQGTALGNLKOIYYNKAITSSEKSAQFLNTLLEKFFTGHPHWNDLLVDLGS 299
Db 222 -----DKHTTCCPCPAPELLGGPSVF--LPFPKP--KDTLM----- 253
QY 300 AATSEYEGSSVDLYGAVYCYQCAGGTGPNKTACTMYGGVTLHDNNRLTEBKVPINLWIDGK 359
Db 254 -----ISRTPEVT-CVVVDVS-----HEDPEVKFNWYVDG- 282
QY 360 QTTVPIDKVKTSKKTQVVOELDQARHYLHKGFGLYNSDSFGGKQVQGLIYVHSEGSTV 419
Db 283 ---VEVHNAKTKPREEQ-----YNSY---RVVSYLTVLHQDWLNGK 318
QY 420 SYDLFDAQQQYPTDLLRIYRDNTTISSTLSLSLYLTTSITWTQTPSTLLVSAGDRVTI 479
Db 319 EY----- 320
QY 480 TCKASQSVNDVAVYQCKPGQSPKLLISYTSRVAGVPRDFSGSGYGTDTLTITSSVQAE 539
Db 321 CKKVS-----NKALPAP---IEKTSKAKGP----- 344
QY 540 DAAVYFCQDDYNSPPFTGGGTKEIKRAADAAPTYSIEPPSSEQLTSGASVVCFLNNFY 599
Db 345 -----REPOVTLTPSREEMTKQVSLTCLVKGY 375
QY 600 KDINVKWKIDGSRQK-----GVLSNMTDQDSKSTYSMSSTLTITKDEYERHNSYTC 654
Db 376 SDIAVENWESNGQPNYKTTTPVLDLSDS-----DGSFFLYSKLTVDKSRWQGNVFC 428
QY 655 THK 657


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QY 420 SYDLFDAQQYPTDLLRIYRDNNTTISSTLSLSLYLTTSIVMTQPTSLVAGDRVTI 479
Db 168 -----TGEIVLTQSPGTLISLSPGERATL 190
QY 480 TCKASQSVND-VAMVYQKQSPKLLISYTSRYAGVDPDRFSGSGYGTDTFTLTISVQA 538
Db 191 SCRASQSVSSYLAWYQKQAPRLLIYGASSRATGIPDRFSGSGGTDTFTLTISRLEP 250
QY 539 EDAAVYFCQDYNSPPTFGGKLEIKRADAAPTIVSIFPPSSQOLTSGGASVVCFLNNFY 598
Db 251 EDFAVYCCQYGGSPPTFGGKLEIKRADAAPTIVSIFPPSSQOLTSGGASVVCFLNNFY 310
QY 599 PKDINVKMKIDGSRQNGVLNSWTDQDSKSTYSMSSTLTLTDEYERHNSYTCETHKT 658
Db 311 PREAKVQKVDNALQSGNSQESVTEQDSKSTYSLSSTLTLSKADYKHKVYACEVTHQ 370
QY 659 STSPIVKSFNENE 671
Db 371 LSSPVTKSFNRGE 383

RESULT 72
US-10-291-265-805
; Sequence 805, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 805
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-805

Query Match 23.9%; Score 841.5; DB 15; Length 384;
Best Local Similarity 30.2%; Pred. No. 2.9e-38;
Matches 203; Conservative 64; Mismatches 95; Indels 311; Gaps 10;

QY 1 EVLQQSGFDLVKPGASVKISKASGYSTGYTHHWKQSPKGLGWIGRINPNNG-VTL 59
Db 20 EVLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSGLSGSGSTY 79
QY 60 YNQKFKDATHLVKDSSTTAYNELSLTSEDSAVYVCARSTMITNYMDYMGQGTSTVTS 119
Db 80 YADSVKGRFTISRDNSKGTLYQMNSLRADDTARYCAKG-----GVELA 124
QY 120 SAKTTPPSVYPLAPGSAAGTNSMTLGLCLVKGPPEPVTVTNWNSGSLSSGVHTPPAVLQS 179
Db 125 STK----- 127
QY 186 DLYTLSSSVTPSPSTWPSPTVTCNVAHPASSTKVDKIVPRDSCGPSEKSEINEKDLRK 239
Db 128 -----PSSIW----- 132
QY 240 KSELQGTALGNLKQIYYNSKAITSSKSAQDLTLNLLFKGFTGHFWYNDLLVLDLGS 299
Db 133 -----RLNPIRY-----WYFDLW-GQGT 150
```

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QY 300 AATSEYEGSSVDLYCAYGYQCAGGTGNKTAQMGVGTLHDNNRLTBEKKVPINLWIDGK 359
Db 151 VTVSGDGGSS-----GGAS----- 167
QY 360 QTTVEIDKVTSKKEVTVOELDLQARHVLHGKFGLYNSDSFGGKVGQGLIVFHSSEGSTV 419
Db 168 ----- 167
QY 420 SYDLFDAQQYPTDLLRIYRDNNTTISSTLSLSLYLTTSIVMTQPTSLVAGDRVTI 479
Db 168 -----TGEIVLTQSPGTLISLSPGERATL 190
QY 480 TCKASQSVND-VAMVYQKQSPKLLISYTSRYAGVDPDRFSGSGYGTDTFTLTISVQA 538
Db 191 SCRASQSVSSYLAWYQKQAPRLLIYGASSRATGIPDRFSGSGGTDTFTLTISRLEP 250
QY 539 EDAAVYFCQDYNSPPTFGGKLEIKRADAAPTIVSIFPPSSQOLTSGGASVVCFLNNFY 598
Db 251 EDFAVYCCQYGGSPPTFGGKLEIKRADAAPTIVSIFPPSSQOLTSGGASVVCFLNNFY 310
QY 599 PKDINVKMKIDGSRQNGVLNSWTDQDSKSTYSMSSTLTLTDEYERHNSYTCETHKT 658
Db 311 PREAKVQKVDNALQSGNSQESVTEQDSKSTYSLSSTLTLSKADYKHKVYACEVTHQ 370
QY 659 STSPIVKSFNENE 671
Db 371 LSSPVTKSFNRGE 383

RESULT 73
US-10-291-265-806
; Sequence 806, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 806
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-806

Query Match 23.9%; Score 841.5; DB 15; Length 384;
Best Local Similarity 30.2%; Pred. No. 2.9e-38;
Matches 203; Conservative 64; Mismatches 95; Indels 311; Gaps 10;

QY 1 EVLQQSGFDLVKPGASVKISKASGYSTGYTHHWKQSPKGLGWIGRINPNNG-VTL 59
Db 20 EVLVESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKGLWVSGLSGSGSTY 79
QY 60 YNQKFKDATHLVKDSSTTAYNELSLTSEDSAVYVCARSTMITNYMDYMGQGTSTVTS 119
Db 80 YADSVKGRFTISRDNSKGTLYQMNSLRADDTARYCAKG-----GVELA 124
QY 120 SAKTTPPSVYPLAPGSAAGTNSMTLGLCLVKGPPEPVTVTNWNSGSLSSGVHTPPAVLQS 179
Db 125 STK----- 127
QY 180 DLYTLSSSVTPSPSTWPSPTVTCNVAHPASSTKVDKIVPRDSCGPSEKSEINEKDLRK 239
```

Db 128 -----PSSW----- 132
QY 240 KSELTALGNLKOIYYNKAITSSEKADQFLNTLLFKGFTGHPWYNDLLVDLST 299
Db 133 -----RLNPIRY-----WYFDLW-CGGTL 150
QY 300 AATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVFINLWIDGK 359
Db 151 VTVSSGGGSS-----GGAS----- 167
QY 360 QTTVPIDKVKTSKEVTVOELDLQARHLYHKGFLYNSDFGKVGRLIVFHSSEGSTV 419
Db 168 ----- 167
QY 420 SYDLFDAQGYPTLLRIYRDNTTISSTLSLSLYLTTISIVMTQTPTSLIVSAGDRVIT 479
Db 168 -----TGEIVLTQSPGTLSPGERATL 190
QY 480 TKASQSVSND-VAWYQKQPGQPKLLISVTSRYAGVDRFSGSGYGTDFTLTISVQA 538
Db 191 SCRASQSVSSYLAWYQKQPGQAPRLIYGCASRATGIDRFSGSGGTDFTLTISRLEP 250
QY 539 EDAVYFCQDYNPPTFGGKTKLEIKRADAAPTIVSIFPPSSEQLTSGGASVVCFLNNFY 598
Db 251 EDPVAVYCCQYGGSPPTFGGKTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCFLNNFY 310
QY 599 PKDINVKWKIDGSRQNGVLNSWTDQDSKDYMSSTLTLTKDEYERHNSYTCETHKT 658
Db 311 PREAKVQKVDNALQSGNSQESVTEQDSKDYMSSTLTLSKADYERHKVYACEVTHQG 370
QY 659 STSPVTKSFNRNE 671
Db 371 LSSPVTKSFNRGE 383

RESULT 74
US-10-291-265-807
; Sequence 807, Application US/10291265
; Publication No. US20030232054A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; APPLICANT: Tang et al
; TITLE OF INVENTION: No. US20030232054A1el Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-017 (785)
; CURRENT APPLICATION NUMBER: US/10/291,265
; CURRENT FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/491,404
; PRIOR FILING DATE: 2000-01-25
; PRIOR APPLICATION NUMBER: 09/617,746
; PRIOR FILING DATE: 2000-07-17
; PRIOR APPLICATION NUMBER: 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 09/633,870
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 944
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 807
; LENGTH: 384
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-291-265-807

Query Match 23.9%; Score 841.5; DB 15; Length 384;
Best Local Similarity 30.2%; Pred. No. 2.9e-38;
Matches 203; Conservative 64; Mismatches 95; Indels 311; Gaps 10;
QY 1 EVOLQSGDPLVKPGASVKISCKASGYFTGYVHWVKOSPGKLEWIGRIPNNG-VTL 59
Db 20 EVOLVESGGGLVQPGGSLRLSCAASGFTTSSYAMSWVRQAPGKLEWVSGLSGGSSTY 79
QY 60 YKQKFKDKATLTVDKSSITAYMELRSLTSEDGAVYVCARSTMTNYMDYWGQGTSTVTS 119

Db 80 YADSVKGFITSRDNSKGTLYLQNSLRADDTARYYCAKG-----GVELA 124
QY 120 SAKTTPPSVYPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTWNSGSLSSGVHTTTPAVLQS 179
Db 125 STK----- 127
QY 180 DLYTLSSSVTVPSSTWPFSETVTCNVAHPASSTKVDDKXIVPRDSGGPSEKSEEINEKDLRK 239
Db 128 -----PSSW----- 132
QY 240 KSELTALGNLKOIYYNKAITSSEKADQFLNTLLFKGFTGHPWYNDLLVDLST 299
Db 133 -----RLNPIRY-----WYFDLW-CGGTL 150
QY 300 AATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVFINLWIDGK 359
Db 151 VTVSSGGGSS-----GGAS----- 167
QY 360 QTTVPIDKVKTSKEVTVOELDLQARHLYHKGFLYNSDFGKVGRLIVFHSSEGSTV 419
Db 168 ----- 167
QY 420 SYDLFDAQGYPTLLRIYRDNTTISSTLSLSLYLTTISIVMTQTPTSLIVSAGDRVIT 479
Db 168 -----TGEIVLTQSPGTLSPGERATL 190
QY 480 TKASQSVSND-VAWYQKQPGQPKLLISVTSRYAGVDRFSGSGYGTDFTLTISVQA 538
Db 191 SCRASQSVSSYLAWYQKQPGQAPRLIYGCASRATGIDRFSGSGGTDFTLTISRLEP 250
QY 539 EDAVYFCQDYNPPTFGGKTKLEIKRADAAPTIVSIFPPSSEQLTSGGASVVCFLNNFY 598
Db 251 EDPVAVYCCQYGGSPPTFGGKTKVDIKRTVAAPSVFIFPPSDEQLKSGTASVVCFLNNFY 310
QY 599 PKDINVKWKIDGSRQNGVLNSWTDQDSKDYMSSTLTLTKDEYERHNSYTCETHKT 658
Db 311 PREAKVQKVDNALQSGNSQESVTEQDSKDYMSSTLTLSKADYERHKVYACEVTHQG 370
QY 659 STSPVTKSFNRNE 671
Db 371 LSSPVTKSFNRGE 383

RESULT 75
US-10-216-484-143
; Sequence 143, Application US/10216484
; Publication No. US20030103976A1
; GENERAL INFORMATION:
; APPLICANT: Serizawa, No. US20030103976A1ufusa
; APPLICANT: Haruyama, Hideyuki
; APPLICANT: Nakahara, Kaori
; APPLICANT: Tamaki, Ikuko
; APPLICANT: Takahashi, Tohru
; TITLE OF INVENTION: Anti-Fas Antibodies
; FILE REFERENCE: 980126CIP/HG
; CURRENT APPLICATION NUMBER: US/10/216,484
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US/09/499,662
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 09/053,583
; PRIOR FILING DATE: 1998-04-01
; NUMBER OF SEQ ID NOS: 165
; SEQ ID NO 143
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Designed heavy
; OTHER INFORMATION: chain of humanized anti-Fas antibody
US-10-216-484-143

Query Match 23.5%; Score 827.5; DB 14; Length 470;
Best Local Similarity 32.5%; Pred. No. 2.1e-37;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 12, 2004, 13:27:15 ; Search time 26.5729 Seconds
(without alignments)
1305.563 Million cell updates/sec

Title: US-09-900-766-1

Perfect score: 3522

Sequence: 1 EVQLQSGPDLVKPGASVKI.....EATHKTSPIVKSNRNES 672

Scoring table: BLOSUM62

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA:*

1: /cgn2_6/prodata/2/1aa/5A-COMB.pep:*

2: /cgn2_6/prodata/2/1aa/5B-COMB.pep:*

3: /cgn2_6/prodata/2/1aa/6A-COMB.pep:*

4: /cgn2_6/prodata/2/1aa/6B-COMB.pep:*

5: /cgn2_6/prodata/2/1aa/6C-COMB.pep:*

6: /cgn2_6/prodata/2/1aa/6D-COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1108.5	31.5	489	5	PCT-US95-11405-35
2	1107	31.4	233	4	US-08-695-692B-8
3	1107	31.4	257	3	US-08-486-099-112
4	1107	31.4	257	3	US-08-360-107A-122
5	1107	31.4	257	3	US-08-484-223B-112
6	1107	31.4	257	3	US-08-919-597-112
7	1107	31.4	257	3	US-08-475-668A-112
8	1107	31.4	257	3	US-08-485-551A-112
9	1107	31.4	257	3	US-08-471-913A-112
10	1107	31.4	257	3	US-08-485-264A-112
11	1107	31.4	257	4	US-08-474-349A-112
12	1107	31.4	257	4	US-08-470-896-112
13	1107	31.4	257	4	US-08-485-546A-112
14	1059.5	30.1	445	1	US-08-353-400-33
15	1059.5	30.1	464	1	US-08-353-400-36
16	1040	29.5	226	3	US-08-896-933-24
17	1040	29.5	226	4	US-09-314-235-24
18	980.5	27.8	711	4	US-09-485-737B-90
19	966	27.4	468	2	US-08-116-247-7
20	960	27.3	212	2	US-08-737-129A-2
21	957	27.2	468	2	US-08-303-569B-7
22	957	27.2	468	2	US-09-795-515-7
23	953.5	27.1	223	5	PCT-US94-14106-51
24	948	26.9	233	4	US-08-695-692B-7
25	948	26.9	257	3	US-08-486-099-113
26	948	26.9	257	3	US-08-360-107A-123
27	948	26.9	257	3	US-08-484-223B-113

28	948	26.9	257	3	US-08-919-597-113	Sequence 113, App
29	948	26.9	257	3	US-08-475-668A-113	Sequence 113, App
30	948	26.9	257	3	US-08-485-551A-113	Sequence 113, App
31	948	26.9	257	3	US-08-471-913A-113	Sequence 113, App
32	948	26.9	257	3	US-08-485-264A-113	Sequence 113, App
33	948	26.9	257	4	US-08-474-349A-113	Sequence 113, App
34	948	26.9	257	4	US-08-470-896-113	Sequence 113, App
35	948	26.9	257	4	US-08-485-546A-113	Sequence 113, App
36	944.5	26.8	239	1	US-08-353-400-37	Sequence 37, Appl
37	944	26.8	233	1	US-08-446-918A-4	Sequence 4, Appl
38	944	26.8	233	2	US-08-580-806-4	Sequence 4, Appl
39	941.5	26.7	219	1	US-08-353-400-34	Sequence 34, Appl
40	933	26.5	222	3	US-08-737-129A-6	Sequence 6, Appl
41	931.5	26.4	232	3	US-08-896-933-23	Sequence 23, Appl
42	931.5	26.4	232	4	US-09-314-235-23	Sequence 23, Appl
43	925	26.3	237	4	US-09-144-776B-2	Sequence 2, Appl
44	921	26.1	233	4	US-09-144-776B-4	Sequence 4, Appl
45	915.5	26.0	254	2	US-08-792-824-10	Sequence 10, Appl
46	915.5	26.0	254	2	US-08-792-824-13	Sequence 13, Appl
47	909.5	25.8	254	2	US-08-792-824-4	Sequence 4, Appl
48	909.5	25.8	254	2	US-08-792-824-7	Sequence 7, Appl
49	904.5	25.7	238	3	US-09-192-545-4	Sequence 4, Appl
50	903.5	25.7	447	6	5455030-1	Patent No. 5455030
51	901	25.6	218	5	PCT-US94-14106-57	Sequence 57, Appl
52	898	25.5	211	4	US-09-170-769A-8	Sequence 8, Appl
53	897.5	25.5	223	5	PCT-US94-14106-55	Sequence 55, Appl
54	895	25.4	215	2	US-08-737-129A-8	Sequence 8, Appl
55	892.5	25.3	599	1	US-08-442-542-18	Sequence 18, Appl
56	892.5	25.3	599	1	US-08-765-469-18	Sequence 18, Appl
57	889.5	25.3	235	4	US-09-423-439-58	Sequence 58, Appl
58	889.5	25.3	235	4	US-09-011-769A-23	Sequence 23, Appl
59	878	24.9	213	2	US-08-737-129A-4	Sequence 4, Appl
60	873	24.8	647	4	US-09-423-439-60	Sequence 60, Appl
61	872	24.8	236	2	US-08-792-824-3	Sequence 3, Appl
62	872	24.8	236	2	US-08-792-824-9	Sequence 9, Appl
63	872	24.8	236	2	US-08-792-824-12	Sequence 12, Appl
64	872	24.8	453	4	US-09-301-593-18	Sequence 18, Appl
65	864	24.5	218	5	PCT-US94-14106-61	Sequence 61, Appl
66	863.5	24.5	472	4	US-09-301-593-30	Sequence 30, Appl
67	861	24.4	215	4	US-09-170-769A-4	Sequence 4, Appl
68	858	24.4	234	5	PCT-US94-07659-4	Sequence 4, Appl
69	855.5	24.3	250	4	US-09-011-769A-21	Sequence 21, Appl
70	855.5	24.3	473	4	US-09-171-945-131	Sequence 131, Appl
71	852.5	24.2	235	2	US-08-303-569B-5	Sequence 5, Appl
72	852.5	24.2	235	2	US-08-116-247-5	Sequence 5, Appl
73	852.5	24.2	235	4	US-09-795-515-5	Sequence 5, Appl
74	850.5	24.1	200	6	5189147-8	Patent No. 5189147
75	841	23.9	454	2	US-07-934-373C-22	Sequence 22, Appl
76	841	23.9	454	3	US-08-437-842B-22	Sequence 22, Appl
77	841	23.9	454	4	US-08-146-206C-22	Sequence 22, Appl
78	841	23.9	454	4	US-09-705-686-22	Sequence 22, Appl
79	841	23.9	454	5	PCT-US93-07833-22	Sequence 22, Appl
80	840	23.9	206	6	5189147-9	Patent No. 5189147
81	834.5	23.7	217	5	PCT-US94-14106-59	Sequence 59, Appl
82	831.5	23.6	247	5	PCT-US94-07659-2	Sequence 2, Appl
83	830	23.6	233	2	US-08-792-824-6	Sequence 6, Appl
84	828.5	23.5	235	3	US-08-444-644-28	Sequence 28, Appl
85	828.5	23.5	235	4	US-08-232-246A-28	Sequence 28, Appl
86	827.5	23.5	215	6	5455030-3	Patent No. 5455030
87	826.5	23.5	235	3	US-08-444-644-42	Sequence 42, Appl
88	826.5	23.5	235	4	US-08-232-246A-42	Sequence 42, Appl
89	825.5	23.4	235	3	US-08-444-644-19	Sequence 19, Appl
90	825.5	23.4	235	4	US-08-232-246A-19	Sequence 19, Appl
91	819	23.3	234	2	US-07-690-192-2	Sequence 2, Appl
92	818.5	23.2	472	4	US-09-301-593-43	Sequence 43, Appl
93	812	23.1	467	2	US-07-916-098A-45	Sequence 45, Appl
94	811.5	23.0	233	3	US-08-444-644-33	Sequence 33, Appl
95	811.5	23.0	233	4	US-08-232-246A-33	Sequence 33, Appl
96	802	22.8	255	2	US-07-690-192-4	Sequence 4, Appl
97	802	22.8	452	3	US-09-027-449-71	Sequence 71, Appl
98	802	22.8	452	3	US-09-026-985-71	Sequence 71, Appl
99	802	22.8	452	4	US-09-121-952A-71	Sequence 71, Appl
100	802	22.8	452	4	US-09-234-340A-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1

PCT-US95-11405-35

Sequence 35, Application PC/TUS9511405

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: PHOSPHOROUS-32 LABELING OF ANTIBODIES

TITLE OF INVENTION: FOR CANCER THERAPY

NUMBER OF SEQUENCES: 38

CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/11405

FILING DATE: 18-SEP-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/308,103

FILING DATE: 16-SEP-1994

ATTORNEY/AGENT INFORMATION:

NAME: SAXE, Bernhard D.

REGISTRATION NUMBER: 28,665

REFERENCE/DOCKET NUMBER: 19733/599/IMIN

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 35:

SEQUENCE CHARACTERISTICS:

LENGTH: 489 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US95-11405-35

Query Match 31.5%; Score 1108.5; DB 5; Length 489;

Best Local Similarity 37.1%; Pred. No. 2.4e-66;

Matches 249; Conservative 60; Mismatches 156; Indels 207; Gaps 7;

QY 1 EVQLQQSGDILVKPGASVKISKASGYSFTGYNHWYKQSPGKLEWIGRINPNNGVTLY 60

DB 23 EVQLVESGGVVQPGSRILRSCSASGDFDTYXXXXXWVRQAPGKLEWIGXXXXXXX 82

QY 61 NQKFKDALTVDKSSITAYNELRLTSEDSAVYVCARSTMITNYVDYWGQTSVTSS 120

DB 83 XXXXXXRFTISRDAKNTFLQMDSLRPEDTGVYFCA-SXXXXXXXWGQGPPTVSS 141

QY 121 AKTTPPSVYPLAPGSAAGTNSMTVLGCLVKGYFPEPVTVTWNSGSLSSGVHTTFAVLQSD 180

DB 142 ASTKGPSVFPPLAPGSKSTSGTAALGCLVKDYPPEPVTVSWNSGALTSVHTTFAVLQSS 201

QY 181 -LYTLSSVTVPSSTWSPSETVTCNVAHPASTKVDKIKIVPRDSGGPSEKSEENKDLRK 239

DB 202 GLYSLSSVTVPSSTWSPSETVTCNVAHPASTKVDKIKIVPRDSGGPSEKSEENKDLRK 241

QY 240 KSELQGTALGNLKOIYYNNSKAITSSSEKADQFLTLLFKGPTGHPWYNLLDLVGLST 299

DB 242 -----KSCD----- 245

QY 300 AATSEYEGSSVDLYGAYGYGQACGTPNKTACMYGGVTLHDNNRLTBEKKVPINLWIDGK 359

Db 246 ----- 245

QY 360 QTVPIDKVKTSKKEVTVQELDLQARHYLHGKFLYNSDSFGGKQVQRLIVHSESESTV 419

DB 246 -----KT-----HTCPPCPM 255

QY 420 SYDLFDAQQQYPTLLRIYRDNNTTSSLSISLYLYTTISVTMTPTSLVLSAGDRVIT 479

DB 256 KYLL-----PTRAAGLLLLAQAQAMADQLTQSPSSLSASVGDRAVIT 297

QY 480 TCKASQSVSNDAVYQQKPGSPKLLISYTSRVAGVDPDRFSGSGYGFDTLTSSVQAE 539

DB 298 TCXXXXXXXWYQQKPGKAPKLLIYXXXXXXGVPDRFSGSGSGTDFFTTSSLOPE 357

QY 540 DAAVYFCQDYNSTPFTGGGKLEIKRADAAPTYSIRPSSSEQLTSGASVVCFLNNFYP 599

DB 358 DIATYCYCXXXXXX-XXFGGQTKVEIKRTVAAPSVFIFPPSDEQLKSGTASVVCFLNNFYP 416

QY 600 KDINVKWKIDGSEKQNGVLSNWTQDSDKSDTYSMSSTLTLTQDEYRHNSTYCEATHKTS 659

DB 417 REAKVQMKVDNALQSGNSQESVTEQDSKSDTYSLSSTLTLSKADYKHKVYACEVTHQGL 476

QY 660 TSPVIVKSFNRNE 671

DB 477 SSPVTKSFNRGE 488

RESULT 2

US-08-695-692B-8

Sequence 8, Application US/08695692B

Patent No. 651499

GENERAL INFORMATION:

APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,

APPLICANT: Johan Hansson, Terje Kalland, Lars

APPLICANT: Abrahamson and Goran Forsberg

TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS

TITLE OF INVENTION: AND THEIR USE

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pravel, Hewitt, Kimball & Krieger

STREET: 1177 West Loop South, 10th Floor

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77027-9095

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/695,692B

FILING DATE: August 12, 1996

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 9601245-5

FILING DATE: March 29, 1996

ATTORNEY/AGENT INFORMATION:

NAME: Krieger, Paul E.

REGISTRATION NUMBER: 25,886

REFERENCE/DOCKET NUMBER: 41986/1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 713-850-0909

TELEFAX: 713-850-0165

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 233 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-695-692B-8

Query Match 31.4%; Score 1107; DB 4; Length 233;

Best Local Similarity 89.7%; Pred. No. 1.2e-66; Mismatches 15; Indels 0; Gaps 0;
Matches 209; Conservative 9;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSADQFLTNLLFKGFTG 285
Db 1 SEKSEINEKDLRKSELORNALSNLKOIYYNEKAITENKESDDQFLENTLLFKGFTG 60
QY 286 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYOCAGTGNKTACMYGGVTLHDNNRLT 345
Db 61 HPWYNDLLVLDGSKATNKYKGVLDLYGAYGYOCAGTGNKTACMYGGVTLHDNNRLT 120
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 405
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
QY 406 RGLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNNTTISSTLSISLYLTT 458
Db 181 RGLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNNTTINSENHLIDLYLTT 233

RESULT 3
US-08-486-099-112
; Sequence 112, Application US/08486099
; Patent No. 6013263
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
; TITLE OF INVENTION: B VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,099
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-031
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-486-099-112

Query Match 31.4%; Score 1107; DB 3; Length 257;
Best Local Similarity 89.7%; Pred. No. 1.3e-66;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSADQFLTNLLFKGFTG 285
Db 25 SEKSEINEKDLRKSELORNALSNLKOIYYNEKAITENKESDDQFLENTLLFKGFTG 84
QY 286 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYOCAGTGNKTACMYGGVTLHDNNRLT 345
Db 85 HPWYNDLLVLDGSKATNKYKGVLDLYGAYGYOCAGTGNKTACMYGGVTLHDNNRLT 144
QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 405
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204
QY 406 RGLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNNTTISSTLSISLYLTT 458
Db 205 RGLIVFHSSEGSTVSYDLFDAQGYPTDLLRIYRDNNTTINSENHLIDLYLTT 257

RESULT 4
US-08-360-107A-122
; Sequence 122, Application US/08360107A
; Patent No. 6017536
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 149
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,107A
; FILING DATE: 20-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-013
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 122:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-360-107A-122

Query Match 31.4%; Score 1107; DB 3; Length 257;
Best Local Similarity 89.7%; Pred. No. 1.3e-66;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSADQFLTNLLFKGFTG 285
Db 25 SEKSEINEKDLRKSELORNALSNLKOIYYNEKAITENKESDDQFLENTLLFKGFTG 84

QY 286 HPWYNDLLVDLGSKDTATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
 DB 85 HPWYNDLLVDLGSKDTATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
 QY 346 BEKKVPINLWIDGKQTTVPIDKVTTSKEVTQELDLQARHYLHGKFGLYNSDSFGGKVQ 405
 DB 145 BEKKVPINLWIDGKQTTVPIDKVTTSKEVTQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
 QY 406 RGLIVFHSSEGSTVSDFDAQGGYPTDLRIYRDNTTISSTLSISLYLYTT 458
 DB 205 RGLIVFHSSEGSTVSDFDAQGGYPTDLRIYRDNTTISSTLSISLYLYTT 257

RESULT 5

US-08-484-223B-112
 ; Sequence 112, Application US/08484223B
 ; Patent No. 6020459
 ; GENERAL INFORMATION:
 ; APPLICANT: Bolognesi, Dani P.
 ; APPLICANT: Matthews, Thomas J.
 ; APPLICANT: Wild, Carl T.
 ; APPLICANT: Barney, Shawn O.
 ; APPLICANT: Lambert, Dennis M.
 ; APPLICANT: Petteway, Stephen R.
 ; APPLICANT: Langlois, Alphonse J.
 ; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
 ; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
 ; NUMBER OF SEQUENCES: 245
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/484,223B
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7872-029
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 112:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 257 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-08-484-223B-112

Query Match 31.4%; Score 1107; DB 3; Length 257;
 Best Local Similarity 89.7%; Pred. No. 1.3e-66;
 Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
 QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSDAQPLTNTLLFKGFFTG 285
 DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSDAQPLTNTLLFKGFFTG 84
 QY 286 HPWYNDLLVDLGSKDTATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345

DB 85 HPWYNDLLVDLGSKDTATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
 QY 346 BEKKVPINLWIDGKQTTVPIDKVTTSKEVTQELDLQARHYLHGKFGLYNSDSFGGKVQ 405
 DB 145 BEKKVPINLWIDGKQTTVPIDKVTTSKEVTQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
 QY 406 RGLIVFHSSEGSTVSDFDAQGGYPTDLRIYRDNTTISSTLSISLYLYTT 458
 DB 205 RGLIVFHSSEGSTVSDFDAQGGYPTDLRIYRDNTTISSTLSISLYLYTT 257

RESULT 6

US-08-919-597-112
 ; Sequence 112, Application US/08919597
 ; Patent No. 6054285
 ; GENERAL INFORMATION:
 ; APPLICANT: Bolognesi, Dani P.
 ; APPLICANT: Matthews, Thomas J.
 ; APPLICANT: Wild, Carl T.
 ; APPLICANT: Barney, Shawn O.
 ; APPLICANT: Lambert, Dennis M.
 ; APPLICANT: Petteway, Stephen R.
 ; APPLICANT: Langlois, Alphonse J.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
 ; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
 ; NUMBER OF SEQUENCES: 273
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/919,597
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/470,896
 ; FILING DATE: 06-JUN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7872-020
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 112:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 257 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-08-919-597-112

Query Match 31.4%; Score 1107; DB 3; Length 257;
 Best Local Similarity 89.7%; Pred. No. 1.3e-66;
 Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
 QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSDAQPLTNTLLFKGFFTG 285
 DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSDAQPLTNTLLFKGFFTG 84
 QY 286 HPWYNDLLVDLGSKDTATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345

Db 85 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 346 EEKKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 EEKKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNTTISSTLSISLYLTT 458
Db 205 RGLIVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNTTINSENHLIDLTYLT 257

RESULT 7
US-08-475-668A-112
; Sequence 112, Application US/08475668A
; Patent No. 6060065
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,668A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-475-668A-112

Query Match 31.4%; Score 1107; DB 3; Length 257;
Best Local Similarity 89.7%; Pred. No. 1.3e-66;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYVNSKAITSEKSDAQFLTNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOGTALGNLKOIYYVNSKAITSEKSDAQFLTNTLLFKGFFTG 84
QY 286 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
Db 85 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 346 EEKKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 EEKKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNTTISSTLSISLYLTT 458

Db 205 RGLIVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNTTINSENHLIDLTYLT 257

RESULT 8
US-08-485-551A-112
; Sequence 112, Application US/08485551A
; Patent No. 6068973
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,551A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-485-551A-112

Query Match 31.4%; Score 1107; DB 3; Length 257;
Best Local Similarity 89.7%; Pred. No. 1.3e-66;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYVNSKAITSEKSDAQFLTNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOGTALGNLKOIYYVNSKAITSEKSDAQFLTNTLLFKGFFTG 84
QY 286 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345
Db 85 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 346 EEKKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 EEKKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 406 RGLIVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNTTISSTLSISLYLTT 458
Db 205 RGLIVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNTTINSENHLIDLTYLT 257

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RESULT 9
US-08-471-913A-112
; Sequence 112, Application US/08471913A
; Patent No. 6093794
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Pettaway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/471-913A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-471-913A-112

Query Match 31.4%; Score 1107; DB 3; Length 257;
Best Local Similarity 89.7%; Pred. No. 1.3e-66;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKXSELOGTALGNLKOIYYNSKAITSEKSDAQFLTNLLFKGFTG 285
DB 25 SEKSEINEKDLRKXSELOGTALGNLKOIYYNSKAITSEKSDAQFLTNLLFKGFTG 84
QY 286 HPWYNDLLVDLGSATSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 345
DB 85 HPWYNDLLVDLGSATSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 144
QY 346 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 405
DB 145 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNNTTISSTLSISLYTT 458
DB 205 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNNTTISSTLSISLYTT 257

RESULT 10
US-08-485-264A-112
; Sequence 112, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:

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; Sequence 112, Application US/08485264A
; Patent No. 6228983
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Pettaway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485-264A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-485-264A-112

Query Match 31.4%; Score 1107; DB 3; Length 257;
Best Local Similarity 89.7%; Pred. No. 1.3e-66;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKXSELOGTALGNLKOIYYNSKAITSEKSDAQFLTNLLFKGFTG 285
DB 25 SEKSEINEKDLRKXSELOGTALGNLKOIYYNSKAITSEKSDAQFLTNLLFKGFTG 84
QY 286 HPWYNDLLVDLGSATSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 345
DB 85 HPWYNDLLVDLGSATSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 144
QY 346 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 405
DB 145 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNNTTISSTLSISLYTT 458
DB 205 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNNTTISSTLSISLYTT 257

RESULT 11
US-08-474-349A-112
; Sequence 112, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:

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; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,546A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-485-546A-112

Query Match 31.4%; Score 1107; DB 4; Length 257;
Best Local Similarity 89.7%; Pred. No. 1.3e-66;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKSDAQLTWLLFKGFTG 285
DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDQFLNTLLFKGFTG 84
QY 286 HPWYNDLLVDLGSATATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 345
DB 85 HPWYNDLLVDLGSADATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 346 BEKKVPINLWIDGKQTTVPIDKVTSEKVTQVELDLOARHYLHGKFGLYNSDSFGKQV 405
DB 145 BEKKVPINLWIDGKQTTVPIDKVTSEKVTQVELDLOARHYLHGKFGLYNSDSFGKQV 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGPDTLLRIYRDNNTISSTLSISLYLTT 458
DB 205 RGLIVFHSSEGSTVSVDLFDAGQGPDTLLRIYRDNNTISSENHLDLYLTT 257

RESULT 14
US-08-353-400-33
; Sequence 33, Application US/08353400
; Patent No. 5665357
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/353,400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 445 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-353-400-33

Query Match 30.1%; Score 1059.5; DB 1; Length 445;
Best Local Similarity 37.5%; Pred. No. 4.1e-63;
Matches 250; Conservative 61; Mismatches 107; Indels 249; Gaps 14;

QY 1 EYVLOQSGPDLYKPGASVKISKASGYSTGYMHWVKQSPKGLIEWIRPNNGVTLY 60
DB 1 QYVLOQPGAEVLYKPGASVQLSKASGYTFTGYTHWVKQSPKGLIEWIRPNNGVTLY 60
QY 61 NQKFKDKATLTVDKSSTTAYMELRLSTSEDSAVYYCARSTMI-TNYVMYMGQGTSTVTS 119
DB 61 NEKFKDKATLTVDKSSTTAYMQLSSLTSEDSAVYYCARAYGYDDAMDYMGQGTSTVTS 120
QY 120 SAKTTPPSVYPLAPGSAQTNSMTVLGCLVKGYPPEPTVTWNSGLSSGHTTFAVLQS 179
DB 121 SAKTTPPSVYPLAPGSAQTNSMTVLGCLVKGYPPEPTVTWNSGLSSGHTTFAVLQS 180
QY 180 DLYTLSSSVTPSPSTWPSSETVTCNVHPASSTKVDKXIVPRDSGGPSEKSEINEKDLRK 239
DB 181 DLYTLSSSVTPSPSTWPSSETVTCNVHPASSTKVDKXIVPRDCG----- 224
QY 240 KSELOQTALGNLKOIYYNSKAITSEKSDAQLTWLLFKGFTTGHWPWYNDLLVDLGS 299
DB 225 -CKPICITVPEVSSVFIPPK-----PKDVLITL----- 253
QY 300 AATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKYPINLWIDGK 359
DB 254 -----TP-KVTCVVVDIS-----KDDPEVQFSWFVD-- 278
QY 360 QTTVPIDKVTSEKVTQVELDLOARHYLHGK-FGL-YNSDSFGKVGQGLIV 410
DB 279 --DVEVHTAQTPREEQFNSTFRSVSELPINHQDWLNGKFKCRVNSAAFPAPIEK--- 332
QY 411 FHSSEGSTVSVDLFDAGQGPDTLLRIYRDNNTISSTLSISLYLTTISVMTQTPTSL 470
DB 333 -----TISK----- 337
QY 471 VSAGDRAVTITTCASQSVNDVAWYQKQKQSPKLLISYTSRYAGVPDRFSGSGYGTDT 530
DB 338 ----- 337
QY 531 LTISVQAEADAAYFCQDDYNSPPTFGGQTKLEIKRADAAPTIVSIFPSSSQTSGGASV 590
DB 338 -----KGRPKAPQVYVITPPKQMAKDKVSL 363
QY 591 VCFLLNFKPDINVKWKIDGSEKQNGVNSWTDDQSKDSTYSMSSTLTTLTKDEYERHNSY 650
DB 364 TCMITDFFPDTVQWNGQPAEN-YKNTQPIMDT-DGSYFVYSKLVNQSINWEAGNTF 421
QY 651 TCEATHK 657
DB 422 TCSVLHE 428

RESULT 15
US-08-353-400-36
```


EARLIER APPLICATION NUMBER: 07/416,530
 EARLIER FILING DATE: 1989-10-03
 NUMBER OF SEQ ID NOS: 34
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 24
 LENGTH: 226
 TYPE: PRT
 ORGANISM: Staphylococcus aureus
 US-09-314-235-24

Query Match 29.5%; Score 1040; DB 4; Length 226;
 Best Local Similarity 85.2%; Pred. No. 3.4e-62;
 Matches 196; Conservative 13; Mismatches 17; Indels 4; Gaps 1;
 QY 229 SEEINEKDLRKSELSQGTALGNLQIYYNKAITSSEKSAQDLTNTLLFKGFTGHPW 288
 DB 1 SEEINEKDLRKSELSQGTALGNLQIYYNKAITSSEKSAQDLTNTLLFKGFTGHPW 60
 QY 289 YNDLLVLDGSTAATSEYEGSSVDLYGAYGYOCAGGTPNKACMYGGVTLHDNNRLTEEK 348
 DB 61 YNDLLVLDGSTAATSEYEGSSVDLYGAYGYOCAGGTPNKACMYGGVTLHDNNRLTEE- 119
 QY 349 KVPINLWIDGKQTTVPIDKVTSSKEVTQELDLQARHYLHGKFGLYNSDSFGGKVORGL 408
 DB 120 ---VAKWIDGKQTTVPIDKVTSSKEVTQELDLQARHYLHGKFGLYNSDSFGGKVORGL 176
 QY 409 IVFHSSEGSTVSVDLFDAGQYPTDLRIYRDNNTISSTLSISLYLYTT 458
 DB 177 IVFHSSEGSTVSVDLFDAGQYPTDLRIYRDNNTISSTLSISLYLYTT 226

RESULT 18
 US-09-485-737B-90
 ; Sequence 90, Application US/09485737B
 ; Patent No. 6350860
 ; GENERAL INFORMATION:
 ; APPLICANT: Bayse, Marie-Ange
 ; APPLICANT: Sablon, Edwin
 ; TITLE OF INVENTION: INTERPERON-GAMMA-BINDING MOLECULES FOR TREATING SEPTIC SHOCK,
 ; FILE REFERENCE: INNS:015
 ; CURRENT APPLICATION NUMBER: US/09/485,737B
 ; CURRENT FILING DATE: 2000-02-14
 ; PRIOR APPLICATION NUMBER: PCT/EP 98/05165
 ; PRIOR FILING DATE: 1998-08-14
 ; PRIOR APPLICATION NUMBER: EPO 98870139.7
 ; PRIOR FILING DATE: 1998-06-18
 ; PRIOR APPLICATION NUMBER: EPO 97870122.5
 ; PRIOR FILING DATE: 1997-08-18
 ; NUMBER OF SEQ ID NOS: 104
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 90
 ; LENGTH: 711
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: SYNTHETIC
 US-09-485-737B-90

Query Match 27.8%; Score 980.5; DB 4; Length 711;
 Best Local Similarity 35.3%; Pred. No. 1.4e-57;
 Matches 254; Conservative 103; Mismatches 180; Indels 183; Gaps 23;
 QY 1 BVQLQQSQDPLVKPGASVKISKASGYSFTGYNMHWKQSPGKLEWIGRINPNNGVTLY 60
 DB 21 QVQLVQSGSELKPKGASVKISKASGYSFTGYNMHWKQSPGKLEWIGRINPNNGVTLY 80
 QY 61 NQKFKDKATLVDSKSTAYNELSLTSEDSAVTYCARSTWITNYVDYWGQGTSTVVS 120
 DB 81 VDDFKGKRVFSLDTSVSAAYLQISLKAEDTATYFCARRGF---YAMDYWGQGTSTVVS 137
 QY 121 AKTTPPSVYPLAPGASAAQTNSMVTGLCLVKYGFPPEVPTVTVNSGSLSSGVTHTTFAVLQSD 180

DB 138 ASTKGPSVFPLAPSSKSTSGGTAALGLCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 197
 QY 181 -LYTLSSSVTPSPSTWPESTVTCNVAHPASSTKVDKKIIPRDS-----GG 224
 DB 198 GLYSLSVVTVFSSSLGTQTYICNVNHPKSTKVDKRVPEKSCDKTHTCPCPAPPELLGG 257
 QY 225 PS-----EKSEEI-----NEKDLRKSELSQGTALGNLQIYYNKAITSSEKSAQDLTNTLLFKGFTGHPW 288
 DB 258 PSVFLFPPPKDPTLMISRTPEVTVVVDVSHEDPEVKFNWYVDGVEVHNATKPKREEQYN 317
 QY 259 S-----KAITSS-EK-----SADQ 271
 DB 318 STYRVSVLVTVLHQWLNGKVKYKSNKALPASIEKTIISKAKGQRPQVPTLPPSREE 377
 QY 272 FLTN-----TLLEKFGFTGHPWINDLLVDLGSTA-ATSEYEGSS--VDLYGAYGYOCAGG 324
 DB 378 MTKNQVSLTCLVKGFV-----SDIAVEWESNGQPNKYKTPPVLDSDGSGFFLYSKL-- 430
 QY 325 TENKACMYGGV-----TLHD--NNRLTEEK-----KVPINLWIDGKQTTVPIDKY 368
 DB 431 TVDKSRWQCGNVFSCVMHEALHNHYTOKSLSPKLGSGSQVQLVQSGSELKPKGASV 490
 QY 369 KTSKKEVTQELDLQARHYLHGKFGLYNSDSFGGKVORGLIVFHSSEGSTVSVDLFDAGQ 428
 DB 491 KISK-----ASGYTFDYGCMWVKQAPGGGLKMWGWINITYGTESTVVD--DFKG 538
 QY 429 QPDTLLRIYRDNNTISSTLSIS-----LYLT----- 457
 DB 539 RF-----VFLSDTSVSAAYLQISLKAEDTATYFCARRGFYAMDYWGQGTSTVTVSSGGG 592
 QY 458 -----TSIVMTOTPTSLYSAGDRVTITCKASQSVSNVDVAMVYQKPGQSPKLLI 506
 DB 593 GSGGSGSGSGGSDIVLTQSPATMSASPERVTLTCSASSISY-MFWYHQRPGQSPRLII 651
 QY 507 SYTSRYAGVPRFSGSGYGTFTLTISVQAEDAAVYFCQDYNPSPTFGGKLEIKR 566
 DB 652 YDTSNLAGVPARFSGSGSTSYSLTISRMPEDEPATYFCHQSSGSPPTFGGKLEIKR 711

RESULT 19
 US-08-116-247-7
 ; Sequence 7, Application US/08116247
 ; Patent No. 5929212
 ; GENERAL INFORMATION:
 ; APPLICANT: Jolliffe, Linda K.
 ; APPLICANT: Zivin, Robert A.
 ; APPLICANT: Adair, John R.
 ; APPLICANT: Achwal, Diljeet S.
 ; TITLE OF INVENTION: CD3 Specific Recombinant Antibody
 ; NUMBER OF SEQUENCES: 29
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Woodcock Wasburn Kurtz Mackiewicz & No. 5929212ris
 ; STREET: One Liberty Place - 46th Floor
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/116,247
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 07/743,377
 ; FILING DATE: 10-OCT-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Paintin, Francis A.
 ; REGISTRATION NUMBER: 19,386
 ; REFERENCE/DOCKET NUMBER: CARP-0011

QY 301 ATSEYEGSSVDLYGAYYGOCAGTGNKATCMYGVTLHDNNRLTEBKKVPINLWIDGKQ 360
Db 247 -----PCKCPAEN-----LLGSPSVF----- 262
QY 361 TTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDPSGGKVQGLIVFHSSEGSTVS 420
Db 263 -----IPPKIKDVLMI-----SUSPIVT 281
QY 421 YDLFDAQGVYPTLLRIYRDNNTTSSLSISLYTTSIVMTQTPTSLLSAGDRVTIT 480
Db 282 CVVVDVSEDDP-----VQISFVANVEVHTAQOT----- 312
QY 481 CKASQSVNDVANYQKFGSPKLLISYSSRAGVDRFSGSGYGTDTLLTSSVQARD 540
Db 313 -----HREDYNLSLRV----- 324
QY 541 AAVYFQOQDYNPPTFGGTGKLEIKRAD-----AAPTIVSIPPSSEQLT 584
Db 325 SALPIQHQMWSGKEP-----KCKVNNKDLPAPIERTISKPGSVRAPQVYVLPPEEEMT 380
QY 585 SGGASVVCFLNNYPKDINVKWIDGSERON-----GVLSNWTDDQSKDSTYSMSLTTL 639
Db 381 KKQVTLTCMVTDMPEDIVYEWMTNNGKTELNYKNTFVLDS-----DGSYFMYSKLRV 433
QY 640 TKDEYERHNSYTCETHK-TSTSPIVKSENR 669
Db 434 EKWVWERNYSYCVVHGLNHHHTTKSPSR 464

RESULT 23
PCT-US94-14106-51
; Sequence 51, Application PC/TUS9414106
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Process for Generating Specific Antibodies
; NUMBER OF SEQUENCES: 61
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 223 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-14106-51
Query Match 27.1%; Score 953.5; DB 5; Length 223;
Best Local Similarity 83.0%; Pred. No. 2e-56;
Matches 185; Conservative 12; Mismatches 23; Indels 3; Gaps 2;
QY 1 EVOLQSGPDLVKPGASVAKISKASGYFTGYMHVWKSPGKLEWIGRINPNNGVTLY 60
Db 1 EVOLQSGPELWMPGASVKISKATGYTLSSYWLWVKSPGHEWIGLISILFGSGSAHY 60
QY 61 NQFKDKAILTVDKSSTTAYMELRSLTSDSAVYCARSTMTINY--VMDYWGQGSTVTV 118
Db 61 NEKFKGATFTVDTSSNTAYMQLSLTSBDSAIVYCARGD-YGNYGDYDYGQGTTLTV 119
QY 119 SSAKTTTPPSVYPLAPGSAQTNSMVTGLGVKGFPEPVTVTWNSGSLSSGVHTTFAVLQ 178
Db 120 SSAKTTTPPSVYPLAPGSAQTNSMVTGLGVKGFPEPVTVTWNSGSLSSGVHTTFAVLQ 179
QY 179 SDLYTLSSSVYTPSSWPSETVTCNVAHPASSTKVDKIVPRD 221
Db 180 SDLYTLSSSVYTPSSWPSETVTCNVAHPASSTKVDKIVPRD 222

RESULT 24

US-08-695-692B-7
; Sequence 7, Application US/08695692B
; Patent No. 6514498
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlisten,
; APPLICANT: Johan Hansson, Terje Kalland, Lars
; APPLICANT: Abrahamson and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; TITLE OF INVENTION: AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,692B
; FILING DATE: August 12, 1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9601245-5
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 41986/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-695-692B-7

Query Match 26.9%; Score 948; DB 4; Length 233;
Best Local Similarity 76.4%; Pred. No. 5e-56;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
QY 226 SEKSEENEKDLRKSELOQTALGNLKOIYYVNSKAITSSSEKSDQFLTNTLLFKGFTG 285
Db 1 SEKSEENEKDLRKSELOQTALGNLKOIYYVNSKAITSSSEKSDQFLTNTLLFKGFTG 60
QY 286 HPWYNDLLVLGSTAATSEYEGSSVDLYGAYYGOCAGTGNKATCMYGVTLHDNNRLT 345
Db 61 HSWYNDLLVDPDSKDIDVKYKKVDLYGAYYGOCAGTGNKATCMYGVTLHDNNRLT 120
QY 346 BEKKVPINLWIDGQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDPSGGKVQ 405
Db 121 BEKKVPINLWIDGQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDPSGGKVQ 180
QY 406 RGLIVFHSSEGSTVSVDLFDQAQGVYPTLLRIYRDNNTTSSLSISLYT 458
Db 181 RGLIVFHSSEGSTVSVDLFDQAQGVYPTLLRIYRDNNTTSSLSISLYT 233
RESULT 25
US-08-486-099-113
; Sequence 113, Application US/08486099
; Patent No. 6013263
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.

APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS B VIRUS TRANSMISSION
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/486,099
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-486-099-113

Query Match 26.9%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 5.7e-56;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKXSEIQGTALGNLKOIYYNSKAITSSSEKSAQDQFLNTLLFKGFTG 285
DB 25 SEKSEINEKDLRKXSEIQGTALGNLKOIYYNEKAKTENKESHQDQFLQHTILFKGFTD 84

QY 286 HPWYNDLLVDLGSATSEYEGSSVDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLT 345
DB 85 HSWYNDLLVDFSKDIDVKYKGGKVDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLT 144

QY 346 BEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGGKVQ 405
DB 145 BEKKVPINLWDGKQTTVPLETVKTKNKQNTVQELDLQARHYLQEKYLYNSDVFDCQVQ 204

QY 406 RGLIVFHSSEGSTSVSYDLFDAGQYPTDLRIYRDNNTTISSTLSISLYLTT 458
DB 205 RGLIVFHTSTEPSVNYDLFGAGQYNTLLRIYRDNKNTINSENMHIDIYLYTS 257

RESULT 26
US-08-360-107A-123
Sequence 123, Application US/08360107A
Patent No. 6017536
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.

APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/360,107A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-360-107A-123

Query Match 26.9%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 5.7e-56;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKXSEIQGTALGNLKOIYYNSKAITSSSEKSAQDQFLNTLLFKGFTG 285
DB 25 SEKSEINEKDLRKXSEIQGTALGNLKOIYYNEKAKTENKESHQDQFLQHTILFKGFTD 84

QY 286 HPWYNDLLVDLGSATSEYEGSSVDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLT 345
DB 85 HSWYNDLLVDFSKDIDVKYKGGKVDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLT 144

QY 346 BEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGGKVQ 405
DB 145 BEKKVPINLWDGKQTTVPLETVKTKNKQNTVQELDLQARHYLQEKYLYNSDVFDCQVQ 204

QY 406 RGLIVFHSSEGSTSVSYDLFDAGQYPTDLRIYRDNNTTISSTLSISLYLTT 458
DB 205 RGLIVFHTSTEPSVNYDLFGAGQYNTLLRIYRDNKNTINSENMHIDIYLYTS 257

RESULT 27
US-08-484-223B-113
Sequence 113, Application US/08484223B
Patent No. 6020459
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.

```
;/ TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
;/ TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
;/ TITLE OF INVENTION: TRANSMISSION
;/ NUMBER OF SEQUENCES: 245
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Pennie & Edmonds LLP
;/ STREET: 1155 Avenue of the Americas
;/ CITY: New York
;/ STATE: New York
;/ COUNTRY: USA
;/ ZIP: 10036-2711
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: Patent in Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/484,223B
;/ FILING DATE: 07-JUN-1995
;/ CLASSIFICATION: 435
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Coruzzi, Laura A.
;/ REGISTRATION NUMBER: 30,742
;/ REFERENCE/DOCKET NUMBER: 7872-023
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (212) 790-9090
;/ TELEFAX: (212) 869-9741/8864
;/ TELEX: 66141 PENNIE
;/ INFORMATION FOR SEQ ID NO: 113:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 257 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS:
;/ TOPOLOGY: unknown
;/ MOLECULE TYPE: protein
;/ US-08-484-223B-113

Query Match 26.9%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 5.7e-56;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKQIYYNKAITSSEKSAOFLNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLKQIYYNEKAKTENKESHDFLQHTILFKGFFTD 84
QY 286 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYOCAGGTPNKTCACMYGGVTLHNNRLT 345
Db 85 HSWYNDLLVDFDSKDIYDKYKGVKVDLYGAYGYOCAGGTPNKTCACMYGGVTLHNNRLT 144
QY 346 BEKKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 BEKKVPINLWIDGKQNTVPLETVKTNKKNVTVOELDLQARRYLQEKYLYNSDSVFDGKVQ 204
QY 406 RGLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNTTISSTLSLSLYLTT 458
Db 205 RGLIVFHTSTEPSVNYDLFGAQGOYSNTLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 28
US-08-919-597-113
; Sequence 113, Application US/08919597
; Patent No. 6054265
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
```

```
;/ NUMBER OF SEQUENCES: 273
;/ CORRESPONDENCE ADDRESS:
;/ ADDRESSEE: Pennie & Edmonds
;/ STREET: 1155 Avenue of the Americas
;/ CITY: New York
;/ STATE: New York
;/ COUNTRY: USA
;/ ZIP: 10036-2711
;/ COMPUTER READABLE FORM:
;/ MEDIUM TYPE: Floppy disk
;/ COMPUTER: IBM PC compatible
;/ OPERATING SYSTEM: PC-DOS/MS-DOS
;/ SOFTWARE: Patent in Release #1.0, Version #1.30
;/ CURRENT APPLICATION DATA:
;/ APPLICATION NUMBER: US/08/919,597
;/ FILING DATE:
;/ CLASSIFICATION:
;/ PRIOR APPLICATION DATA:
;/ APPLICATION NUMBER: US 08/470,896
;/ FILING DATE: 06-JUN-1995
;/ ATTORNEY/AGENT INFORMATION:
;/ NAME: Coruzzi, Laura A.
;/ REGISTRATION NUMBER: 30,742
;/ REFERENCE/DOCKET NUMBER: 7872-020
;/ TELECOMMUNICATION INFORMATION:
;/ TELEPHONE: (212) 790-9090
;/ TELEFAX: (212) 869-9741/8864
;/ TELEX: 66141 PENNIE
;/ INFORMATION FOR SEQ ID NO: 113:
;/ SEQUENCE CHARACTERISTICS:
;/ LENGTH: 257 amino acids
;/ TYPE: amino acid
;/ STRANDEDNESS:
;/ TOPOLOGY: unknown
;/ MOLECULE TYPE: protein
;/ US-08-919-597-113

Query Match 26.9%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 5.7e-56;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKQIYYNKAITSSEKSAOFLNTLLFKGFFTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLKQIYYNEKAKTENKESHDFLQHTILFKGFFTD 84
QY 286 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYOCAGGTPNKTCACMYGGVTLHNNRLT 345
Db 85 HSWYNDLLVDFDSKDIYDKYKGVKVDLYGAYGYOCAGGTPNKTCACMYGGVTLHNNRLT 144
QY 346 BEKKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 BEKKVPINLWIDGKQNTVPLETVKTNKKNVTVOELDLQARRYLQEKYLYNSDSVFDGKVQ 204
QY 406 RGLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNTTISSTLSLSLYLTT 458
Db 205 RGLIVFHTSTEPSVNYDLFGAQGOYSNTLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 29
US-08-475-668A-113
; Sequence 113, Application US/08475668A
; Patent No. 6060065
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
```

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US/08/475.668A
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-026
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-475-668A-113

Query Match 26.9%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 5.7e-56;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSEKSDQFLNTLLFKGFTG 285
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESHDFLOHTILFKGFTD 84
QY 286 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTENKTCMYGGVTLHNNRLT 345
DB 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTENKTCMYGGVTLHNNRLT 144
QY 346 BEKKVPINLWDGKQTTPIDKVTSKKEVTVOELDLQARHLYHGKGLYNSDSFGKVKQ 405
DB 145 BEKKVPINLWDGKQNTVPLETVTKNKNVTVOELDLQARHLYHGKGLYNSDSFGKVKQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPDTLRLIYRDNTTISSTLSISLYLYTT 458
DB 205 RGLIVFHTSTEPSVNYDLFGAGQGYNTLLRIYRDNKTINSENHMDIYLYTS 257

RESULT 30
US-08-485-551A-113
Sequence 113, Application US/08485551A
Patent No. 6068973
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Pettaway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA

ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US/08/485.551A
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-551A-113

Query Match 26.9%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 5.7e-56;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSEKSDQFLNTLLFKGFTG 285
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESHDFLOHTILFKGFTD 84
QY 286 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTENKTCMYGGVTLHNNRLT 345
DB 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTENKTCMYGGVTLHNNRLT 144
QY 346 BEKKVPINLWDGKQTTPIDKVTSKKEVTVOELDLQARHLYHGKGLYNSDSFGKVKQ 405
DB 145 BEKKVPINLWDGKQNTVPLETVTKNKNVTVOELDLQARHLYHGKGLYNSDSFGKVKQ 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPDTLRLIYRDNTTISSTLSISLYLYTT 458
DB 205 RGLIVFHTSTEPSVNYDLFGAGQGYNTLLRIYRDNKTINSENHMDIYLYTS 257

RESULT 31
US-08-471-913A-113
Sequence 113, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Pettaway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

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/
/
/   COMPUTER: IBM PC compatible
/   OPERATING SYSTEM: PC-DOS/MS-DOS
/   SOFTWARE: PatentIn Release #1.0, Version #1.30
/   CURRENT APPLICATION DATA:
/   APPLICATION NUMBER: US/08/471,913A
/   FILING DATE: 07-JUN-1995
/   CLASSIFICATION: 435
/   ATTORNEY/AGENT INFORMATION:
/   NAME: Coruzzi, Laura A.
/   REGISTRATION NUMBER: 30,742
/   REFERENCE/DOCKET NUMBER: 7872-030
/   TELECOMMUNICATION INFORMATION:
/   TELEPHONE: (212) 790-9090
/   TELEFAX: (212) 869-9741/8864
/   TELEX: 66141 PENNIE
/   INFORMATION FOR SEQ ID NO: 113:
/   SEQUENCE CHARACTERISTICS:
/   LENGTH: 257 amino acids
/   TYPE: amino acid
/   STRANDEDNESS:
/   TOPOLOGY: unknown
/   MOLECULE TYPE: Protein
/   US-08-471-913A-113

Query Match      26.9%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 5.7e-56;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKQIYYNYSKAITSEKSDQFLNTLLFKGFTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLKQIYYNEKAKTENKESHDFLOHTILFKGFTD 84
QY 286 HPWNLLVLDLSTAAITSEYEGSSVDLYGAYGYQCAGGTPNKTCMVGTVLHNNRLT 345
Db 85 HSWNLLVDFDSKDIVDKYKGVKVDLYGAYGYQCAGGTPNKTCMVGTVLHNNRLT 144
QY 346 EEKVPINLWIDGQTTVPIDKVTSKKEVTQELDQARHYLHGKFGLYNSDSFGKQV 405
Db 145 EEKVPINLWLDGKQNTVPLETVTKNKXNVTVQELDQARRYLQEKYLYNSDVFQKQV 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYTT 458
Db 205 RGLIVFHTSTEPSVNDLFDAGQGYNTLLRIYRDNTKNTSENHNDIYLYTS 257

RESULT 32
US-08-485-264A-113
; Sequence 113, Application US/08485264A
; Patent No. 6228983
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

/
/
/   COMPUTER: IBM PC compatible
/   OPERATING SYSTEM: PC-DOS/MS-DOS
/   SOFTWARE: PatentIn Release #1.0, Version #1.30
/   CURRENT APPLICATION DATA:
/   APPLICATION NUMBER: US/08/485,264A
/   FILING DATE: 07-JUN-1995
/   CLASSIFICATION: 435
/   ATTORNEY/AGENT INFORMATION:
/   NAME: Coruzzi, Laura A.
/   REGISTRATION NUMBER: 30,742
/   REFERENCE/DOCKET NUMBER: 7872-021
/   TELECOMMUNICATION INFORMATION:
/   TELEPHONE: (212) 790-9090
/   TELEFAX: (212) 869-9741/8864
/   TELEX: 66141 PENNIE
/   INFORMATION FOR SEQ ID NO: 113:
/   SEQUENCE CHARACTERISTICS:
/   LENGTH: 257 amino acids
/   TYPE: amino acid
/   STRANDEDNESS:
/   TOPOLOGY: unknown
/   MOLECULE TYPE: protein
/   US-08-485-264A-113

Query Match      26.9%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 5.7e-56;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOQTALGNLKQIYYNYSKAITSEKSDQFLNTLLFKGFTG 285
Db 25 SEKSEINEKDLRKSELOQTALGNLKQIYYNEKAKTENKESHDFLOHTILFKGFTD 84
QY 286 HPWNLLVLDLSTAAITSEYEGSSVDLYGAYGYQCAGGTPNKTCMVGTVLHNNRLT 345
Db 85 HSWNLLVDFDSKDIVDKYKGVKVDLYGAYGYQCAGGTPNKTCMVGTVLHNNRLT 144
QY 346 EEKVPINLWIDGQTTVPIDKVTSKKEVTQELDQARHYLHGKFGLYNSDSFGKQV 405
Db 145 EEKVPINLWLDGKQNTVPLETVTKNKXNVTVQELDQARRYLQEKYLYNSDVFQKQV 204
QY 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYTT 458
Db 205 RGLIVFHTSTEPSVNDLFDAGQGYNTLLRIYRDNTKNTSENHNDIYLYTS 257

RESULT 33
US-08-474-349A-113
; Sequence 113, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
; TITLE OF INVENTION: VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
```

```
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-474-349A-113

Query Match      26.9%; Score 948; DB 4; Length 257;
Best Local Similarity 76.4%; Pred. No. 5.7e-56;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEEEINEKDLRKSELOGTALGNLKOIYYNSKAITSEKSDAQPLTNTLLFKGFFTG 285
Db 25 SEKSEEEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESHDOFLQHTILFKGFFTD 84
QY 286 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYOCAGGTPNKTCACMYGGVTLHDNNRLT 345
Db 85 HSWYNDLLVDFDSKDIDVYKYGKVDLYGAYGYOCAGGTPNKTCACMYGGVTLHDNNRLT 144
QY 346 BEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 BEKVPINLWLDGKQNTVPLETVTKNKNVTVOELDLQARRYLOEKYNLYNSDVFDDGVQ 204
QY 406 RGLIVFHSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYLYTT 458
Db 205 RGLIVFHTSTEPSVNYDLFGAQQGYNSLTLRIYRDNTKINSNMHIDIYLYTS 257

RESULT 34
US-08-470-896-113
Sequence 113, Application US/08470896
Patent No. 6479055
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,896
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
```

```
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-896-113

Query Match      26.9%; Score 948; DB 4; Length 257;
Best Local Similarity 76.4%; Pred. No. 5.7e-56;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEEEINEKDLRKSELOGTALGNLKOIYYNSKAITSEKSDAQPLTNTLLFKGFFTG 285
Db 25 SEKSEEEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESHDOFLQHTILFKGFFTD 84
QY 286 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYOCAGGTPNKTCACMYGGVTLHDNNRLT 345
Db 85 HSWYNDLLVDFDSKDIDVYKYGKVDLYGAYGYOCAGGTPNKTCACMYGGVTLHDNNRLT 144
QY 346 BEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
Db 145 BEKVPINLWLDGKQNTVPLETVTKNKNVTVOELDLQARRYLOEKYNLYNSDVFDDGVQ 204
QY 406 RGLIVFHSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYLYTT 458
Db 205 RGLIVFHTSTEPSVNYDLFGAQQGYNSLTLRIYRDNTKINSNMHIDIYLYTS 257

RESULT 35
US-08-485-546A-113
Sequence 113, Application US/08485546A
Patent No. 6518013
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,546A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-028
TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-546A-113

Query Match 26.8%; Score 948; DB 4; Length 257;
Best Local Similarity 76.4%; Pred. No. 5.7e-56;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSADOFNTLLFKGFFTG 285
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESHDFLOHTILFKGFFTD 84

QY 286 HPWNLLVDLGSTAATSEYSSVDLYGAYGYQCAGTTPNKATCMYGGVTLHDNNRLT 345
DB 85 HSWNDLLVDFSDKOIVDKYKGGKVDLYGAYGYQCAGTTPNKATCMYGGVTLHDNNRLT 144

QY 345 EEKVPINLWIDGKOTVPIDKVTSKKEVTVOELDLQARHLYHGKFLYNSDSFGKVQ 405
DB 145 EEKVPINLWIDGKQNTVLETVKTNKNVTVQELDLQARRYLQEKYINLYNSDVFQKVQ 204

QY 406 RGLIVFHSSEGSVSYDLDAQQYPTDLLRIYRDNTTSSLSLSLYTT 458
DB 205 RGLIVFHTSTPSVNYDLFGAQQSYNTLLRIYRDNTKINSENHIDILYTS 257

RESULT 36
US-08-353-400-37
Sequence 37, Application US/08353400
Patent No. 5665357
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 37
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/353,400
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9324819.3
FILING DATE: 03-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9411089.7
FILING DATE: 03-JUN-1994
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-353-400-37

Query Match 26.8%; Score 944.5; DB 1; Length 239;
Best Local Similarity 78.1%; Pred. No. 8.9e-56;
Matches 185; Conservative 22; Mismatches 19; Indels 11; Gaps 3;

QY 445 SSTSLSISLYTT-----SIVMTQPTSLVSAGDRVTITCKASQSVND-----VAVY 494
DB 3 SQAQVILLILLWVGTCGDIWVSQSPSSLAVSAGEKVTMSCKSSQLNSRTRKYLAWY 62

QY 495 QQKPGQPKLLISYTSRYAGVDRFSGSGYGTDTLTITSSVQAEDAAYFCQDYNSPP 554
DB 63 QQRPGQPKLLIYWASTRTSGVDRFSGSGGTDTLTITSSVQAEDLAIYCKQSY-TLR 121

QY 555 TFGGKTLEIKRADAAFTVSIFPPSSBQLTSGGASVVCFLNFPKPDINVKWKIDGSRQ 614
DB 122 TFGGKTLEIKRADAAFTVSIFPPSSBQLTSGGASVVCFLNFPKPDINVKWKIDGSRQ 181

QY 615 NGVLSNWTDDQSKDSTYSMSSTLTLTDKDEYERHNSYTCETHKTSTSPIVKSFNRNE 671
DB 182 NGVLSNWTDDQSKDSTYSMSSTLTLTDKDEYERHNSYTCETHKTSTSPIVKSFNRNE 238

RESULT 37
US-08-446-918A-4
Sequence 4, Application US/08446918A
Patent No. 5705151
GENERAL INFORMATION:
APPLICANT: Dow, Steve W.
APPLICANT: Elmslie, Robyn E.
TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,918A
FILING DATE: 18-MAY-1995
CLASSIFICATION: 552
ATTORNEY/AGENT INFORMATION:
NAME: Kovarik, Joseph E.
REGISTRATION NUMBER: 33,005
REFERENCE/DOCKET NUMBER: 2879-29
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-446-918A-4

Query Match 26.8%; Score 944; DB 1; Length 233;
Best Local Similarity 76.3%; Pred. No. 9.3e-56;
Matches 177; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 227 EKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSADOFNTLLFKGFFTG 286
DB 2 EKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESHDFLOHTILFKGFFTDH 61

QY 287 FWYNDLLVDLGSTAATSEYSSVDLYGAYGYQCAGTTPNKATCMYGGVTLHDNNRLTE 346
DB 62 SWYNDLLVDFSDKOIVDKYKGGKVDLYGAYGYQCAGTTPNKATCMYGGVTLHDNNRLTE 121

QY 347 EKKVPINLWIDGKOTVPIDKVTSKKEVTVOELDLQARHLYHGKFLYNSDSFGKVQ 406
DB 122 EKKVPINLWIDGKQNTVLETVKTNKNVTVQELDLQARRYLQEKYINLYNSDVFQKVQ 181

QY 407 GLIVFHSSEGSVSYDLDAQQYPTDLLRIYRDNTTSSLSLSLYTT 458
DB 182 GLIVFHTSTPSVNYDLFGAQQSYNTLLRIYRDNTKINSENHIDILYTS 233

RESULT 38
US-08-580-806-4
; Sequence 4, Application US/08580806
; Patent No. 5935568
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmslie, Robyn E.
; APPLICANT: Potter, Terence A.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,806
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-29-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-580-806-4

Query Match 26.8%; Score 944; DB 2; Length 233;
Best Local Similarity 76.3%; Pred. No. 9,3e-56;
Matches 177; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
QY 227 EKSEINEKDLRKSELQGTALGNLQIYYNNSKATTSSEKSDAQFLNTLLFKGFTGH 286
Db 2 EKSEINEKDLRKSELQGTALGNLQIYYNNSKATTSSEKSDAQFLNTLLFKGFTGH 61
QY 287 PWYNDLLVDLSTAASTSEYSGSSVDLYCAVYGCAGTGNKTCMYGGVTLHDNNRLTE 346
Db 62 SWYNDLLVDFDSKDIYDKYKGVLDLYGAYGYCAGTGNKTCMYGGVTLHDNNRLTE 121
QY 347 EKKVPINLWIDKQTTVPIDKVTISKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQVOR 406
Db 122 EKKVPINLWIDKQNTVLETKINKNVTYQELDLQARHYLQEKYLYNSDVFQKQVOR 181
QY 407 GLIVFHSSEGVTSVDLFDAGQVPTLLRLRYRNTTISSTLSLSLYLT 458
Db 182 GLIVFHTSPSVNVDLFGAGQVSNLTLLRIYRDKNTINSENHDIYLYTS 233

RESULT 39
US-08-353-400-34
; Sequence 34, Application US/08353400
; Patent No. 5665357
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PROTEINS
; NUMBER OF SEQUENCES: 37
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/353,400
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9324819.3
; FILING DATE: 03-DEC-1993
; PRIOR APPLICATION NUMBER: GB 9411089.7
; FILING DATE: 03-JUN-1994
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 219 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-353-400-34
Query Match 26.7%; Score 941.5; DB 1; Length 219;
Best Local Similarity 83.0%; Pred. No. 1.3e-55;
Matches 181; Conservative 19; Mismatches 11; Indels 7; Gaps 2;
QY 460 IVWTOTPTSLVSGADRVITTCASQSVND-----VAVYQKPGQSPKLLISYTSRY 513
Db 2 IVWSQSPSSLAVSAGEKVTMSCKSSLLNSRTRKNYLAWYQORPGQSPKLLIYNASTRT 61
QY 514 AGVPDRFSGSGYGTDTLTITSSVQAEAAVYFCQDYNSPTFGGKTKLEIKRADAAPT 573
Db 62 SGVPDRFSGSGYGTDTLTITSSVQAEAAVYFCQDYNSPTFGGKTKLEIKRADAAPT 120
QY 574 SIFFPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSEKQNGVLSNWTQDQSKDSTYSM 633
Db 121 SIFFPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSEKQNGVLSNWTQDQSKDSTYSM 180
QY 634 SSTLTLTDKEXERHNSYTCETHKTSTSPIVKSENRNE 671
Db 181 SSTLTLTDKEXERHNSYTCETHKTSTSPIVKSENRNE 218
RESULT 40
US-08-737-129A-5
; Sequence 6, Application US/08737129A
; Patent No. 5885816
; GENERAL INFORMATION:
; APPLICANT: Ikao FUJII et al.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY
; TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,129A
; FILING DATE: No. 5885816member 15, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.

REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 222 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-737-129A-6

Query Match 26.5%; Score 933; DB 2; Length 232;
Best Local Similarity 82.6%; Pred. No. 4.7e-55;
Matches 180; Conservative 12; Mismatches 24; Indels 2; Gaps 1;

QY 6 QSGPDLVKQASVKISKCKASGYFTGYMHVWVKQSPGKLEWIGRINPNNGVTLNKKPK 65
DB 2 ESGPELVKPGSVTISKASGYFTTSMWVVRQPGQGLEWIGRIYPGSGDNNYNGKPK 61

QY 66 DKATLTWKSSTAYMELSLTSEDGAVYYCAR--STMITNVMYDYGOGTSTVYSSAKT 123
DB 62 VKATLTARSSSTVYVHLSSLTSDVSAVFCARFHYDRSRVAMDWGGTSTVYSSAKT 121

QY 124 TSPSVYPLAPGSAQNSMTVLCGLVKGYFPEPTVTVWNSGSLSSGVHTFPVAVLQSDLYT 183
DB 122 TSPSVYPLAPGSAQNSMTVLCGLVKGYFPEPTVTVWNSGSLSSGVHTFPVAVLQSDLYT 181

QY 184 LSSSVTPSPSTWPESTVTCNVAPASSTKVKKIVPRD 221
DB 182 LSSSVTPSPSTWPESTVTCNVAPASSTKVKKIVPRD 219

RESULT 41
US-08-896-933-23
; Sequence 23, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-23

Query Match 26.4%; Score 931.5; DB 3; Length 232;
Best Local Similarity 76.0%; Pred. No. 6.3e-55;
Matches 177; Conservative 21; Mismatches 34; Indels 1; Gaps 1;

QY 226 SEKSEINEKDLRKSELOQTALGNLQIYYNSKAITSEKSADQFLTNLLFKGFFTG 285
DB 1 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHQFL-HTILFKGFFTD 59

QY 286 HPWYNDLLVDLGSTAATSEVSGSVLYGYGQACGTPNKTCMYGGVTLHNNRLT 345
DB 60 HSWYNDLLVDFDSKQIVDKYKGVLYGYGQACGTPNKTCMYGGVTLHNNRLT 119

QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFLYNSDSFGKVKQ 405
DB 120 EEKVPINLWLDGKQNTVPLETVTKNKNVTVOELDQARRYLQEKYLNLYNSDVFDGKVKQ 179

QY 406 RGLIVFHSSEGSTVSYDLFDAQQGYPTDILLRIYRDNTTISSTLSISLYLTT 458
DB 180 RGLIVFHTSTEPSVNYDLFGAQQGYNTLLRIYRDNTKNTINSENHMDIYLYTS 232

RESULT 42
US-09-314-235-23
; Sequence 23, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; EARLIER FILING DATE: 1999-05-18
; EARLIER FILING DATE: 1997-07-18
; EARLIER FILING DATE: 1994-06-02
; EARLIER FILING DATE: 1992-06-01
; EARLIER FILING DATE: 1991-04-17
; EARLIER FILING DATE: 1990-01-17
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-314-235-23

Query Match 26.4%; Score 931.5; DB 4; Length 232;
Best Local Similarity 76.0%; Pred. No. 6.3e-55;
Matches 177; Conservative 21; Mismatches 34; Indels 1; Gaps 1;

QY 226 SEKSEINEKDLRKSELOQTALGNLQIYYNSKAITSEKSADQFLTNLLFKGFFTG 285
DB 1 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHQFL-HTILFKGFFTD 59

QY 286 HPWYNDLLVDLGSTAATSEVSGSVLYGYGQACGTPNKTCMYGGVTLHNNRLT 345
DB 60 HSWYNDLLVDFDSKQIVDKYKGVLYGYGQACGTPNKTCMYGGVTLHNNRLT 119

QY 346 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFLYNSDSFGKVKQ 405
DB 120 EEKVPINLWLDGKQNTVPLETVTKNKNVTVOELDQARRYLQEKYLNLYNSDVFDGKVKQ 179

QY 406 RGLIVFHSSEGSTVSYDLFDAQQGYPTDILLRIYRDNTTISSTLSISLYLTT 458
DB 180 RGLIVFHTSTEPSVNYDLFGAQQGYNTLLRIYRDNTKNTINSENHMDIYLYTS 232

RESULT 43
US-09-144-776B-2
; Sequence 2, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army WPMC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)

```

; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-144-776B-2

Query Match 26.3%; Score 925; DB 4; Length 257;
Best Local Similarity 75.1%; Pred. No. 2e-54;
Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNYSKAITSEKSDAFLNTLLFKGPTG 285
Db 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNYSKAITSEKSDAFLNTLLFKGPTD 84
QY 286 HPYNDLLVLDGSTAATSEYEGSSVDLYGAYGYCCAGGTPNKTCMYGGVTLHDNNRLT 345
Db 85 HSYNDLLVLDGSTAATSEYEGSSVDLYGAYGYCCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 346 BEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLGYNLSDSFGKVQ 405
Db 145 BEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLGYNLSDSFGKVQ 204
QY 406 RGLIVFHTSTPFSVNYDLFDAQGQYPTLLRIYRDNTTISSTLSISLYTT 458
Db 205 RGLIVFHTSTPFSVNYDLFDAQGQYPTLLRIYRDNTTISSTLSISLYTT 257

RESULT 44
US-09-144-776B-4
; Sequence 4, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA

; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
;
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
;
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-144-776B-2

Query Match 26.3%; Score 925; DB 4; Length 257;
Best Local Similarity 75.1%; Pred. No. 2e-54;
Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;

QY 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNYSKAITSEKSDAFLNTLLFKGPTG 285
Db 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNYSKAITSEKSDAFLNTLLFKGPTD 84
QY 286 HPYNDLLVLDGSTAATSEYEGSSVDLYGAYGYCCAGGTPNKTCMYGGVTLHDNNRLT 345
Db 85 HSYNDLLVLDGSTAATSEYEGSSVDLYGAYGYCCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 346 BEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLGYNLSDSFGKVQ 405
Db 145 BEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLGYNLSDSFGKVQ 204
QY 406 RGLIVFHTSTPFSVNYDLFDAQGQYPTLLRIYRDNTTISSTLSISLYTT 458
Db 205 RGLIVFHTSTPFSVNYDLFDAQGQYPTLLRIYRDNTTISSTLSISLYTT 257

RESULT 44
US-08-792-824-10
; Sequence 10, Application US/08792824
; Patent No. 5932449
; GENERAL INFORMATION:
; APPLICANT: EMANUEL, PETER A.
; APPLICANT: BURANS, JAMES P.
; APPLICANT: VALDES, JAMES J.
; APPLICANT: MOHYER, ELDERAWI E.
; TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. Army Chemical and Biological Defense
; ADDRESS: Command
; STREET: Office of the Chief Counsel, Bldg E4435
; CITY: Aberdeen Proving Ground
; STATE: MD
; COUNTRY: U.S.
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,824
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Biffoni, U. J.
; REGISTRATION NUMBER: 39,908
; REFERENCE/DOCKET NUMBER: DAM 431-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 410-671-1158
; TELEFAX: 410-671-2534
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-792-824-10

```

```

Query Match          26.0%; Score 915.5; DB 2; Length 254;
Best Local Similarity 79.2%; Pred. No. 8.3e-54;
Matches 179; Conservative 15; Mismatches 27; Indels 5; Gaps 2;

QY 1 EVQLQSGPDLVKPGASVKISKASGYFTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 23 EVQLQSGAELVKPGASVKLSCTASGFIKDTFMHWVKQRPQGLEWIGRIDPANGNTEY 82
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NQKFKDKATLVDKSTTAYMELRSITSDSAVYICARSTMTINYMDYWGQGTSTVTS 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 DPKFGKATITADTSSNTVNLQSLTSEDTAVYICASGGELG---FPYWGQGTSLTVSA 139
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 AKTTPSVPLAPGSAQTNSMTVLCGLVKGFPEPVTVTWNSGSLSSGVHTFPVAVLQSD 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 140 AKTTPSVPLAPGSAQTNSMTVLCGLVKGFPEPVTVTWNSGSLSSGVHTFPVAVLQSD 199
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 181 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKVDDKIVPRD--SGG 224
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 200 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKVDDKIVPRDCTSGG 245
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

RESULT 46
US-08-792-824-13
; Sequence 13, Application US/08792824
; Patent No. 5932449
; GENERAL INFORMATION:
; APPLICANT: EMANUEL, PETER A.
; APPLICANT: BURANS, JAMES P.
; APPLICANT: VALDES, JAMES J.
; APPLICANT: MOHYEE, ELDEFRAWI E.
; TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. Army Chemical and Biological Defense
; ADDRESSEE: Command
; STREET: Office of the Chief Counsel, Bldg E4435
; CITY: Aberdeen Proving Ground
; STATE: MD
; COUNTRY: U.S.
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,824
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Biffoni, U. J.
; REGISTRATION NUMBER: 39,908

```

```

; REFERENCE/DOCKET NUMBER: DAM 431-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 410-671-1158
; TELEFAX: 410-671-2534
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-792-824-13

```

```

Query Match          26.0%; Score 915.5; DB 2; Length 254;
Best Local Similarity 79.2%; Pred. No. 8.3e-54;
Matches 179; Conservative 15; Mismatches 27; Indels 5; Gaps 2;

QY 1 EVQLQSGPDLVKPGASVKISKASGYFTGYMHVWKQSPGKLEWIGRINPNNGVTLY 60
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 23 EVQLQSGAELVKPGASVKLSCTASGFIKDTFMHWVKQRPQGLEWIGRIDPANGNTEY 82
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 61 NQKFKDKATLVDKSTTAYMELRSITSDSAVYICARSTMTINYMDYWGQGTSTVTS 120
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 83 DPKFGKATITADTSSNTVNLQSLTSEDTAVYICASGGELG---FPYWGQGTSLTVSA 139
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 121 AKTTPSVPLAPGSAQTNSMTVLCGLVKGFPEPVTVTWNSGSLSSGVHTFPVAVLQSD 180
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 140 AKTTPSVPLAPGSAQTNSMTVLCGLVKGFPEPVTVTWNSGSLSSGVHTFPVAVLQSD 199
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

QY 181 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKVDDKIVPRD--SGG 224
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 200 LYTSSSVTPSPSTWSPSETVTCNVAHPASSTKVDDKIVPRDCTSGG 245
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```

RESULT 47
US-08-792-824-4
; Sequence 4, Application US/08792824
; Patent No. 5932449
; GENERAL INFORMATION:
; APPLICANT: EMANUEL, PETER A.
; APPLICANT: BURANS, JAMES P.
; APPLICANT: VALDES, JAMES J.
; APPLICANT: MOHYEE, ELDEFRAWI E.
; TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. Army Chemical and Biological Defense
; ADDRESSEE: Command
; STREET: Office of the Chief Counsel, Bldg E4435
; CITY: Aberdeen Proving Ground
; STATE: MD
; COUNTRY: U.S.
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,824
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Biffoni, U. J.
; REGISTRATION NUMBER: 39,908
; REFERENCE/DOCKET NUMBER: DAM 431-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 410-671-1158
; TELEFAX: 410-671-2534
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

```

MOLECULE TYPE: protein
US-08-792-824-4
Query Match 25.8%; Score 909.5; DB 2; Length 254;
Best Local Similarity 78.8%; Pred. No. 2.1e-53;
Matches 178; Conservative 15; Mismatches 28; Indels 5; Gaps 2;
QY 1 EVQLQQSGPDLVKPGASVKISKASGYSFTGYHWHVKQSPGKLEWIGRINPNNGVTLY 60
DB 23 EVQLQQSGAELVKPGASVKLSCTASGNIKDTFMHWKQRPQGLEWIGRIDPANGTEY 82
QY 61 NQKFKDKATLVDSKSTTAYNELRLSDESAVYICARSTMTINYNVDYWGQGTSTVTS 120
DB 83 DPKFGQKATITADTSNTVNLQSLSLSDTAVYICASGGELG---PPYWGQGLTVLSA 139
QY 121 AKTTPSPVPLAPGSAATQNSMTLGLVKGYFPPEPVTVTWNSGSLSSGSHVHTFPVQLSD 180
DB 140 AKTTPSPVPLAPGSAATQNSMTLGLVKGYFPPEPVTVTWNSGSLSSGSHVHTFPVQLSD 199
QY 181 LYTSSSVTVPSSTWSPSETVTCNVAHPASSTKVDKIVPRD--SGG 224
DB 200 LYTSSSVTVPSSTWSPSETVTCNVAHPASSTKVDKIVPRDCTSGG 245

RESULT 48
US-08-792-824-7
; Sequence 7, Application US/08792824
; Patent No. 5932449
; GENERAL INFORMATION:
; APPLICANT: EMANUEL, PETER A.
; APPLICANT: BURANS, JAMES P.
; APPLICANT: VALDES, JAMES J.
; APPLICANT: MOHVEE, ELDEFRAWI E.
; TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. Army Chemical and Biological Defense
; ADDRESSEE: Command
; STREET: Office of the Chief Counsel, Bldg E4435
; CITY: Aberdeen Proving Ground
; STATE: MD
; COUNTRY: U.S.
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,824
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Biffoni, U. J.
; REGISTRATION NUMBER: 39,908
; REFERENCE/DOCKET NUMBER: DAM #31-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 410-671-1158
; TELEFAX: 410-671-2534
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 254 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-792-824-7

Query Match 25.8%; Score 909.5; DB 2; Length 254;
Best Local Similarity 78.8%; Pred. No. 2.1e-53;
Matches 178; Conservative 15; Mismatches 28; Indels 5; Gaps 2;
QY 1 EVQLQQSGPDLVKPGASVKISKASGYSFTGYHWHVKQSPGKLEWIGRINPNNGVTLY 60
DB 23 EVQLQQSGAELVKPGASVKLSCTASGNIKDTFMHWKQRPQGLEWIGRIDPANGTEY 82
QY 61 NQKFKDKATLVDSKSTTAYNELRLSDESAVYICARSTMTINYNVDYWGQGTSTVTS 120
DB 83 DPKFGQKATITADTSNTVNLQSLSLSDTAVYICASGGELG---PPYWGQGLTVLSA 139
QY 121 AKTTPSPVPLAPGSAATQNSMTLGLVKGYFPPEPVTVTWNSGSLSSGSHVHTFPVQLSD 180
DB 140 AKTTPSPVPLAPGSAATQNSMTLGLVKGYFPPEPVTVTWNSGSLSSGSHVHTFPVQLSD 199
QY 181 LYTSSSVTVPSSTWSPSETVTCNVAHPASSTKVDKIVPRD--SGG 224
DB 200 LYTSSSVTVPSSTWSPSETVTCNVAHPASSTKVDKIVPRDCTSGG 245

DB 23 EVQLQQSGAELVKPGASVKLSCTASGNIKDTFMHWKQRPQGLEWIGRIDPANGTEY 82
QY 61 NQKFKDKATLVDSKSTTAYNELRLSDESAVYICARSTMTINYNVDYWGQGTSTVTS 120
DB 83 DPKFGQKATITADTSNTVNLQSLSLSDTAVYICASGGELG---PPYWGQGLTVLSA 139
QY 121 AKTTPSPVPLAPGSAATQNSMTLGLVKGYFPPEPVTVTWNSGSLSSGSHVHTFPVQLSD 180
DB 140 AKTTPSPVPLAPGSAATQNSMTLGLVKGYFPPEPVTVTWNSGSLSSGSHVHTFPVQLSD 199
QY 181 LYTSSSVTVPSSTWSPSETVTCNVAHPASSTKVDKIVPRD--SGG 224
DB 200 LYTSSSVTVPSSTWSPSETVTCNVAHPASSTKVDKIVPRDCTSGG 245

RESULT 49
US-09-192-545-4
; Sequence 4, Application US/09192545
; Patent No. 6118044
; GENERAL INFORMATION:
; APPLICANT: Karasuyama, Hajime
; APPLICANT: Yonekawa, Hiromichi
; APPLICANT: Taya, Choji
; APPLICANT: Matsuo, Kunie
; TITLE OF INVENTION: Transgenic Animal Allergy Models and Methods for Their Use
; FILE REFERENCE: 799p79570
; CURRENT APPLICATION NUMBER: US/09/192,545
; EARLIER FILING DATE: 1998-11-13
; EARLIER FILING DATE: 1997-11-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 4
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: Description of Artificial Sequence: Designed heavy
US-09-192-545-4

Query Match 25.7%; Score 904.5; DB 3; Length 238;
Best Local Similarity 79.5%; Pred. No. 4.2e-53;
Matches 175; Conservative 18; Mismatches 22; Indels 5; Gaps 2;
QY 457 TTSIVMTQTPTSLIYAGDRVTITCKASQSV--SND---VAVYQKPGQSKLLISYTS 511
DB 18 SSDVLMTQTPSLPVLGSDQASISCRSQSIVHSGNTYLEWYLOKPGQSKLLIYKVS 77
QY 512 RVAGVDPDRFGSGGYGTDFTLTITSSVQAEADAAYFCQDYNSPPTFGGTTKLEIKADAAP 571
DB 78 RFGVDPDRFGSGSGTDFTLKISRVEAEDLGYYVCFQSHVPLTFGAGTKLEKADAAP 137
QY 572 TVSIIFPPSSEQLTSGGASVVCFLNNPYPKIDINVKKIDGSEBRQNLVNSWTDQDSKSTY 631
DB 138 TVSIIFPPSSEQLTSGGASVVCFLNNPYPKIDINVKKIDGSEBRQNLVNSWTDQDSKSTY 197
QY 632 SMSSTLTLDKDEYERHNSYTCATHKTSPTVKSFNNE 671
DB 198 SMSSTLTLDKDEYERHNSYTCATHKTSPTVKSFNNE 237

RESULT 50
5455030-1
; Patent No. 5455030
; APPLICANT: LAJNER, ROBERT C.; BIRD, ROBERT E.; HARDMAN, KARL
; TITLE OF INVENTION: IMMUNOTHERAPY USING SINGLE CHAIN
; POLYPEPTIDE BINDING MOLECULES
; NUMBER OF SEQUENCES: 24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/40,440
; FILING DATE: 1-APR-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 512,910
; FILING DATE: 25-APR-1990

```
; APPLICATION NUMBER: 299,617
; FILING DATE: 19-JAN-1989
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 92,110
; FILING DATE: 02-SEP-1987
; APPLICATION NUMBER: 902,971
; FILING DATE: 01-SEP-1986
; SEQ ID NO:1
; LENGTH: 447
; 5455030-1

Query Match      25.7%; Score 903.5; DB 6; Length 447;
Best Local Similarity 32.9%; Pred. No. 1.1e-52;
Matches 222; Conservative 69; Mismatches 121; Indels 263; Gaps 15;

QY 1 EVOLQSGPDLVPCGASVKLSCKASGYSTFYGMHVKSPGKGLWIGRINPNNGVTLY 60
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 EVOLVESGGLVPCG-SLKLSCAAGFTFISYGMVVRQTPDKRLEWVATISGGSTYTY 59
QY 61 NQFKDKAKATLVKDSSTAYMELRSITSEDSAVVYCAR---STMITN-YVMDVWGQTSV 116
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
60 PDSVKGRFTISRDNAKNTLYLQMSGLKSEDTANYICARRITTVLLDYDYAMVWGQTSV 119
QY 117 TVSSAKTTPSVPLAPGSAQNSMVTGLCLVKGYFPEPVFTVWNSGSLSGVHTFPFAV 176
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
120 TVSSAKTTPSVPLAPGSAQNSMVTGLCLVKGYFPEPVFTVWNSGSLSGVHTFPFAV 179
QY 177 LQSDLYTLSSSVTPSPSTPSETVTCNVAHPASTKVDKKIIPRDSGGPSEKSEELNEXD 236
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
180 LQSDLYTLSSSVTPSPSTPSETVTCNVAHPASTKVDKKIIPRDCG----- 226
QY 237 LRKKSLOQTALGNLKIYYNSKAITSEKSAQDLTNTLLFKGFTGHPWYNLLVLDL 296
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
227 ----CKPCICTPEVSSVFIFPPK-----PKDVLITIL----- 255
QY 297 GSTAATSEVGGSSVDLYGAYGYQCAGGTGPKTACMYGGVTLHNNRLTEKKVPINLMI 356
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
256 -----TP-KVTCVVVDIS-----KDDPEVQFSWPFV 279
QY 357 DGRQTTVPIDKVKTSKEV-----TVQELDLQARHYLHGKFGLYNSDS--FGGKVQRG 407
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
280 D----DVEVHTAGTQPREQFDSSTSVSELPLMHQDWLNGKEFKCRVDSAAFPAPIEK- 334
QY 408 LIVFHSSEGSTSVSYDLFDAQGGVPTLLRIYRNTTISSTISLSLYLTTSIVMTQPT 467
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
335 -----TISKT----- 339
QY 468 SLLVSAGDRVTITCKASQSVNDVANYQKPGQPKLLISYTSRRYAGVDPDRFGSGYGT 527
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
340 ----- 339
QY 528 DFTLTISVQAEADAAYVFCQDYNSPPTFGGKTKLEIKRAADAAPTIVSIPIPPSSEQLTSGG 587
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
340 -----KGRPKAPQVYTIPTPPKEQVAKDX 362
QY 588 ASVVCFNNFYPKDINVKNKIDGSRQN-----GVLSNWTDDQSKDSTYSMSSTTLTKD 642
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
363 VSLTCMTIDFFPDIDTVEWDGQPAENYKNTQRIQNT-----DGSYFYVSKLDVQKS 415
QY 643 EVERHNSYTCETHK 657
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
416 NWEAGTFTICSVLHE 430

RESULT 51
PCT-US94-14106-57
; Sequence 57, Application PC/TUS9414106
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Process for Generating Specific Antibodies
; NUMBER OF SEQUENCES: 61
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
```

```
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14106
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 57:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 218 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US94-14106-57

Query Match      25.6%; Score 901; DB 5; Length 218;
Best Local Similarity 80.6%; Pred. No. 6.4e-53;
Matches 174; Conservative 9; Mismatches 29; Indels 4; Gaps 1;

QY 460 IWMQTPTSLVLSAGDRVTITCKASQSVSND----VANYQKPGQPKLLISYTSRRYAG 515
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
2 IWMQTSPASLAVSLGQRATISCRVRSQSVSTSSHSHMYQKPGQPKLLIKYASNLESG 61
QY 516 VPDFSGSGYGTDTFTLTISVQAEADAAYVFCQDYNSPPTFGGKTKLEIKRAADAAPTIVSI 575
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
62 VPARFSGSGSGTDTFTLNHPVEEEDTATYYCOHSWEIPTYTFGGGKTKLEIKRAADAAPTIVSI 121
QY 576 FPPSEQLTSGASVVCFLANNFYPKDINVKNKIDGSRQNGVLNSWTDQDSKDSYMS 635
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
122 FPPSEQLTSGASVVCFLANNFYPKDINVKNKIDGSRQNGVLNSWTDQDSKDSYMS 181
QY 636 TLTLTKDYEYRHSNYTCEATHTKSTSPVKSFNENE 671
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
182 TLTLTKDYEYRHSNYTCEATHTKSTSPVKSFNENE 217

RESULT 52
US-09-170-769A-8
; Sequence 8, Application US/09170769A
; Patent No. 6444206
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: LETURCO, Didier
; APPLICANT: MORIATRY, Ann
; APPLICANT: ULEVITCH, Richard
; APPLICANT: TOBIAS, Peter
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING CD14 MEDIATED CELL ACTIVA
; FILE REFERENCE: SCRIP1140-3
; CURRENT APPLICATION NUMBER: US/09/170,769A
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: US 08/070,160
; PRIOR FILING DATE: 1993-05-28
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 8
; LENGTH: 211
; TYPE: PRT
; ORGANISM: Murine
; US-09-170-769A-8

Query Match      25.5%; Score 898; DB 4; Length 211;
Best Local Similarity 81.4%; Pred. No. 9.7e-53;
Matches 171; Conservative 15; Mismatches 24; Indels 0; Gaps 0;

QY 462 MTQPTSLVLSAGDRVTITCKASQSVSNDVANYQKPGQPKLLISYTSRRYAGVDPDRFS 521
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 MTQPTSLVLSAGDRVTITCKASQSVSNDVANYQKPGQPKLLISYTSRRYAGVDPDRFS 60
QY 522 GSGYGTDTFTLTISVQAEADAAYVFCQDYNSPPTFGGKTKLEIKRAADAAPTIVSI 581
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 GSGYGTDTFTLTISVQAEADAAYVFCQDYNSPPTFGGKTKLEIKRAADAAPTIVSI 120
QY 582 QLTSGASVVCFLANNFYPKDINVKNKIDGSRQNGVLNSWTDQDSKDSYMSSTLT 641
```

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Db 121 QLTGGGASVVCFLNFPKIDINVKWKIDGSRQGVLSNWTDDQSKDSTYSMSSTLTITK 180
Qy 642 DEYERHNSYTCETHKTSPIVKSFNNE 671
Db 181 DEYERHNSYTCETHKTSPIVKSFNNE 210

RESULT 53
PCT-US94-14106-55
; Sequence 55, Application PC/TUS9414106
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Process for Generating Specific Antibodies
; NUMBER OF SEQUENCES: 61
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/14106
; FILING DATE:
; TELEPHONE:
; TELEFAX:
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 223 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-14106-55

Query Match 25.5%; Score 897.5; DB 5; Length 223;
Best Local Similarity 79.4%; Pred. No. 1.1e-52;
Matches 177; Conservative 12; Mismatches 31; Indels 3; Gaps 2;

Qy 1 EVQLQSGFPIVKPGASVKISKASGYSFTGYMHWVKQSPGKLEWIGRINPNNGVTLY 60
Db 1 EVQLQSGAELMPPGASVKISKATGYTLSSSLWLVKQSPGKLEWIGRIGELFGSGAHY 60

Qy 61 NQKFKDKATLVDRKSTTAYMELRSLTSEDGAVYICARSTMITNY--VMDYWGQGTSTV 118
Db 61 NEKFKGKATFTVDSSNTAYMQLSLSLSEDGAVYICARGD-YGNYGDFYWGQGTSTV 119

Qy 119 SSAKTPPSVPLAPGSAQAQNSMWTLCGLVKGFFPEPVTWNSSGSLSGVHTFPVLQ 178
Db 120 PSAKTPPSVPLAPGSAQAQNSMWTLCGLVKGFLPEPVTWNSSGSLSGVHTFPVLQ 179

Qy 179 SDLYTLSSSVTPSPSTPSETVTCNVAHPASSTKVDKIVPRD 221
Db 180 SDLYTLSSSVTPSPSTPSETVTCNVAHPASSTKVDKIVPRD 222

RESULT 54
US-08-737-129A-8
; Sequence 8, Application US/08737129A
; Patent No. 5885816
; GENERAL INFORMATION:
; APPLICANT: IKUO FUJII et al.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTISELECTIVELY
; TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
```

```
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,129A
; FILING DATE: No. 5885816member 15, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-737-129A-8

Query Match 25.4%; Score 895; DB 2; Length 215;
Best Local Similarity 80.2%; Pred. No. 1.6e-52;
Matches 170; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

Qy 460 IVMTOTPTSLVSGDRVTITCKASQSVSNVDVAVYQKPGQSPKLLISYTSRYAGVDR 519
Db 2 LVMTQTPSSMYASLGERVTITCKASQSDINIVLWVQKPGKSPKALIVRTNGLVDGVPSR 61

Qy 520 FSGSGYGTFTLTISVQAEAAVFCQDYNSTPFGGKLEIKRADAAPTVSIPTPS 579
Db 62 FSGSGSGQDYSLTISLEVEDMGIVYCLQYDEFPYTFGGGKLEIKRADAAPTVSIPTPS 121

Qy 580 SGLTSGGASVVCFLNFPKIDINVKWKIDGSRQGVLSNWTDDQSKDSTYSMSSTLT 639
Db 122 SGLTSGGASVVCFLNFPKIDINVKWKIDGSRQGVLSNWTDDQSKDSTYSMSSTLT 181

Qy 640 TKDEYERHNSYTCETHKTSPIVKSFNNE 671
Db 182 TKDEYERHNSYTCETHKTSPIVKSFNNE 213

RESULT 55
US-08-442-542-18
; Sequence 18, Application US/08442542
; Patent No. 5686600
; GENERAL INFORMATION:
; APPLICANT: Carozzi, Nadine B.
; APPLICANT: Koziel, Michael G.
; TITLE OF INVENTION: Antibodies which Bind to Insect Gut
; TITLE OF INVENTION: Proteins and their Use
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: NY
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,542
; FILING DATE: 16-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/267,641
```


Db 487 -----TISKT----- 491
Qy 468 SLLVSAGDRVTITCKASQSVNDVAVYQKPGQSKLLISYTSRVAGVDPDRFGSGCYGT 527
Db 492 ----- 491
Qy 528 DFTLTSSVQABDAAVYFCQDYNSPPTFGGTYKLEIKRADAPTYSIFPPSSEQLTSGG 587
Db 492 -----KGRPKAPOVYTIPTTPEQOMAKDK 514
Qy 588 ASVVCFLNNFYKPDINVKWKIDGSEON-----GVLSWTDQDSKDYSGMSSTLTITKD 642
Db 515 VSLTCMTDFPDITVWQNGQPAENYKNTQPIMT-----NGSYFYVSKLNVQKS 567
Qy 643 EYERHNSYTCBATHK 657
Db 568 NWEAGNTFTCSVLHE 582

RESULT 57

US-09-423-439-58

; Sequence 58, Application US/09423439

; Patent No. 6339070

; GENERAL INFORMATION:

; APPLICANT: EMERY, Stephen Charles

; BLAKEY, David Charles

; TITLE OF INVENTION: CHEMICAL COMPOUNDS

; NUMBER OF SEQUENCES: 60

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pillsbury Winthrop, L.L.P.

; STREET: 1100 New York Ave., N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: MS Word

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/423,439

; FILING DATE: 09-NOV-1999

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB98/01294

; FILING DATE: 05-MAY-1998

; APPLICATION NUMBER: GB 9709421.3

; FILING DATE: 10-MAY-1997

; INFORMATION FOR SEQ ID NO: 58:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 235 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 58:

US-09-423-439-58

Query Match

Best Local Similarity 25.3%; Score 889.5; DB 4; Length 235;

Matches 172; Conservative 19; Mismatches 31; Indels 1; Gaps 1;

Qy 449 LSISLYLTTISIVMTQTPTSLVSAGDRVTITCKASQSVNDVAVYQKPGQSKLLISY 508

Db 13 ISASVIMSRGQTVLSQSPAILSGAPEKVTMTCRASSVTY-IHWYQKPGSSPKSWIYA 71

Qy 509 TSSRVAGVDPDRFGSGCYGTDTLTITSSVQABDAAVYFCQDYNSPPTFGGTYKLEIKRAD 568

Db 72 TSNLASGVPAFPGSGSGTSLTISRVEADAATYICQHWSSKRPPTFGGTYKLEIKRAD 131

Qy 569 AAPTYSIFPPSSEQLTSGASVVCFLNNFYKPDINVKWKIDGSEONGVLSWTDQDSKD 628

Db 132 AAPTYSIFPPSSEQLTSGASVVCFLNNFYKPDINVKWKIDGSEONGVLSWTDQDSKD 191

Qy 629 AAPTYSIFPPSSEQLTSGASVVCFLNNFYKPDINVKWKIDGSEONGVLSWTDQDSKD 671

Db 132 AAPTYSIFPPSSEQLTSGASVVCFLNNFYKPDINVKWKIDGSEONGVLSWTDQDSKD 191
Qy 629 STYSMSSTLTITCKEYERHNSYTCATHKTSTSPIVKSFNRNE 671
Db 192 STYSMSSTLTITCKEYERHNSYTCATHKTSTSPIVKSFNRNE 234

RESULT 58

US-09-011-769A-23

; Sequence 23, Application US/09011769A

; Patent No. 6436691

; GENERAL INFORMATION:

; APPLICANT: SLATER, Anthony M.

; BLAKEY, David C.

; DAVIES, David H.

; HENNEQUIN, John F.

; HENNEQUIN, Laurent F.A.

; MARSHAM, Peter R.

; DOWELL, Robert I.

; TITLE OF INVENTION: Chemical Compounds

; NUMBER OF SEQUENCES: 87

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pillsbury Madison & Sutro, LLP

; STREET: 1100 New York Ave., N.W.

; CITY: Washington

; STATE: D.C.

; COUNTRY: U.S.A.

; ZIP: 20005

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 1.44 Mb disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: MS Word

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/011,769A

; FILING DATE: 13-Feb-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/GB96/01975

; FILING DATE: 13-AUG-1996

; APPLICATION NUMBER: GB 9612295.7

; FILING DATE: 12-JUN-1996

; APPLICATION NUMBER: GB 9611019.2

; FILING DATE: 25-MAY-1996

; APPLICATION NUMBER: GB 9516810.0

; FILING DATE: 16-AUG-1995

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 235 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-09-011-769A-23

Query Match

Best Local Similarity 25.3%; Score 889.5; DB 4; Length 235;

Matches 172; Conservative 19; Mismatches 31; Indels 1; Gaps 1;

Qy 449 LSISLYLTTISIVMTQTPTSLVSAGDRVTITCKASQSVNDVAVYQKPGQSKLLISY 508

Db 13 ISASVIMSRGQTVLSQSPAILSGAPEKVTMTCRASSVTY-IHWYQKPGSSPKSWIYA 71

Qy 509 TSSRVAGVDPDRFGSGCYGTDTLTITSSVQABDAAVYFCQDYNSPPTFGGTYKLEIKRAD 568

Db 72 TSNLASGVPAFPGSGSGTSLTISRVEADAATYICQHWSSKRPPTFGGTYKLEIKRAD 131

Qy 569 AAPTYSIFPPSSEQLTSGASVVCFLNNFYKPDINVKWKIDGSEONGVLSWTDQDSKD 628

Db 132 AAPTYSIFPPSSEQLTSGASVVCFLNNFYKPDINVKWKIDGSEONGVLSWTDQDSKD 191

Qy 629 AAPTYSIFPPSSEQLTSGASVVCFLNNFYKPDINVKWKIDGSEONGVLSWTDQDSKD 671

Db 192 \$TYSMSSTLTITLKDEYERHNSYTCETHKTSPIVKSFNRE 234

RESULT 59
US-08-737-129A-4
; Sequence 4, Application US/08737129A
; Patent No. 5865816
; GENERAL INFORMATION:
; APPLICANT: IKUO FUJII et al.
; TITLE OF INVENTION: CATALYTIC ANTIBODIES ENANTIOSELECTIVELY
; TITLE OF INVENTION: HYDROLYSING AMINO ACID ESTER DERIVATIVES
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wenderoth, Lind & Ponack
; STREET: 805 Fifteenth Street, N.W., #700
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,129A
; FILING DATE: No. 5885916member 15, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Warren M. Cheek, Jr.
; REGISTRATION NUMBER: 33,367
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-8850
; TELEFAX:
; TELEX:
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 213 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-737-129A-4

Query Match 24.9%; Score 878; DB 2; Length 213;
Best Local Similarity 81.1%; Pred. No. 2.1e-51;
Matches 172; Conservative 13; Mismatches 25; Indels 2; Gaps 2;

QY 460 IVMTOPTSLYSAGDRVYITCKASOSVNDVAVYQKQSPKLLISYTSRYAGVDR 519
Db 2 LVMTQPALMSAPGKMTWCASSISY-NHWYQKFGTPPKRWIYGTSLKTSGVPAR 60

QY 520 FSGSGYGTFTLTISVQAEADAAVYFCQDYNSPPTFGGKLEIKRADAAPTIVFPFS 579
Db 61 FSGSGSGTSFSLTISMEAEADATVYCHQ-RSSYPTFGGKLEIKRADAAPTIVFPFS 119

QY 580 SEQLTSGGASVUCFLNFPKIDINVKWKIDGSRQNGVLSNWTDDQSKDSTYSMSSTLT 639
Db 120 SEQLTSGGASVUCFLNFPKIDINVKWKIDGSRQNGVLSNWTDDQSKDSTYSMSSTLT 179

QY 640 TKDEYERHNSYTCETHKTSPIVKSFNRE 671
Db 180 TKDEYERHNSYTCETHKTSPIVKSFNRE 211

RESULT 60
US-09-423-439-60
; Sequence 60, Application US/09423439
; Patent No. 6339070

GENERAL INFORMATION:
APPLICANT: EMERY, Stephen Charles
BLAKEY, David Charles
TITLE OF INVENTION: CHEMICAL COMPOUNDS
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pillsbury Winthrop, L.L.P.
STREET: 1100 New York Ave., N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/423,439
FILING DATE: 09-No. 6339070-1999
CLASSIFICATION: <UNKNOWN>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB98/01294
FILING DATE: 05-MAY-1998
APPLICATION NUMBER: GB 9709421.3
FILING DATE: 10-MAY-1997
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 647 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-09-423-439-60

Query Match 24.8%; Score 873; DB 4; Length 647;
Best Local Similarity 37.3%; Pred. No. 1.9e-50;
Matches 247; Conservative 66; Mismatches 184; Indels 166; Gaps 27;

QY 1 EVOIQSGPDLVKPGASVKISKASGYSTGYVYHWTQSPGKLEWIGRI-NPENGVTL 59
Db 20 EVKLVEGSGGLVQPGGSLRUSCATSGTFTDYNNWVRQPPGKALEWLGFINRGANGYTT 79

QY 60 -YNQKFKDKATLTVDKSTTAYMELRLTSDTSVAVYCARSTMTNVMYVWGQSTVTV 118
Db 80 EYSASVKGRFTISRDKSQSLYLQMTLRAEDSATYICTDRGLRFY-FDYWGQSTLTV 138

QY 119 SSAKTTPSVYPLAPGSAQAQNSMVTLCGLVKGYFPPEPVTVTWNSGSLSGVHTFPVLQ 178
Db 139 SSAKTTPSVYPLAPGSAQAQNSMVTLCGLVKGYFPPEPVTVTWNSGSLSGVHTFPVLQ 198

QY 179 SDLYTLASSVTPSSTWPSSETVTCNVAHPASSTKVDKKIIPRD-----SGGPSE 227
Db 199 SDLYTLASSVTPSSTWPSSETVTCNVAHPASSTKVDKKIIPRDGCGGGGGGGGGGSG 258

QY 228 KSEBI-----NE-----KDLRKSELO-GT-----ALGNLKKIYYNKAITSSEKS 268
Db 259 KRDNVLQAATDEQPAVTKLELVNIETGTGDAEGIAAGNFLEAKNLGFTVTRSKS 318

QY 269 ADQFLTNILFKGFTGHPWYNDLL-----VDLGSTAAATSEYEGSSVDLYGAYYQCA 322
Db 319 AGLVVGNDIV--GKIKRGGKNLLMSHMDTVLKGILAKAPFVEGDKAYG-----P 369

QY 323 GGTENKACMYGG--VTLHNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOEL 380
Db 370 GIADDK-----GGNAVILHTLKLL-----KEYGYRD- 395

QY 381 DLQARHYLHGKFG-----LYNSDSFGGKVGQRLIVFHSSEGSTVSYDLFDAGQGVPTLLR 436
Db 396 -----YGTITVLFTND-----BEKSGFSGRDLIQBEAKLADYVLS 430

QY 437 IYRDNNTISSTLSLSILYLTSTIWMQT-----PTSLLYSAGRVITTC 481

Db 431 F--BPTSAGDEKLSIG-----TSGIAYQVNVITKASHAGAPLGNVALVEASDLVLRM 484
QY 482 KASQSVN-DVAVYQQRGQSKLLISYTS-----SRVAGVDPDRSGSGYGTDTLTISSV 536
Db 485 NIDKAKVLRFNWTIAKAGVNSNIPASATLNADRYA-----RNEDFDAAMKTL 534
QY 537 QAEDAAVVFQODY-----NSPPTFG--GQTKLEIKRA-----DAAPTVAIFPPSSBQLT 584
Db 535 ZERAQKKLPADVKVIVTRGRPAFNAGEGKKLVDAKAVYKAGGTLGV-----EERT 589
QY 585 SGG 587
Db 590 GGG 592

RESULT 61
US-08-792-824-3
; Sequence 3, Application US/08792824
; Patent No. 5932449
; GENERAL INFORMATION:
; APPLICANT: EMANUEL, PETER A.
; APPLICANT: BURANS, JAMES P.
; APPLICANT: VALDES, JAMES J.
; APPLICANT: MOHYEE, ELDEFRAWI E.
; TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. Army Chemical and Biological Defense
; ADDRESSEE: Command
; STREET: Office of the Chief Counsel, Bldg E4435
; CITY: Aberdeen Proving Ground
; STATE: MD
; COUNTRY: U.S.
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,824
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Biffoni, U. J.
; REGISTRATION NUMBER: 39,908
; REFERENCE/DOCKET NUMBER: DAM 431-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 410-671-1158
; TELEFAX: 410-671-2534
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-792-824-3

Query Match 24.8%; Score 872; DB 2; Length 236;
Best Local Similarity 78.3%; Pred. No. 6.1e-51;
Matches 166; Conservative 18; Mismatches 28; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVLSAGDRVTITCKASQSVNSDVAVYQQRGQSKLLISYTSRYAGVDPDR 519
Db 24 IQMTQSPASLSASVGETVTITCRASGNTHNYLAWYQQRGQSKPOLLYVNAKTLADGVPSR 83
QY 520 FSGSGYGTDTLTISSVQAEADAAYVFCQDYNSPPTFGGQTKLEIKRADAAPTVAIFPPS 579
Db 84 FSGSGGTQYSLKINSLOPEDFGSYCQHFWSPTWTFGGQTKLEIKRADAAPTVAIFPPS 143
QY 580 SEQLTSGGASVVCFLNFPKDNVKKIDGSRQGVNSWTDQDSDKSTYSMSSTLTL 639
Db 144 SEQLTSGGASVVCFLNFPKDNVKKIDGSRQGVNSWTDQDSDKSTYSMSSTLTL 203

RESULT 63
US-08-792-824-12
; Sequence 12, Application US/08792824

QY 640 TKDEYERHNSYTCETHKTSPIVKSFNRE 671
Db 204 TKDEYERHNSYTCETHKTSPIVKSFNRE 235

RESULT 62
US-08-792-824-9
; Sequence 9, Application US/08792824
; Patent No. 5932449
; GENERAL INFORMATION:
; APPLICANT: EMANUEL, PETER A.
; APPLICANT: BURANS, JAMES P.
; APPLICANT: VALDES, JAMES J.
; APPLICANT: MOHYEE, ELDEFRAWI E.
; TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: U.S. Army Chemical and Biological Defense
; ADDRESSEE: Command
; STREET: Office of the Chief Counsel, Bldg E4435
; CITY: Aberdeen Proving Ground
; STATE: MD
; COUNTRY: U.S.
; ZIP: 21010-5423
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/792,824
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Biffoni, U. J.
; REGISTRATION NUMBER: 39,908
; REFERENCE/DOCKET NUMBER: DAM 431-96
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 410-671-1158
; TELEFAX: 410-671-2534
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 236 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-792-824-9

Query Match 24.8%; Score 872; DB 2; Length 236;
Best Local Similarity 78.3%; Pred. No. 6.1e-51;
Matches 166; Conservative 18; Mismatches 28; Indels 0; Gaps 0;

QY 460 IVMTQPTSLVLSAGDRVTITCKASQSVNSDVAVYQQRGQSKPOLLYVNAKTLADGVPSR 519
Db 24 IQMTQSPASLSASVGETVTITCRASGNTHNYLAWYQQRGQSKPOLLYVNAKTLADGVPSR 83
QY 520 FSGSGYGTDTLTISSVQAEADAAYVFCQDYNSPPTFGGQTKLEIKRADAAPTVAIFPPS 579
Db 84 FSGSGGTQYSLKINSLOPEDFGSYCQHFWSPTWTFGGQTKLEIKRADAAPTVAIFPPS 143
QY 580 SEQLTSGGASVVCFLNFPKDNVKKIDGSRQGVNSWTDQDSDKSTYSMSSTLTL 639
Db 144 SEQLTSGGASVVCFLNFPKDNVKKIDGSRQGVNSWTDQDSDKSTYSMSSTLTL 203

RESULT 63
US-08-792-824-12
; Sequence 12, Application US/08792824

Patent No. 5932449
GENERAL INFORMATION:
APPLICANT: EMANUEL, PETER A.
APPLICANT: BURANS, JAMES P.
APPLICANT: VALDES, JAMES J.
APPLICANT: MOHVEE, ELDEFRAWI E.
TITLE OF INVENTION: DETECTION OF BOTULINUM TOXIN
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: U.S. Army Chemical and Biological Defense
ADDRESS: Command
STREET: Office of the Chief Counsel, Bldg E4435
CITY: Aberdeen Proving Ground
STATE: MD
COUNTRY: U.S.
ZIP: 21010-5423
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/792,824
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Biffoni, U. J.
REGISTRATION NUMBER: 39,908
REFERENCE/DOCKET NUMBER: DAM 431-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: 410-671-1158
TELEFAX: 410-671-2534
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 236 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-792-824-12

Query Match 24.8%; Score 872; DB 2; Length 236;
Best Local Similarity 78.3%; Pred. No. 6.1e-51;
Matches 166; Conservative 18; Mismatches 28; Indels 0; Gaps 0;
QY 460 IVMQTPTLLVSAGDRVITTKASQSVNDVAVYQKPGQPKLLISYTSRYAGVDR 519
Db 24 IQMTQSPASLSASVGETVITTCRASGNIHNLAWYQKQKSPQLLVYNAKTLADGVR 83
QY 520 FSGSGYGTDFLTLSISSVQAEADAVYFCQDYNPPTFGGKLEIKRADAAPTYSIFPPS 579
Db 84 FSGSGSGTQYSLKINSIQPEDFGYYCOHFWSTPTFTGGTKLEIKRADAAPTYSIFPPS 143
QY 580 SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLSNWDQDSKDSYMSSTLTL 639
Db 144 SEQLTSGGASVVCFLNNFYPKDINVKWKIDGSRQNGVLSNWDQDSKDSYMSSTLTL 203
QY 640 TKDEYERHNSYTCEATHKTSSTPIVKSFNRE 671
Db 204 TKDEYERHNSYTCEATHKTSSTPIVKSFNRE 235

RESULT 64
US-09-301-593-18
Sequence 16, Application US/09301593A
Patent No. 6455677
GENERAL INFORMATION:
APPLICANT: Park, John E.
APPLICANT: Garin-Chesa, Pilar
APPLICANT: Bamberger, Uwe
APPLICANT: Leger, Olivier
APPLICANT: Saldanha, Jose W.
APPLICANT: Rettig, Wolfgang J.
TITLE OF INVENTION: FAP-specific Antibody with Improved Productivity

FILE REFERENCE: 0652.1890001
CURRENT APPLICATION NUMBER: US/09/301.593A
CURRENT FILING DATE: 1999-04-29
EARLIER APPLICATION NUMBER: EP 98107925.4
EARLIER FILING DATE: 1998-04-30
EARLIER APPLICATION NUMBER: US 60/086,049
EARLIER FILING DATE: 1998-05-18
NUMBER OF SEQ ID NOS: 108
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 18
LENGTH: 453
TYPE: PRT
ORGANISM: Homo sapiens
US-09-301-593-18

Query Match 24.8%; Score 872; DB 4; Length 453;
Best Local Similarity 34.1%; Pred. No. 1.4e-50;
Matches 227; Conservative 56; Mismatches 143; Indels 240; Gaps 17;
QY 2 VLOQSGPDLVPGASVKISCKASGYSFTGYMHVWVKQSPGKLEWIGRINPNNGVTLN 61
Db 1 VLOQSGPELVPGASVMSCKTSRYTFTYTHVQSHGKSLWIGGINPNNGINPNY 60
QY 62 QKFKDKATLTVDKSSTTAYMELRLTSDSAYVYCARSTMITNY----VMDYWGQGSVT 117
Db 61 QKFKGRATLTVGKSSSTAYMELRLTSDSAYVYCARRIAYGYDEGHAMDYWGQGSVT 120
QY 118 VSSAKTTPPSVYPLAPGSAATNSMTGLCLVKGYFPEPVTVTVNSGSLSSGVHTFPAVL 177
Db 121 VSSASTKGPSVFPLAPSSKSTSGGTAAALGLCLVKDYFPEPVTVSVNSGALTSGVHTFPAVL 180
QY 178 QSD-LYTLSSSVTVPSSWPTSETVTCNVAPASSTKVDKIVPRDGGSPSEKSEINEKD 236
Db 181 QSSGLYSLSSVTVFPSSSLGTQTYICNVNHPKSTKVDKVEPKSC-----226
QY 237 LRKXSELQGTALGNLKOIYYNNSKAITSSSEKSAQDFTNTLLFGFTGHPWYNDLLVDL 296
Db 227 -----DKHTCTCPCPAPELGGPSVF--LPFPKP--KDTLM--258
QY 297 GSTAATSEYSGSVLDLYGAYYQYQAGTPTNKTACMYGGVTLHDNRLTEKKYPINLWI 356
Db 259 -----ISRTPEVT--CVVDVS-----HEDFEVKFNWY 285
QY 357 DGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQRLGVLVHSE 416
Db 286 DG-----VEVHNAKTPREEQ-----YNSTY--RVSVTLTVLHQDWL 320
QY 417 STVSYDLDFAQGYPDLLRIYRDNNTISSTLSLSISLYLTTSIWMQTPTSLLSVAGDR 476
Db 321 NGKEY-----325
QY 477 VTITCKASQSVNDVAVYQKPGQPKLLISYTSRYAGVDRPDRSGSGYGTDFLTLSV 536
Db 326 ---XCKVS-----NKAAP--LEKTSKAKGP-----349
QY 537 QAEDAAVFCQDYNPPTFGGKLEIKRADAAPTYSIFPPSSEQLTSGGASVVCFLNN 596
Db 350 -----REPQVYTLPPSREEMTKQVSLTCLVK 377
QY 597 FYPKDINVKWKIDGSRQN-----GVLSNWDQDSKDSYMSSTLTLTKDEYERHNSYT 651
Db 378 FYPSDIAVESNQPENNYKTTTPVLDS-----DGSFELYSKLIIVDKSRWQGNVFS 430
QY 652 CEATHK 657
Db 431 CSVMHE 436

RESULT 65
PCT-US94-41106-61
Sequence 61, Application PC/TUS9441106
GENERAL INFORMATION:
APPLICANT:

Matches 169; Conservative 11; Mismatches 31; Indels 4; Gaps 1;
 QY 462 MTOTPTSLVAGDRVTITCKASQSYNDV-...AWQKPGQSPKLLISYSSRVAGVP 517
 Db 1 MTQSPASLAVSLQORAPYCRASESDSYNSFLHWYQKPGQPPKLLIYRASNLQSGIP 60
 QY 518 DFGSGGYGDTFTLTSSVQAEADAAVYFCQDYNSPFTFGGGLKLEIKRADAAPTYSIIFP 577
 Db 61 ARFSGSGRTDFTLTINPVEADVAATYVCOQSNEDPTTSGGGLKLEIKRADAAPTYSIIFP 120
 QY 578 PSSEQLTSGGASVVCPLNNFYPKDINVKKIDGSRQNGVLNWDQDSDKSTYSMSSTL 637
 Db 121 PSSEQLTSGGASVVCPLNNFYPKDINVKKIDGSRQNGVLNWDQDSDKSTYSMSSTL 180
 QY 638 TLTKDEYERHNSYTCETHKTSPIVKSFRNE 671
 Db 181 TLTKDEYERHNSYTCETHKTSPIVKSFRNE 214

RESULT 68
 PCT-US94-07659-4
 ; Sequence 4, Application PC/TUS9407659
 ; GENERAL INFORMATION:
 ; APPLICANT: Young, Peter
 ; APPLICANT: Gross, Mitchell
 ; APPLICANT: Jonak, Zdenka L.
 ; APPLICANT: Theisen, Timothy
 ; APPLICANT: Hurler, Mark
 ; APPLICANT: Jackson, Jeffrey R.
 ; TITLE OF INVENTION: Recombinant and Humanized IL-1 beta
 ; TITLE OF INVENTION: Antibodies for Treatment of IL-1 Mediated Inflammatory
 ; TITLE OF INVENTION: Disorders in Man
 ; NUMBER OF SEQUENCES: 21
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SmithKline Beecham Corporation - Corp.
 ; ADDRESSEE: Intellectual Property
 ; STREET: 709 Swedeland Road
 ; CITY: King of Prussia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19406-2799
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US94/07659
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/090,534
 ; FILING DATE: 09-JUL-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Sutton, Jeffrey A.
 ; REGISTRATION NUMBER: 34,028
 ; REFERENCE/DOCKET NUMBER: P50171-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (610) 270-5024
 ; TELEFAX: (610) 270-5090
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 234 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; PCT-US94-07659-4

Query Match 24.4%; Score 858; DB 5; Length 234;
 Best Local Similarity 72.9%; Pred. No. 5.2e-50;
 Matches 167; Conservative 19; Mismatches 39; Indels 4; Gaps 1;
 QY 447 TSLISILYLYTT-----SIVMTPTSLVAGDRVTITCKASQSYNDVAVYQKPGQSP 502

Db 5 TOVLALLLWLTGARCIDQMTQSPASLSASVGEIVTITCRASGNIHNYLWYQKQKQSP 64
 QY 503 KLLISYSSRVAGVDPDRPSGSGYGTDFLTLTSSVQAEADAAVYFCQDYNSPFTFGGGLK 562
 Db 65 QLLVYNAKTLADGVPSRPSGSGSTQYSLKINSIQPEDFGSYQCQHFWSIPIYTFGGGTL 124
 QY 563 BIKRADAAPTYSIIFPPSEQLTSGGASVVCPLNNFYPKDINVKKIDGSRQNGVLNWSWT 622
 Db 125 EINRADAAPTYSIIFPPSEQLTSGGASVVCPLNNFYPKDINVKKIDGSRQNGVLNWSWT 184
 QY 623 DQSKDSTYSMSSTLTLTCKDEYERHNSYTCETHKTSPIVKSFRNE 671
 Db 185 DQSKDSTYSMSSTLTLTCKDEYERHNSYTCETHKTSPIVKSFRNE 233

RESULT 69
 US-09-011-769A-21
 ; Sequence 21, Application US/09011769A
 ; Patent No. 6436691
 ; GENERAL INFORMATION:
 ; APPLICANT: SLATER, Anthony M.
 ; BLAKE, David C.
 ; DAVIES, David H.
 ; HENNAM, John F.
 ; HENNEQUIN, Laurent F.A.
 ; MARSHAM, Peter R.
 ; DOWELL, Robert I.
 ; TITLE OF INVENTION: Chemical Compounds
 ; NUMBER OF SEQUENCES: 87
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pillsbury Madison & Sutro, LLP
 ; STREET: 1100 New York Ave., N.W.
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: U.S.A.
 ; ZIP: 20005
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 1.44 Mb disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: MS Word
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/011,769A
 ; FILING DATE: 13-Feb-1998
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/GB96/01975
 ; FILING DATE: 13-AUG-1996
 ; APPLICATION NUMBER: GB 9612295.7
 ; FILING DATE: 12-JUN-1996
 ; APPLICATION NUMBER: GB 9611019.2
 ; FILING DATE: 25-MAY-1996
 ; APPLICATION NUMBER: GB 9516810.0
 ; FILING DATE: 16-AUG-1995
 ; INFORMATION FOR SEQ ID NO: 21:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 250 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 21:
 US-09-011-769A-21

Query Match 24.3%; Score 855.5; DB 4; Length 250;
 Best Local Similarity 72.9%; Pred. No. 8.4e-50;
 Matches 164; Conservative 24; Mismatches 34; Indels 3; Gaps 3;
 QY 1 EVQLQQSGPDLVQPKASVKISKASGYSTGYMHWKQSPGKLEWIGRI-NFNNGVTL 59
 Db 20 EVKLVEGGGLVQPGGRLRISCATSGFTFTDYNNWYRQPPGKALEWLGFGIKNAGYTT 79
 QY 60 -YNQKFKDKATLTVDKSTTAYMELRSLTSDSAAVYCARSTMTINYMDYWGQGTSTV 118

Db 80 EYASVKGRTISRDKSQSILYLQWNTLRAEDSATYICTRDRGLRFF-FDYWGQGITLTV 138
QY 119 SSAKTTTPSVPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTVNSGSLSSGVHTFPAVLQ 178
Db 139 SSAKTTTPSVPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTVNSGSLSSGVHTFPAVLQ 198
QY 179 SDLYTLSSSVTPSPSTPSEVTCNVAHPASSTKVDKKIVPRDSG 223
Db 199 SDLYTLSSSVTPSPSTPSEVTCNVAHPASSTKVDKKIVPRDCG 243

RESULT 70

US-09-171-945-131
; Sequence 131, Application US/09171945
; Patent No. 6277599
; GENERAL INFORMATION:
; APPLICANT: Emery, Stephen
; APPLICANT: Copley, Clive Graham
; APPLICANT: Edge, Michael Derek
; TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said
; FILE REFERENCE: Monoclonal Antibody, and Their Therapeutic Use in an Adept System
; CURRENT APPLICATION NUMBER: US/09/171.945
; CURRENT FILING DATE: 1998-10-29
; PRIOR APPLICATION NUMBER: GB9703103.3
; PRIOR FILING DATE: 1997-02-14
; PRIOR APPLICATION NUMBER: GB9609405.7
; PRIOR FILING DATE: 1996-05-04
; PRIOR APPLICATION NUMBER: PCT/GB97/01165
; PRIOR FILING DATE: 1997-04-29
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 131
; LENGTH: 473
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: humanized
US-09-171-945-131

Query Match 24.3%; Score 855.5; DB 3; Length 473;
Best Local Similarity 72.9%; Pred. No. 1.9e-49;
Matches 164; Conservative 24; Mismatches 34; Indels 3; Gaps 3;
QY 1 EVQLQSGPDLVKPQASVKISCKASGYSTFTGYMHMWKQSPGKLEWIGRI-NPNNGVTIL 59
Db 243 EYKLVESGGLVQPGGSLRLSCATSGFTFTDYNNWVRQPPGKALEWLGFIGNKANGYTT 302
QY 60 -YNQKFKDKATLTVDKSTTAYMELRSLTSDSAVYVCARSTMITNYMDYWGQGTSTV 118
Db 303 EYASVKGRTISRDKSQSILYLQWNTLRAEDSATYICTRDRGLRFF-FDYWGQGITLTV 361
QY 119 SSAKTTTPSVPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTVNSGSLSSGVHTFPAVLQ 178
Db 362 SSAKTTTPSVPLAPGSAQAQNSMVTGLCLVKGYFPEPVTVTVNSGSLSSGVHTFPAVLQ 421
QY 179 SDLYTLSSSVTPSPSTPSEVTCNVAHPASSTKVDKKIVPRDSG 223
Db 422 SDLYTLSSSVTPSPSTPSEVTCNVAHPASSTKVDKKIVPRDCG 466

RESULT 71

US-08-303-569B-5
; Sequence 5, Application US/08303569B
; Patent No. 5859205
; GENERAL INFORMATION:
; APPLICANT: Acair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5859205ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/303.569B
; FILING DATE: 07-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yanko
; REGISTRATION NUMBER: 35.719
; REFERENCE/DOCKET NUMBER: CARP-0032
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-303-569B-5
Query Match 24.2%; Score 852.5; DB 2; Length 235;
Best Local Similarity 74.9%; Pred. No. 1.2e-49;
Matches 167; Conservative 18; Mismatches 37; Indels 1; Gaps 1;
QY 449 LSIISLYTTSIVMTQTPTSLLLVSAGDRVITTCASQSVNDVAVYQKPGQSPKLLISY 508
Db 13 ISAVIISRGQVILTCSPAINASPEKVTMTCSASSSVY-MNYYQKSGTSPKRWIYD 71
QY 509 TSSRVAGVPDRFSGSGYGTDFLTITSSVQAEDAAVYFCQDYNSPPTFGGKLEIKLAD 568
Db 72 TSLKASGVPAHFRGSGSGTSYSLTISGAEADAAVYCCQWSSNPFTTSGSGTKLEINRAD 131
QY 569 AAPTIVSIIPPSSEQLTSGASVVCFLNNFYKIDINVKWKIDGSEFQNGVLNSWTDQDSK 628
Db 132 TAPTIVSIIPPSSEQLTSGASVVCFLNNFYKIDINVKWKIDGSEFQNGVLNSWTDQDSK 191
QY 629 STYSMSSTLTLDKDYERHNSYTCETHKTSPIVKSFNRE 671
Db 192 STYSMSSTLTLDKDYERHNSYTCETHKTSPIVKSFNRE 234
RESULT 72
US-08-116-247-5
; Sequence 5, Application US/08116247
; Patent No. 5923212
; GENERAL INFORMATION:
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Zivin, Robert A.
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; TITLE OF INVENTION: CD3 Specific Recombinant Antibody
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5929212ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/116,247
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/743,377
; FILING DATE: 10-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Paintin, Francis A.
; REGISTRATION NUMBER: 19,386
; REFERENCE/DOCKET NUMBER: CARP-0011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-116-247-5

Query Match      24.2%; Score 852.5; DB 2; Length 235;
Best Local Similarity 74.9%; Pred. No. 1.2e-49;
Matches 167; Conservative 18; Mismatches 37; Indels 1; Gaps 1;

QY 449 LSISLYLTTISVMTQPTSLVSAGDRVTITCKASQSVNDVAVYQKPGOSP KLLISY 508
Db 13 ISASVIISRGQIVLTQSPAIMSASPGKVTMTCSASSSVSY-MNYYQKSGTSPKRWIYD 71

QY 509 TSSRYAGVPRFSGSGYGTDFLTITSSVQAEADAAYVFCQDYNSPPTFGGKLEIKRAD 568
Db 72 TSKLASGVPAHFHFGSGSGTSYSLTISGMEADAATYCCQWSSNPFTFGSGTKLEINRAD 131

QY 569 AAPTVSIFPPSSSEQLTSGGASVVCFLNNFPKDIINVKWKIDGSRQNGVLSNWTQDQSKD 628
Db 132 TAPTVSIFPPSSSEQLTSGGASVVCFLNNFPKDIINVKWKIDGSRQNGVLSNWTQDQSKD 191

QY 629 STYSMSSTLTITKDEYERHNSYTCETHKTSPIVKSFNNE 671
Db 192 STYSMSSTLTITKDEYERHNSYTCETHKTSPIVKSFNNE 234

RESULT 73
US-09-795-515-5
; Sequence 5, Application US/09795515
; Patent No. 6632927
; GENERAL INFORMATION:
; APPLICANT: Adair, John R.
; APPLICANT: Athwal, Diljeet S.
; APPLICANT: Emtage, John S.
; TITLE OF INVENTION: Humanised Antibodies
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESS: Woodcock Washburn Kurtz Mackiewicz & No. 6632927ris
; STREET: One Liberty Place - 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM: disk
; MEDIUM TYPE: Floppy
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,515
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/846,658
; FILING DATE: 01-MAY-1997
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; ATTORNEY/AGENT INFORMATION:
; NAME: Trujillo, Doreen Yarko
; REGISTRATION NUMBER: 35,719
; REFERENCE/DOCKET NUMBER: CARP-0057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 235 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-795-515-5

Query Match      24.2%; Score 852.5; DB 4; Length 235;
Best Local Similarity 74.9%; Pred. No. 1.2e-49;
Matches 167; Conservative 18; Mismatches 37; Indels 1; Gaps 1;

QY 449 LSISLYLTTISVMTQPTSLVSAGDRVTITCKASQSVNDVAVYQKPGOSP KLLISY 508
Db 13 ISASVIISRGQIVLTQSPAIMSASPGKVTMTCSASSSVSY-MNYYQKSGTSPKRWIYD 71

QY 509 TSSRYAGVPRFSGSGYGTDFLTITSSVQAEADAAYVFCQDYNSPPTFGGKLEIKRAD 568
Db 72 TSKLASGVPAHFHFGSGSGTSYSLTISGMEADAATYCCQWSSNPFTFGSGTKLEINRAD 131

QY 569 AAPTVSIFPPSSSEQLTSGGASVVCFLNNFPKDIINVKWKIDGSRQNGVLSNWTQDQSKD 628
Db 132 TAPTVSIFPPSSSEQLTSGGASVVCFLNNFPKDIINVKWKIDGSRQNGVLSNWTQDQSKD 191

QY 629 STYSMSSTLTITKDEYERHNSYTCETHKTSPIVKSFNNE 671
Db 192 STYSMSSTLTITKDEYERHNSYTCETHKTSPIVKSFNNE 234

RESULT 74
5189147-8
; Patent No. 5189147
; APPLICANT: SAITO, HARUO; KRANZ, DAVID M.; ELSEN, HERMAN N.;
; TONEGAWA, SUSUMU
; TITLE OF INVENTION: METEORODIMERIC T LYMPHOCYTE RECEPTOR
; ANTIBODY
; NUMBER OF SEQUENCES: 21
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/271,216
; FILING DATE: 14-NOV-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 666,988
; FILING DATE: 31-OCT-1984
; APPLICATION NUMBER: 620,122
; FILING DATE: 13-JUN-1984
; SEQ ID NO: 8
; LENGTH: 200
5189147-8

Query Match      24.1%; Score 850.5; DB 6; Length 200;
Best Local Similarity 78.3%; Pred. No. 1.4e-49;
Matches 170; Conservative 13; Mismatches 17; Indels 17; Gaps 3;

QY 1 EVQLQQSGPDLVKEGASVKISCKASGYSTFGYYMHVWKQSPGKLEWIGINPNNGVTLY 60
Db 1 EVQLQQSGAELVRAGSSVKSKASGYTFTSYGINVWKQRPQGQLEWIGINPNNGVINY 60

QY 61 NQKFKDKATLTVDKSSSTAYMELRSLTSEDSAVYVCARSTWITNYVMYDYGQGTSTVTSS 120
Db 61 NEKEFGKXTLLTVDKSSSTAYMQLRSLTSEDSAVYFCARS-----HYFG-----G 104

QY 121 AKTTPPSVYPLAPGSAATNSMTVLGCLVKGYPEPVTVTWNSGLSSGSHVHTPAVLQSD 180
Db 105 AKTTPPSVYPLAPGSAATNSMTVLGCLVKGYPEPVTVTWNSGLSSGSHVHTPAVLQSD 164

QY 181 LYTLLSSSVTPSSSTWPSSETVTCNVHPASSSTKVDKKI 217
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Db 165 TY-LSSSVTPSSPRPSETVTCNVAHPASSTKVDK1 200
 RESULT 75
 US-07-934-373C-22
 ; Sequence 22: Application US/07934373C
 ; Patent No. 5821337
 ; GENERAL INFORMATION:
 ; APPLICANT: Paul J. Carter
 ; APPLICANT: Leonard G. Presta
 ; TITLE OF INVENTION: Immunglobulin Variants
 ; NUMBER OF SEQUENCES: 48
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatIn (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/934.373C
 ; FILING DATE: 21-Aug-1992
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US92/05126
 ; FILING DATE: 15-JUN-1992
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 07/715272
 ; FILING DATE: 14-JUN-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Lee, Wendy M.
 ; REGISTRATION NUMBER: 40,378
 ; REFERENCE/DOCKET NUMBER: P0709P2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-1994
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 454 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; US-07-934-373C-22

Query Match 23.9%; Score 841; DB 2; Length 454;
 Best Local Similarity 33.2%; Pred. No. 1.7e-48;
 Matches 222; Conservative 58; Mismatches 146; Indels 242; Gaps 18;
 QY 1 EVQLQSGPDLVKPGASVKISKAGSYFTGYMHVWVKQSPCKGLEWIGRINPNNGVTLY 60
 Db 1 QVQLQSGPELVKPGASVKISKAGSYFTGYMHVWVKQSPCKGLEWIGRINPNNGVTLY 60
 QY 61 NQKFKDKATLVVDKSSITAYVELSLTSEDGAVYICARSTMTNY-----VMDYWGOGTS 115
 Db 61 NQKFKDKATLVVDKSSITAYVELSLTSEDGAVYICARSTMTNY-----VMDYWGOGTS 115
 QY 116 VTSSAKTTPPSVPLAPGSAQNSVMTLGLVKGYFPEPVTVTWNSGSLSSGVHTFPA 175
 Db 120 VTSSASTKGSFVPLAPGSAQNSVMTLGLVKGYFPEPVTVTWNSGSLSSGVHTFPA 175
 QY 176 VLQSD-LYTLSSSVTPSSVTPSETVTCNVAHPASSTKVDKVIIPRDSGGPSEKSEBINE 234
 Db 180 VLQSSGLYSLSSVTPSSVTPSSVTPSETVTCNVAHPASSTKVDKVIIPRDSGGPSEKSEBINE 234
 QY 235 KDLRKSELOGTALGNLQIYYNYSKAITSEKSAQDLTNTLLPKGFFFTCHPMYNDLLV 294
 Db 228 -----DKHTTCCPCPAPELLGGPSVF--LFPKP--KDTLM 259

QY 295 DLGSTAATSEYEGSSVDLYGAYGYQCAGGTENKTACWYGGVTLHDNRLTEKKVPINL 354
 Db 260 -----ISRPEVT-CVVVDV-----HEDEVEKFNW 284
 QY 355 WIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGGKVGQRIIVFHSS 414
 Db 285 YVDG----VEVHNAKTPREEQ-----YNSTY--RVSVLTVLHQD 319
 QY 415 EGSVTSYDLFDAQGGYPTLLRIYEDNTTISTSLISLYLYTTSIVMTQPTSLIUSAG 474
 Db 320 WLNGKEY----- 326
 QY 475 DRVTITCKASQSVSNDVAWYQOKPGQSPKLLISYTSRYAGVDPDRFSGSGYGTDTLTIS 534
 Db 327 -----KCKVS-----NKALPAP--LEKTIKAKGP----- 350
 QY 535 SVOAEDAAVYFCQDYNSPPTFGGKLEIKRADAAPTIVSIFPPSSSEQLTSGGASVVCFL 594
 Db 351 -----REPQVYTLPPSREEMTKNQVSLTCLV 376
 QY 595 NNFYFKDINVKWKIDGSEKQ-----GVLSNWTQDQSKDSTYSMSSTLTLTAKDEYERHNS 649
 Db 377 KGFYPSDIAVEWESNGQPNKYKITPPVLD-----DGSFFLYSKLTVDKSRWQGNV 429
 QY 650 YTCEATHK 657
 Db 430 FSCSVWHE 437
 Search completed: August 12, 2004, 13:34:01
 Job time : 33.5729 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 12, 2004, 13:26:25 ; Search time 7.37083 Seconds
(without alignments)
3040.721 Million cell updates/sec

Title: US-09-900-766-2

Perfect score: 1218

Sequence: 1 SEKSEINEKDLRKSEIQG.....RDNTTISSTLSLSLYLYTT 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 78:**

1: pir1:**

2: pir2:**

3: pir3:**

4: pir4:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1107	90.9	257	2 A28179	enterotoxin E prec
2	948	77.8	257	2 A28664	enterotoxin A prec
3	918	75.4	260	2 C89384	enterotoxin P [imp
4	611	50.2	258	2 A33953	enterotoxin D prec
5	420.5	34.5	258	2 H83968	enterotoxin Sen [i
6	372.5	30.6	260	2 E89969	enterotoxin SeO [i
7	311	25.5	242	2 C89991	extracellular ente
8	296.5	24.3	242	2 C89969	extracellular ente
9	284.5	23.4	266	2 S11885	enterotoxin C3 - S
10	282	23.2	239	2 D89969	enterotoxin SEM [i
11	277.5	22.8	266	2 A60114	enterotoxin C-2 pr
12	269.5	22.1	251	1 S23659	exotoxin type A pr
13	268.5	22.0	266	1 ENSAB6	enterotoxin B prec
14	263.5	21.6	266	1 ENSAC1	enterotoxin C-1 pr
15	253.5	20.8	236	2 S18783	exotoxin type A pr
16	251.5	20.6	236	2 S18789	exotoxin A precurs
17	248.5	20.4	236	2 S18786	exotoxin type A pr
18	241	19.8	258	2 G89968	extracellular ente
19	220	18.1	250	1 A26152	streptococcal pyro
20	190	15.6	136	2 A89969	enterotoxin YENT2
21	178	14.6	157	2 A89942	hypothetical prote
22	155.5	12.8	235	2 A30509	exotoxin C precurs
23	115	9.4	62	2 H89941	hypothetical prote
24	100	8.2	234	1 XCSA51	toxic shock syndro
25	98	8.0	133	2 B89969	enterotoxin Yent1
26	98	8.0	227	2 G89967	exotoxin 14 [impor
27	98	8.0	234	2 B89992	toxic shock syndro
28	96	7.9	552	2 T41863	chitinase chi-A or
29	94	7.7	231	2 D89907	exotoxin 11 [impor

30	94	7.7	979	2 JQ0894	Pil5 protein - Myc
31	91.5	7.5	993	2 AB1905	outer membrane sec
32	1634	7.5	1634	2 B64410	DNA-directed DNA p
33	88	7.2	419	1 C53312	thymidine phosphor
34	88	7.2	543	2 A53310	phoromone cad1 bin
35	88	7.2	788	2 A71076	hypothetical prote
36	87.5	7.2	1946	2 AE1449	hypothetical prote
37	87	7.1	914	2 TC8081	probable myrosinas
38	87	7.1	988	2 TC8102	myrosinase-binding
39	86.5	7.1	722	2 E71403	hypothetical prote
40	86.5	7.1	1449	2 T30857	glucosyltransferas
41	86	7.1	1388	2 T38720	chromodomain helic
42	85.5	7.0	638	2 AH0340	putative autotransp
43	85.5	7.0	1449	2 T30552	glucosyltransferas
44	85	7.0	1090	2 AG1749	glycosidase homolo
45	84.5	6.9	443	2 S23771	outer membrane por
46	84	6.9	232	2 F89807	exotoxin 13 [impor
47	83.5	6.9	282	2 A41025	aspergillopepsin I
48	83.5	6.9	292	2 B89807	exotoxin 9 [impor
49	83	6.8	226	2 G89806	exotoxin 6 [impor
50	83	6.8	444	2 H83624	probable porin PAO
51	83	6.8	2893	2 A64556	toxin-like outer m
52	82.5	6.8	328	2 F64187	p-aminobenzoate sy
53	82.5	6.8	455	2 S39663	aminopeptidase hom
54	82.5	6.8	600	1 D65000	NADH2 dehydrogenas
55	82.5	6.8	600	2 B91025	NADH dehydrogenase
56	82.5	6.8	600	2 C85869	NADH dehydrogenase
57	82	6.7	123	2 E84752	hypothetical prote
58	82	6.7	466	2 S36209	dep protein precur
59	82	6.7	631	2 S70908	transferrin-bindin
60	82	6.7	644	2 T33730	hypothetical prote
61	82	6.7	745	2 D82568	conserved hypothet
62	82	6.7	843	2 H72204	pullulanase - Ther
63	82	6.7	888	2 C90595	hypothetical prote
64	81.5	6.7	227	2 C89808	exotoxin 15 [impor
65	81.5	6.7	374	2 AH1903	hypothetical prote
66	81.5	6.7	1269	2 A90267	proteinase related
67	81.5	6.7	2288	2 T29999	hypothetical prote
68	81	6.7	411	2 AI1161	flagellar hook pro
69	81	6.7	411	2 AI1520	flagellar hook pro
70	81	6.7	611	2 T15410	hypothetical prote
71	81	6.7	992	2 T28421	probable DNA-direc
72	81	6.7	2167	2 A71489	cell wall-associat
73	80.5	6.6	1395	2 S25997	gene atpA intron 1
74	80.5	6.6	1704	2 A55426	gingipain R (EC 3 .
75	80.5	6.6	1883	2 C82875	hypothetical prote
76	80	6.6	345	2 A64370	adenylosuccinate s
77	80	6.6	411	2 B69006	phosphoglycerate k
78	80	6.6	501	2 C86460	probable cytochrom
79	80	6.6	1151	2 A45226	integrin alpha-1 c
80	80	6.6	2044	2 AB1180	probable peptidogl
81	80	6.6	2902	2 C71953	toxin-like outer m
82	79.5	6.5	445	2 E86440	probable chloropla
83	79.5	6.5	637	2 S36523	El protein - human
84	79.5	6.5	692	2 B64381	hypothetical prote
85	79	6.5	453	2 D71064	probable phospho-s
86	79	6.5	478	2 F90497	hypothetical prote
87	79	6.5	490	2 D82668	dihydrolipoamide d
88	79	6.5	551	2 G72865	chitinase - Autogr
89	79	6.5	1025	2 S69790	fibronectin-bindin
90	79	6.5	1518	2 A44811	glucosyltransferas
91	79	6.5	3890	2 C89921	hypothetical prote
92	78.5	6.4	232	2 B89807	exotoxin 12 [impor
93	78.5	6.4	396	2 S56954	protein YBR162C ho
94	78.5	6.4	413	2 S59650	hypothetical prote
95	78.5	6.4	468	2 T25475	hypothetical prote
96	78.5	6.4	475	2 C86863	N-acetylmuramoyl-L
97	78.5	6.4	762	2 A34355	cell surface prote
98	78.5	6.4	1959	2 AG1085	hypothetical prote
99	78	6.4	359	2 G82197	RstA1/RstA2 protei
100	78	6.4	376	1 JQ0474	alcohol dehydrogen

ALIGNMENTS

RESULT 1

A28179

enterotoxin E precursor - Staphylococcus aureus

C:Species: Staphylococcus aureus

C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 15-Oct-1999

C:Accession: A28179

R:Couch, J.L.; Soltis, M.T.; Betley, M.J.

J. Bacteriol. 170, 2954-2960, 1988

A:Title: Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gene.

A:Reference number: A28179; MUID:88257005; PMID:3384800

A:Accession: A28179

A:Molecule type: DNA

A:Residues: 1-257 <COU>

A:Cross-references: GB:M21319; NID:g153001; PIDN:AAA26617.1; PID:g153002

C:Superfamily: enterotoxin B

Query Match 90.9%; Score 1107; DB 2; Length 257;

Best Local Similarity 89.7%; Pred. No. 9.7e-88; Indels 0; Gaps 0;

Matches 209; Conservative 9; Mismatches 15;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESDQFLNTLLFKGFFTG 60

DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESDQFLNTLLFKGFFTG 84

QY 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYCCAGGTPNKTKACMYGGVTLHDNNELT 120

DB 85 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYCCAGGTPNKTKACMYGGVTLHDNNELT 144

QY 121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180

DB 145 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204

QY 181 RGLIVFHSSEGSTVSYDLFDAQQGYPTLLRIYRDNTTISSTLSISLYLYTT 233

DB 205 RGLIVFHSSEGSTVSYDLFDAQQGYPTLLRIYRDNTTISSTLSISLYLYTT 257

RESULT 2

A28664

enterotoxin A precursor - Staphylococcus aureus

C:Species: Staphylococcus aureus

C>Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 15-Oct-1999

C:Accession: A28664; A29566

R:Berlev, M.J.; Mekalanos, J.J.

J. Bacteriol. 170, 34-41, 1988

A:Title: Nucleotide sequence of the type A staphylococcal enterotoxin gene.

A:Reference number: A28664; MUID:88086892; PMID:3335483

A:Accession: A28664

A:Molecule type: DNA

A:Residues: 1-257 <BET>

A:Cross-references: GB:M18970; NID:g153120; PIDN:AAA26681.1; PID:g153121

A:Experimental source: strain FR1337

R:Huang, I.X.; Hughes, J.L.; Bergdoll, M.S.; Schantz, E.J.

J. Biol. Chem. 262, 7006-7013, 1987

A:Title: Complete amino acid sequence of staphylococcal enterotoxin A.

A:Reference number: A29566; MUID:87222293; PMID:3584106

A:Accession: A29566

A:Molecule type: protein

A:Residues: 25-241, 'S', 243-257 <HUA>

A:Gene: entA

C:Genetics:

A:Map position: 6

C:Superfamily: enterotoxin B

Query Match

Best Local Similarity 77.8%; Score 948; DB 2; Length 257;

Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESDQFLNTLLFKGFFTG 60

DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESDQFLNTLLFKGFFTG 84

QY 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYCCAGGTPNKTKACMYGGVTLHDNNELT 120

DB 85 HSWYNDLLVDLFDKIDVKGKGVLDLYGAYGYCCAGGTPNKTKACMYGGVTLHDNNELT 144

QY 121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180

DB 145 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204

QY 181 RGLIVFHSSEGSTVSYDLFDAQQGYPTLLRIYRDNTTISSTLSISLYLYTT 233

DB 205 RGLIVFHSSEGSTVSYDLFDAQQGYPTLLRIYRDNTTISSTLSISLYLYTT 257

RESULT 3

C89984

enterotoxin P [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus

C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001

C:Accession: C89984

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.

A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: C89984

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-260 <KUR>

A:Cross-references: GB:BA000018; PID:g13701743; PIDN:BA843036.1; GSPDB:GN00149

A:Experimental source: strain N315

C:Genetics:

A:Gene: sep

C:Superfamily: enterotoxin B

Query Match

Best Local Similarity 75.4%; Score 918; DB 2; Length 260;

Matches 170; Conservative 21; Mismatches 42; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTSSSEKSDQFLNTLLFKGFFTG 60

DB 28 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTSSSEKSDQFLNTLLFKGFFTG 87

QY 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYCCAGGTPNKTKACMYGGVTLHDNNELT 120

DB 88 HQWYNDLLVDLGSKDTANIYKGGKVDLYGVYGYCTGTPFKTACMYGGVTLHDNNQLE 147

QY 121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180

DB 148 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 207

QY 181 RGLIVFHSSEGSTVSYDLFDAQQGYPTLLRIYRDNTTISSTLSISLYLYTT 233

DB 208 RGLIEFHSSGSDSVGYDLFGAQQGYPTQLRIYRDNTTISSTLSISLYLYTT 260

RESULT 4

A33953

enterotoxin D precursor - Staphylococcus aureus

C:Species: Staphylococcus aureus

C>Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 15-Oct-1999

C:Accession: A33953

R:Bayles, K.W.; Iandolo, J.J.

J. Bacteriol. 171, 4799-4806, 1989

A:Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin I

A:Reference number: A33953; MUID:89359112; PMID:2549000

A:Accession: A33953

A:Status: Preliminary

A:Molecule type: DNA

A:Residues: 1-258 <BAY>

A:Cross-references: GB:M28521; NID:g1492109; PIDN:AAB06195.1; PID:g7558691

QY 187 HSEGSTVSYDLFPAQGGYPTDRLRIYRNTTISSTLSISL 228
 Db 194 HMDGNSFSYDLFTYGYLPEFLKIYKDNKTVDSTQFHLDV 235

RESULT 8

extracellular enterotoxin type I precursor [imported] - Staphylococcus aureus (strain N3)
 C:Species: Staphylococcus aureus
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: C89969
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
 A:Reference number: A89758; PMID:21311952; PMID:11418146
 A:Accession: C89969
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-242 <KUR>
 A:Cross-references: GB:BA000018; PID:gl3701621; PIDN:BA42914.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: sei
 C:Superfamily: enterotoxin B

Query Match 24.3%; Score 296.5; DB 2; Length 242;
 Best Local Similarity 32.4%; Pred. No. 4.7e-18;
 Matches 77; Conservative 39; Mismatches 85; Indels 37; Gaps 10;
 QY 8 NEKDLRKSELOQ-TALGNLKQIY----YNSKAITSEKSADQFLNTLLFKGFTGHP 62
 Db 17 NIKL---TYAQDIDGVGNLRFYTKHDYIDLKGVTDKLP----IANQLEFS--IG-- 64
 QY 63 WYNDLLVDLGTAASTSEYSGSDVLYGAYGYQCAGTPNKTACMGVTLHDNNRLTEE 122
 Db 65 -TNDLISESNWDEISFKGKKLDFIDYNGPC-----KSKYMYGGATL-SQYLNLSA 116
 QY 123 KKVPIINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFG-GK--- 178
 Db 117 RKIPINLWNGKHKTISTDKIATNKKLVTAQEIIDVKLRVLOEYNIYGHNTGKKEYG 176
 QY 179 -----VQRLVHFSSSEGSTVSYDLFPAQGGYPTDRLRIYRNTTISSTLSISL 228
 Db 177 YKSKFYSGFNNGKVLFLHNLNKSFSYDLFTYGDGLGFLPSFLKIYEDNKIISEKPHLDV 234

RESULT 9

S11885
 enterotoxin C3 - Staphylococcus aureus
 C:Species: Staphylococcus aureus
 C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 16-Jul-1999
 C:Accession: S11885
 R:Hoover, C.J.; Hackett, S.P.; Bohach, G.A.
 Mol. Gen. Genet. 220, 323-333, 1990
 A:Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence comparison
 A:Reference number: S11885; PMID:90220508; PMID:2325627
 A:Accession: S11885
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-266 <HOV>
 A:Cross-references: GB:X51661; NID:G46570; PIDN:CA335972.1; PID:G46571
 C:Superfamily: enterotoxin B

Query Match 23.4%; Score 284.5; DB 2; Length 266;
 Best Local Similarity 32.5%; Pred. No. 5.7e-17;
 Matches 76; Conservative 45; Mismatches 94; Indels 19; Gaps 9;
 QY 11 DLKKSSELOQTALGNLKQIYNSKAITSSP-KSADQFLNTLLFKGFTGHPYNDLLV 69
 Db 37 DLKKSSEFTGT-MGNMK--YLYDDHYVSATKVKSVDRFLAHLDIYNSDKKLKNYDKVKT 93

QY 70 DLGSTAATSEYSGSDVLYGAYGYQC-----AGGTENKTACMGVTLHDNNRLTEE 122
 Db 94 ELLNEDLAKYKDEVDVYGSNYVYCVFSSKDNVKGVTGKTCWYGGIYKHEGHNFDNG 153
 QY 123 --KKVPIINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKVKV 180
 Db 154 NLQNLVVRVY-ENKRTISFE-VQTDKKSVTQAELDIKARNFLINKNLYEFNS--SPYE 209
 QY 181 RGLVHFSSSEGSTVSYDLFPAQGGYPTDRLRIYRNTTISSTLSISL 232
 Db 210 TGYIKFIENNGNTFWIDMPPAGPKFDQSKYLMNNDKNTVDSKSVKIEVHLTT 263

RESULT 10

D89969
 enterotoxin SEM [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: D89969
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
 A:Reference number: A89758; PMID:21311952; PMID:11418146
 A:Accession: D89969
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-239 <KUR>
 A:Cross-references: GB:BA000018; PID:gl3701622; PIDN:BAE42915.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: sem
 C:Superfamily: enterotoxin B

Query Match 23.2%; Score 282; DB 2; Length 239;
 Best Local Similarity 29.7%; Pred. No. 8.2e-17;
 Matches 68; Conservative 40; Mismatches 77; Indels 44; Gaps 6;
 QY 23 LGNLKQIYVYNSKAIT--SSEKSADQFLNTLLFKGFTGHPWYNDLLVDLGSTAAATSE- 79
 Db 24 VGVNLNRYGSGYPEDHQISINPENNLHSHQLVF-----SMDNSTVTAAEF 68
 QY 80 -----YEGSSVDLYGAYGYQCAGTPNKTACMGVTLHDNNRLTEEKYPINLWI 131
 Db 69 KNVDDVKFKHADVGVLSYSGYCL-----KNKYIYGGVTL-AGDYLEKRRIPINLWV 122
 QY 132 DGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLY-----NSDSFGGKV 179
 Db 123 NGEHOTISTDKVSTNKKLVTAQEIIDVKLRVLOEYNIYGHNTGKRNKSKFSFSGF 182
 QY 180 QRGLVHFSSSEGSTVSYDLFPAQGGYPTDRLRIYRNTTISSTLSISL 228
 Db 183 NAGKILFHLNDGSPSYDLFTGTQQAESFLKIYNDKNTVETEKPHLDV 231

RESULT 11

A60114
 enterotoxin C-2 precursor - Staphylococcus aureus
 N:Alternate names: enterotoxin C-3 precursor
 C:Species: Staphylococcus aureus
 C:Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 16-Jul-1999
 C:Accession: A60114; A33866
 R:Bohach, G.A.; Schlievert, P.W.
 Infect. Immun. 57, 2249-2252, 1989
 A:Title: Conservation of the biologically active portions of staphylococcal enterotoxins
 A:Reference number: A60114; PMID:89277549; PMID:2543637
 A:Accession: A60114
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-266 <BOH>
 A:Accession: B60114

A:Title: Nucleotide sequence of the enterotoxin B gene from *Staphylococcus aureus*.
A:Reference number: S27350; MUID:86168029; PMID:3957869
A:Accession: S27350
A:Molecule type: DNA
A:Residues: 1-266 <JON>
A:Cross-references: EMBL:M11118; NID:g152999; PIDN:AAA88550.1; PID:g153000
A:Experimental source: strain S6
A:Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3518-3525, 1970
A:Title: The primary structure of staphylococcal enterotoxin B. III. The cyanogen bromide
A:Reference number: A92065; MUID:71007902; PMID:5470821
A:Accession: A92065
A:Molecule type: protein
A:Residues: 28-55, 'NND', '59-68', 'NE', '71', 'FDLIYL', '78-117, 119-127', 'N', '129', 'D', '131-132', 'ENT',
A:Experimental source: strain S-6
B: Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3511-3517, 1970
A:Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, composition
A:Reference number: A92064; MUID:71007901; PMID:5470820
A:Contents: annotation; chymotryptic peptides
R: Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3493-3510, 1970
A:Title: The primary structure of staphylococcal enterotoxin B. I. Isolation, composition
A:Reference number: A92063; MUID:71007900; PMID:5470819
A:Contents: annotation; tryptic peptides
R: Schantz, E.J.; Roessler, W.G.; Wagman, J.; Spero, L.; Dunnehy, D.A.; Bergdoll, M.S.
Biochemistry 4, 1011-1016, 1965
A:Title: Purification of staphylococcal enterotoxin B.
A:Reference number: A90548; MUID:66035792; PMID:4953912
A:Contents: annotation; biological source of protein
R: Akhlov, V.Y.; Kilinsky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.; Moskaleva, E.Y.; Sveshni
Eur. J. Biochem. 209, 823-828, 1992
A:Title: Identification of functionally active fragments of staphylococcal enterotoxin B
A:Reference number: S27240; MUID:93049338; PMID:1425690
A:Accession: S27240
A:Molecule type: protein
A:Residues: 28-42, 128-148 <ALA>
C:Superfamily: enterotoxin B
C:Keywords: enterotoxin; extracellular protein; toxin
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-266/Product: enterotoxin B #status experimental <MAT>
F:120-140/Disulfide bonds: #status experimental

Query Match 22.0%; Score 268.5; DB 1; Length 266;
Best Local Similarity 31.6%; Pred. No. 1.4e-15;
Matches 77; Conservative 44; Mismatches 104; Indels 19; Gaps 8;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSAQDFLNTLLFKGFFTG 60
Db 27 AESQDPKPDDELHKSKFTG-LNENMK-VLYDDNHVSAINVKSIDQFLFDLIYSIKDTK 84

QY 61 HPVNDLLVDLGSTAAITSEYSSVDLYGAYGYQC-----AGTPTNKACMYGG 110
Db 85 LGNYDNRVVEFKNLADKYDKYVDVFGANYTYQCYFSKNTDINSHQTDKREKTCMYGG 144

QY 111 VTLDNNRLTEKKVPINLWDGKQTTVPIDKTSKKEVTVQELDLQARHYLHGKFLY 170
Db 145 VTEHGNQLDKYISITRVFEDGK-NLLSPD-VQTNKKKSVTAQELDIKARNFLINKNL 202

QY 171 NSDSFGKGVQGVILVPHSSSGSTVSYDLFDPAQGYPD--TLRIYRDNTTISSTLSISL 228
Db 203 EFNN--SPYETGYIKFTIENENS-FWYDMPAPGDKFDQSKYLMYNDNKWDSKDKIEV 259

QY 229 YLYT 232
Db 260 YLYT 263

RESULT 14
ENSAC1
enterotoxin C-1 precursor - *Staphylococcus aureus*
C:Species: *Staphylococcus aureus*
C:Date: 15-Nov-1984 #sequence_revision 05-Jan-1996 #text_change 18-Jun-1999

C:Accession: S06356; A01816
R:Bohach, G.A.; Schlievert, P.M.
Mol. Gen. Genet. 209, 15-20, 1987
A:Title: Nucleotide sequence of the staphylococcal enterotoxin C1 gene and relatedness to
A:Reference number: S06356; MUID:88038352; PMID:2823067
A:Accession: S06356
A:Molecule type: DNA
A:Residues: 1-266 <BOH>
A:Cross-references: EMBL:X08915; NID:946586; PIDN:CAA29260.1; PID:946567
R:Schmidt, J.J.; Spero, L.
J. Biol. Chem. 259, 6300-6306, 1983
A:Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1.
A:Reference number: A01816; MUID:83213327; PMID:6189824
A:Accession: A01816
A:Molecule type: protein
A:Residues: 28-75, 'IL', '78-176', 'N', '178-266 <SCH>
C:Genetics:
C:Gene: entC1
C:Superfamily: enterotoxin B
C:Keywords: enterotoxin
F:1-27/Domain: signal sequence #status predicted <SIG>
F:28-266/Product: enterotoxin C-1 #status experimental <MAT>
F:120-137/Disulfide bonds: #status experimental

Query Match 21.6%; Score 263.5; DB 1; Length 266;
Best Local Similarity 30.6%; Pred. No. 3.7e-15;
Matches 75; Conservative 45; Mismatches 104; Indels 21; Gaps 9;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSAQDFLNTLLFKGFF 58
Db 27 AESQDPKPDDELHKSKFTG-LNENMKVLYDDHVS---ATKVSVDKFLAHDLIYNISD 82

QY 59 TCHPWYNDLLVDLGSTAAITSEYSSVDLYGAYGYQC-----AGTPTNKACMYGGV 111
Db 83 KKLKNYDKVKTELLNEGLAKKYDEVVDVYGSYVYVNCYFSSKDNVGVKGTCTMYGGI 142

QY 112 TLHDNNRLTE--KKVPINLWDGKQTTVPIDKTSKKEVTVQELDLQARHYLHGKFL 169
Db 143 TKHEGNHFDNGNLQNLVIRVY-ENKNTISPE-VQTDKKSVTQAEIDIKARNFLINKNL 200

QY 170 NSDSFGKGVQGVILVPHSSSGSTVSYDLFDPAQGYPD--TLRIYRDNTTISSTLSIS 227
Db 201 YEFNS--SPYETGYIKFTIENNGTFFWYDMPAPGDKFDQSKYLMYNDNKTVDSKVKIE 258

QY 228 YLYT 232
Db 259 YLYT 263

RESULT 15
S18783
exotoxin type A precursor (allele 3) - *Streptococcus pyogenes* phage (strain MGAS158 isolate
N:Alternate names: scarlet fever toxin
C:Species: *Streptococcus pyogenes* phage
A:Variety: strain MGAS158 isolate Nebraska; strain MGAS485 isolate Yugoslavia; strain MG
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
A:Accession: S18783; S18793; S18801; S18798
R:Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A:Title: Characterization and clonal distribution of four alleles of the speA gene encodi
A:Reference number: S18782; MUID:92044323; PMID:1940804
A:Accession: S18783
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEL>
A:Cross-references: EMBL:X61568; NID:947289; PIDN:CAA43766.1; PID:947290
A:Experimental source: strain MGAS158 isolate Nebraska unassigned phage
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18793
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEA>
A:Cross-references: EMBL:X61569; NID:947313; PIDN:CAA43767.1; PID:947314

A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NEH>
A:Cross-references: EMBL:X61566; NID:947317; PIDN:CAA43764.1; PID:947318
A:Experimental source: strain MGAS492 isolate United Kingdom unassigned phage
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18799
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-236 <NES>
A:Cross-references: EMBL:X61567; NID:947325; PIDN:CAA43765.1; PID:947326
A:Experimental source: strain MGAS496 isolate Germany unassigned phage
A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C:Genetics:
A:Gene: speA2
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
F:1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F:23-236/Product: exotoxin type A (fragment) #status predicted <MAT>

Query Match 20.4%; Score 248.5; DB 2; Length 236;
Best Local Similarity 31.6%; Pred. No. 6.1e-14;
Matches 73; Conservative 44; Mismatches 95; Indels 19; Gaps 10;

QY 4 SEETNEKDLRKSELOGTAL-GNLKQIYY-YNSKAIT-SSEKSAQDPLTNTLLPKGFFTG 60
DB 17 SQEVAQDPDPQSQRHSLVKNLQNIYFLYEGDPVTHENVKSDQLSHDLIYN---VS 73

QY 61 HPWYNDLLVDLGPSTAATSEYEGSSVDLYGAYGYQC-AGGTPNKTCMVGTVLHNNRL 119
DB 74 GPNYDKLTKELKNQEMATFLPKDNVDIYSEVYHLCVLCENASACIYGVTHNEGNHL 133

QY 120 TEKKVPINLWDGKQTVPIDKVKTSKEVTVQELDLQARHYLHGKGLYNSDSFGGKV 179
DB 134 EIPKKIVKVSIDGIQ-SLSFD-IETNKKMVTQAEIDYKVRKYLTDNKKQYITNGP--SKY 189

QY 180 QRGLIVFHSSEGSTVSVDLFD---AQGQVPTLLRIYRNTTISLSLSI 226
DB 190 ETGYIKIPKNKESFWDFPEPEFTQSKY----LMYKDNELDSNTSQI 236

RESULT 18
G89968
extracellular enterotoxin type G precursor [imported] - Staphylococcus aureus (strain N3)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: G89968
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G89968
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <KUR>
A:Cross-references: GB:BA000018; PID:g13701617; PIDN:BA42910.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: seg
C:Superfamily: enterotoxin B

Query Match 19.8%; Score 241; DB 2; Length 258;
Best Local Similarity 28.8%; Pred. No. 3e-13;
Matches 72; Conservative 48; Mismatches 88; Indels 42; Gaps 12;

QY 3 KSEINKEKDLRKSELOGTALGNLQIYY---YNSKAITSSKSAQDPLTNTLLPKGFFT 59
DB 30 KLDENKVSQYKNN--RGT-MGNVMNLYTSPVVEGRGVNSR---QFUSHDLIFP---I 79
QY 60 GHPWYNDLLVDLGPSTAATSEYEGSSVDLYGAYGYQCA-----GGTPNKTCM 107
A:Gene: yent2

Db 80 EYKSNVKTLENTLANNYKDKKVDIFGVYPYFTCIIPKSEPDINQFEG-----CCM 134
QY 108 YGGVTLH--DNNRLTEKKVPINLWDGKQTVPIDKVKTSKEVTVQELDLQARHYLHG 165
Db 135 YGGLTFNSSENER--DKLITVQVTDNRQSLG--FTITTKNNMTIQELDYKARHLTK 189
QY 166 KFGLYNSDSFGGKVQRGLIVFHSSEGSTVSVDLFDAGQVPT---LLRIYRNTTISST 222
Db 190 EKKLYEFD--GSAFESGYIKETERNKNTSFWDLPKXELVPFVYPYKFLNIYGDKNKVDK 247
QY 223 SLISLSLYLT 232
Db 248 SIKMEVFLNT 257

RESULT 19
A26152
streptococcal pyrogenic exotoxin type A precursor - Streptococcus sp.
N:Alternate names: scarlet fever toxin; SPE type A (spear)
C:Species: Streptococcus sp.
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A26152
R:Johnson, L.P.; L'Italien, J.J.; Schlievert, P.M.
Mol. Gen. Genet. 203, 354-356, 1986
A:Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to Staf
A:Reference number: A26152; MUID:86284313; PMID:3526093
A:Accession: A26152
A:Molecule type: DNA
A:Residues: 1-250 <JOH>
C:Superfamily: enterotoxin B
C:Keywords: exotoxin

Query Match 18.1%; Score 220; DB 1; Length 250;
Best Local Similarity 28.9%; Pred. No. 1.9e-11;
Matches 66; Conservative 42; Mismatches 99; Indels 22; Gaps 9;

QY 14 KXSELOGTALGNLQIYY-YNSKAITSE--KSADQELTNTLLPKGFFTGHFWNDLLVD 70
DB 35 KPSQLQRNLVKTFKIYIFFMVRLTVTHENVKSDQLSHDLIYN---VSGPNYDKLKE 91

QY 71 LGSTAAATSEYEGSSVDLYGAYGYQC-AGGTPNKTCMVGTVLHNNRLTEKKVPINL 129
DB 92 LKNQEMATFLPKDNVDIYSEVYHLCVLCENASACIYGVTHNEGNHLEIPKIVKV 151

QY 130 WIDGKQT-TVPIDKVKTSKEVTVQELDLQARHYLHGKGLYNSDSFGGKVQRGLIVFHS 188
DB 152 SIDGIQSLSPDIEQIKNG---NCSRISTYVRKYLTDNKKQYITNGP--SKYETGVKIFIP 205

QY 189 SEGSTVSVDLFD---AQGQVPTLLRIYRNTTISLSLSIYLT 232
DB 206 KNKESFWDFPEPEFTQSKY----LMYKDNELDSNTSQIEVLYLT 249

RESULT 20
A89969
enterotoxin YENT2 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: A89969
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: A89969
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <KUR>
A:Cross-references: GB:BA000018; PID:g13701619; PIDN:BA42912.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: yent2

Query Match 15.6%; Score 190; DB 2; Length 136;
Best Local Similarity 34.1%; Pred. No. 3.2e-09;
Matches 46; Conservative 25; Mismatches 54; Indels 10; Gaps 5;

QY 103 KTACMYGGVTLHDNNRTEKKV--PINLW---DGRQTTVPIDKVTSKKEVTQVQLD 157
DB 2 KKTQWGGVTEHDGNQDKNNSTNSHNLIKVYENERSLSFD-IPTNKNITQAQIDY 60

QY 158 QARYHLCKFGLYNSDFGGKVGQGLIVFHSSEGSTVSYDLFDAQGQ--YPTLLRIYRD 215
DB 61 KVRNYLLKHNLYBFS--SPYETGYIKFIEGSGHSFYDLMPSGKKFYPTKYLIIYND 118

QY 216 NTTISSTLSISLYL 230
DB 119 NKTVESKSNVVEHL 133

RESULT 21
A89942
hypothetical protein SA1430 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C/Accession: A89942
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: A89942
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-157 <KUR>
A:Cross-references: GB:BA000018; PID:gl3701400; PIDN:BA842694.1; GSPDB:GN00149
A:Experimental source: strain N315
A:Genetics:
A:Gene: SA1430

Query Match 14.6%; Score 178; DB 2; Length 157;
Best Local Similarity 31.4%; Pred. No. 4.2e-08;
Matches 37; Conservative 21; Mismatches 59; Indels 2; Gaps 1;

QY 1 SEKSEINEKLRKSELOGTALGNLKOIYYNSKAITSSSEKSDAQFLTWLLPKGFTG 60
DB 42 TNSAIEYSDLHKSKFDSKRLSNKQSFNPTQ--LENKNTNDRLLKHLDFHMFVN 99

QY 61 HPWYNDLLVLDLSTAAATSEYEGSSVDLYGAYGYOCAGTGNKACMYGGVTLHDNNR 118
DB 100 VASKDFKVERENALSKKFNKINIDIVAGSYSECHGATNKTCQSYGGVTLSDNNK 157

RESULT 22
A30509
exotoxin C precursor - Streptococcus pyogenes
C:Species: Streptococcus pyogenes
C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 17-Mar-2000
C/Accession: A30509
R;Goshorn, S.C.; Schlievert, P.M.
Infect. Immun. 56, 2518-2520, 1988
A:Title: Nucleotide sequence of streptococcal pyrogenic exotoxin type C.
A:Reference number: A30509; MUID:88314303; PMID:3045005
A:Accession: A30509
A:Molecule type: DNA
A:Residues: 1-235 <GOS>
A:Cross-references: GB:M39514; NID:gl53820; PIDN:AAA27017.1; PID:gl53821
C:Superfamily: enterotoxin B
C:Keywords: exotoxin

Query Match 12.8%; Score 155.5; DB 2; Length 235;
Best Local Similarity 24.2%; Pred. No. 6.1e-06;
Matches 57; Conservative 37; Mismatches 77; Indels 65; Gaps 11;

QY 47 FLTNTLLFKGFTGH-----PW-YNDLLVLDLGSTAA-----TSE 79
DB 11 FIITVILISTYTHQSDSKDISNVKSDLLYAITPYDYKDCRVNFTTHLIDTQK 70

QY 80 YEGSS-----VDLYGAYGYOCAGTGNKACMYGGVTLHDNNRL 119
DB 71 YRGKDYIISSESYEASQKFRDDHVDVFGFLYINSHTG-----EYIYGGITPAQNNKV 125

QY 120 TEEKKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDLCARHYLHGKFLYNSDS--FGG 177
DB 126 NH--KULGNLFISGSOQNLNKKIILEKDIVTFQIDFKIRKYLMDNKKIYDATSPYVSG 183

QY 178 KVQRGLIVFHSSEGSTVSYDLFDA--QGOYPTLLRIYRDNTTISSTLSLS--LSYL 230
DB 184 RIEIG-----TKDGKHEQIDLFDSNPGTRSDIFAK-YKDNRIINMKNSHFDIYL 233

RESULT 23
H89941
hypothetical protein SA1429 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C/Accession: H89941
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H89941
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-62 <KUR>
A:Cross-references: GB:BA000018; PID:gl3701399; PIDN:BA842693.1; GSPDB:GN00149
A:Experimental source: strain N315
A:Genetics:
A:Gene: SA1429

Query Match 9.4%; Score 115; DB 2; Length 62;
Best Local Similarity 32.1%; Pred. No. 0.0032;
Matches 18; Conservative 16; Mismatches 22; Indels 0; Gaps 0;

QY 176 GKKVQSGGLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNTTISSTLSISLYL 231
DB 5 GGDIVKGVKYNHDDQCNVEYDFYNLNGEYGYEVLKMYADNKTINRDLHLDIYLF 60

RESULT 24
XCSAS1
toxic shock syndrome toxin-1 precursor - Staphylococcus aureus
N:Alternate names: TSST-1
C:Species: Staphylococcus aureus
C>Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 18-Jun-1999
C/Accession: A24606; B24606
R;Blomster-Hautamaa, D.A.; Kreiswirth, B.N.; Kornblum, J.S.; Novick, R.P.; Schlievert, P.
J. Biol. Chem. 261, 15783-15786, 1986
A:Title: The nucleotide and partial amino acid sequence of toxic shock syndrome toxin-1.
A:Reference number: A24606; MUID:87057222; PMID:3782090
A:Accession: A24606
A:Molecule type: DNA
A:Residues: 1-234 <BIO>
A:Cross-references: GB:J02615; NID:gl53122; PIDN:AAA26682.1; PID:gl53123.
A:Accession: B24606
A:Molecule type: protein
A:Residues: 41-106; 199-224 <BIO>
A:Note: the authors translated the codon ACT for residue 20 as Ile and GGG for residue 1;
C:Superfamily: toxic shock syndrome toxin
C:Keywords: toxic shock syndrome; toxin
F;1-40/Domain: signal sequence #status predicted <SIG>
F;41-234/Product: toxin shock syndrome toxin-1 #status experimental <MAT>

Query Match 8.2%; Score 100; DB 1; Length 234;
Best Local Similarity 24.5%; Pred. No. 0.36;

A;Cross-references: GB:BA000018; PID:g13700320; PIDN:BAB41618.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: set14
C;Superfamily: toxic shock syndrome toxin

Query Match 8.0%; Score 98; DB 2; Length 227;
Best Local Similarity 26.4%; Pred.No.0.51;
Matches 53; Conservative 28; Mismatches 78; Indels 42; Gaps 9

Qy 8 NEKDRLKSELOCTALGNLKOIY-YTNSKAITSSEKSADOFNTLLFKGFTTGHPWYNDD 66
Db 33 NQSYNKXDK-----EALYYTYTKTWEMKNISALKHGENLRFX--PRGIKIQLV 81

Qy 67 LVLGLGSTAASTSEYGSSV-----DLYGAYGYQCAGGT--PNKTACMGVGVTLDHNN 117
Db 82 LPNGDSKFQORSYEGDLVFVQEKRDGHIFY---TVGGVIQNKKTS----GVWSAPIL 134

Qy 118 RTEEEKVPINLWDIKOTTPIDKVTSKEVTQVELDQAHHYLHGKFGLYNSDFSG 177
Db 135 NISXKK-----GEDAFVKGPYPPIYEKITLKELDYLKRKHLEKYGLYKTIKSDG 185

Qy 178 KVQRGLIVFHSSEGSTVSVDL 198
Db 186 RVKISL-----KDGsfynldl 201

RESULT 27
B89992
toxic shock syndrome toxin-1 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: B89992
R.;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui,
ma, A.; Mizutani-Ue, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Seki,
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A99756; PMID:21311952; PMID:11418146
A;Accession: B89992
A>Status: preliminary
A:Molecule type: DNA
A;Residues: 1-234 <Kur>
A;Cross-references: GB:BA000018; PID:g13701806; PIDN:BAB43089.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: tsst
C;Superfamily: toxic shock syndrome toxin

Query Match 8.0%; Score 98; DB 2; Length 234;
Best Local Similarity 24.6%; Pred.No.0.53;
Matches 49; Conservative 33; Mismatches 57; Indels 60; Gaps 13

Qy 25 NLKQI---YYNSKAITSSE-----KSAQQFLNTLLFKGFTTGHPWYNDDL-- 68
Db 45 NIKLDDWYSGSPTFTNSEVLDNSLGSMRIKNTDGSII-SLIIFPS-----PYISPAPT 98

Qy 69 ---VDLGSATATSEYGESSVDLYGAYGYQCAGGTNPKTACMGVGVTLDHNNRLTEEEKV 125
Db 99 GEKVUL-NTRKTKSQHTS---EGTYIHFOISGVT-----NTEKLPPIEL 140

Qy 126 PINLMWDKGQTVV---PIDKVTSKEVTQVEILDQAHHYLHGKFGLY-NSDSFG--KV 179
Db 141 PLKRVHKGDPLKYWP-----KPDKQLASTLDLFIRHQLTQHIGLYRSSDKTTGGYWKI 196

Qy 180 QRGLIVFHSSEGSTVSVDL 198
Db 197 T-----MNDGSTVQSDEL 208

RESULT 28
T41863
Chitinase chi-A orf126 - Bombyx mori nuclear polyhedrosis virus (isolate T3)

C;Species: Bombyx mori nuclear polyhedrosis virus, BmNPV
A;Variety: isolate T3
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C;Accession: T41863
R;Gomi, S.; Majima, K.; Maeda, S.
J. Gen. Virol. 80, 1323-1337, 1999
A;Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
A;Reference number: Z2020; MUID:99281911; PMID:10355780
A;Accession: T41863
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-552 <RAM>
A;Cross-references: EMBL:L33180; NID:g3745835; PIDN:AAC63792.1; PID:g3745945
A;Experimental source: isolate T3
C;Superfamily: Serratia marcescens chitinase

Query Match 7.9%; Score 96; DB 2; Length 552;
Best Local Similarity 24.9%; Pred. No. 2.5;
Matches 46; Conservative 23; Mismatches 68; Indels 48; Gaps 11;

QY 32 YNSKAITS---SEKSAOQLTWLLPKGFTHPWYNLDLVLGSTAAATSEYEGSGVDLY 88
Db |||:::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
359 YDKIAVVNAEAKSLDKIFLMTYDFKG-----AWSN---TDLGYOTTVPAPSWNSEELY 410
QY 89 GAYIGYQC---AGGTENKT---ACMYG----GVTLHDN-NRLTEEEKKVIN-LWIDGKQT 136
Db |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
411 TTHYAVDALLEGQVDENKIIVGMVGRGWGTGVTNTNGYFSGTGNGPVGSGTWEDG--- 467
QY 137 TVPIDKVTKSKKEVTVOELDLOARHYLHGKFGLYNSDSFGGKVQRGLIYPHSSEGSTVSX 196
Db |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
468 -----VVDYRQIQKOLNNY-----VYTFDS-----AAQAAYVPDKSGLISF 505
QY 197 DLPDA 201
Db |:
506 DSIDS 510

RESULT 29
D89807
exotoxin II [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: D89807
R;Ruroda, M.; Ohira, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Uji, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: D89807
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-231 <XUR>
A;Cross-references: GB:BA000018; PID:g13700317; PIDN:BAB41615.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: setII

Query Match 7.7%; Score 94; DB 2; Length 231;
Best Local Similarity 23.6%; Pred. No. 1.2;
Matches 43; Conservative 27; Mismatches 84; Indels 28; Gaps 6;

QY 2 EKGEENEKDLRKKSELQGTALGNLKQIY-YNSKAITSS--KSADQLTWLLFKGP 57
Db |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
32 EKGERVQH-----LYDIKDLRYYSSESFEFSNISGKYENTNGSNVVRNQE 78
QY 58 FTGHWPYNDLLVLGGSTAATASEYEGSGSDLYGAAYGVQQCGGTPNKTCAMYGCVTVLHDDN 117
Db |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
79 QKHQLFP---LLGKDKDYKKGLEQNVFVKELL-----DPNGELSTVGVTCKNNK 128
QY 118 RLTEEEKKVINLWDGKQTTVPIDKVKTSKKEVTVOELDLOARHYLHGKFGLYNSDSFG 177
Db |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
129 SSTETHTLFVNK-VYGNLGDASIDSFLINKEEVELKLDELDFKIRKQAVEKGLYKGTIKY 187

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Qy 24 GNLKQIYYNSKAITSEKSA---DOFLNTLTLFKGFTGHPWYNLLDLVGLSTAAT--- 77
Db 420 GNLRDYSAFNHSTAAPSPITSLPDPYETPNFLGLDNTTSAQASSNLQVLEQTNRVR 479

Qy 78 ----SEYEGSSVDLYGAYGYQ-CAGGTPTNKTACMYGGVTLHDNNRLTEKKV-PINLWI 131
Db 480 FVPNADYNGQANUTFRWDCSGNVAGGTTGVAAVNGNATFSSNTLTASITVSPINNP 539

Qy 132 DGKQTTVPIDVKVTSKKEVTVQELDQARHYLHGKFGLYNSDS-----FGCKVQVGH 184
Db 540 QG---TTGLDKLYGTANEDIIN--GNEGNDYLFGRAGNDTLDGEGNDVYFGG---TGND 591

Qy 185 VFHSSEGSTVS 196
Db 592 TLDGEGSDLLY 603

RESULT 32
E64410
DNA-directed DNA polymerase (EC 2.7.7.7) family B, intein containing precursor - Methanococcus
N;Contains: DNA endonuclease (EC 3.1.1.1) PI-I; DNA endonuclease (EC 3.1.1.1) PI-II; DNA
C;Species: Methanococcus jannaschii
C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Sep-1996
C;Accession: E64410
R;Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
; Reich, C.I.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Werrick, J.M.; Glodek, A.;
; Olson, J.D.; Sadow, P.W.; Hanna, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A;Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C
A;Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A;Reference number: A64300; MUID:56337999; PMID:8688087
A;Accession: E64410
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1634 <BUL>
A;Cross-references: GB:U67532; GB:L77117; NID:g1591559; PID:g1591563; TIGR:MJ0885; PID:g
C;Genetics:
A;Map position: REV816304-811400
A;Start codon: TTG
C;Function: <DPL>
A;Description: as DNA-directed DNA polymerase, catalyzes the polymerization of DNA at th
C;Function: <EN1>
A;Description: as DNA endonuclease PI-Mjai, catalyzes the hydrolysis of internal phospho
C;Function: <EN2>
A;Description: as DNA endonuclease PI-Mjai, catalyzes the hydrolysis of internal phosph
C;Superfamily: DNA-directed DNA polymerase KOD
C;Keywords: endonuclease; hydrolase; nucleotidyltransferase; protein splicing
F;1-425/795-882,1359-1634/Product: DNA-directed DNA polymerase family B #status predicted
F;1-425/Domain: DNA-directed DNA polymerase family B extein 1 #status predicted <XT1>
F;426-794/Product: DNA endonuclease PI-I (pol B extein 1) #status predicted <MNT2>
F;795-882/Domain: DNA-directed DNA polymerase family B extein 2 #status predicted <XT2>
F;883-1358/Product: DNA endonuclease PI-II (pol B extein 2) #status predicted <MNT3>
F;1358-1634/Domain: DNA-directed DNA polymerase family B extein 3 #status predicted <XT3>
F;425-795/Cross-link: peptide (Arg-Ser) #status predicted
F;882-1359/Cross-link: peptide (Arg-Ser) #status predicted

Query Match 7.5%; Score 91; DB 2; Length 1634;
Best Local Similarity 21.6%; Pred. No. 27;
Matches 50; Conservative 36; Mismatches 79; Indels 79; Gaps 10;

Qy 12 LRKSELOGTALGNLKOIYYNSKAITSEKSAADQFLTNLLFKGFTGHPWYNLLVDL 71
Db 614 VRKKGKTAITLGCCKADYILKEIEIL---KNKERYLPAIL-RGPFEGDGYVTVRRV 669

Qy 72 GSTAATSEYB-----GSSVDLYGAYGYQACAGGTPTNKTACMYGGVTLHDNNRLTEKKVP 126
Db 670 VVNGQTNVYDKIFIASLLDLRLGIKVSF-----YYYSVEERGKLRV 713

Qy 127 INWIDGKQTVTFIDVKVTS-----KKEVTVQELDQARHYLHGKFGLYNSD----- 173
Db 714 IEIFSKG-----DLIKFISILSF-SRRKNLLNBIIRQKTLTKIGDYGFYDLDDVCVS 766

Qy 174 --SFGGKV-----ORGLIVFHSSEGS-TVSYDLFLDAQGGYPDDL 209
Db 767 LESYKGEVYDLTLEGRPPYFANGILTHNSLYPSIIISYNI-----SPDTL 811

RESULT 33
CS3312
thymidine phosphorylase (EC 2.4.2.4) - Mycoplasma pirum (strain BER)
C;Species: Mycoplasma pirum
C;Date: 23-Oct-1998 #sequence_revision 23-Oct-1998 #text_change 23-Dec-2002
C;Accession: CS3312
R;Tham, T.N.; Ferris, S.; Kovacic, R.; Montagnier, L.; Blanchard, A.
J. Bacteriol. 175, 5281-5285, 1993
A;Title: Identification of Mycoplasma pirum genes involved in the salvage pathways for n
A;Reference number: A53312; MUID:93352438; PMID:8349569
A;Accession: CS3312
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-419 <THA>
A;Cross-references: GB:L13289; NID:g401781; PIDN:AAA25432.1; PID:g401784
C;Genetics:
A;Genetic code: SGC3
C;Superfamily: thymidine phosphorylase/pyrimidine-nucleoside phosphorylase
C;Keywords: glycosyltransferase; pentosyltransferase

Query Match 7.2%; Score 88; DB 1; Length 419;
Best Local Similarity 27.0%; Pred. No. 8.3;
Matches 38; Conservative 22; Mismatches 57; Indels 24; Gaps 7;

Qy 47 FLTNLLFKG-FFTHGHPWYNLLDLVGLSTAATSE-----YEGSSVDLYGAYG 93
Db 57 FLTKAMTDSGKIYKFXHPEYKIKLIDKHSTGIGIGKVSIALRPILVSPDLGVAKLSGRGLG 116

Qy 94 YQCAGGTPTNKTACMYGGVTLHDNNRLTEKKV--PINLWIDGK-QTTVPIDVKVTSKKEV 150
Db 117 F--TGGTIDKLE-----SINVNTDIDLNKSKILNIAINMFIQNTDIVPADKLLYAUDRV 170

Qy 151 --TVQELDLQARHYLHGKFG 169
Db 171 TGTVDLSLPLIAASILSKKFL 191

RESULT 34
A53310
phenomone CAD1 binding protein precursor - Enterococcus faecalis plasmid PAD1
N;Alternate names: TraC
C;Species: Enterococcus faecalis
C;Date: 08-Sep-1995 #sequence_revision 08-Sep-1995 #text_change 20-Aug-1999
C;Accession: A53310
R;Tanimoto, K.; An, F.Y.; Clewell, D.B.
J. Bacteriol. 175, 5260-5264, 1993
A;Title: Characterization of the traC determinant of the Enterococcus faecalis hemolysin-
A;Reference number: A53310; MUID:93352433; PMID:8349566
A;Accession: A53310
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-543 <TAN>
A;Cross-references: NID:L19532; NID:g388267; PIDN:AAA72024.1; PID:g388269
C;Genetics:
A;Gene: traC
A;Genome: plasmid
C;Superfamily: dipeptide transport protein

Query Match 7.2%; Score 88; DB 2; Length 543;
Best Local Similarity 21.3%; Pred. No. 12;
Matches 46; Conservative 31; Mismatches 61; Indels 78; Gaps 10;

Qy 33 NSKAITSEKSAADQFLTNLLFKGFTGH-----PWYNDLLVDLGSTAATSEY- 80
Db 146 NAKELAGKQSKSE-----TLAVKS--NGNKTIELEKPTPIYFDLL-----ALRAYP 192

Qy 81 -EGSSVDLYGAYGYQACAGGTPTNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQTV 139

```

Db 193 VQKAIKEYGKDY-----GTSQKSVITNGAFNLTSLEGVGTSDK-----W-----TIS 235
Qy 140 IDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQORGLIVFHSSEGSTVSVDLF 199
Db 236 KNKEYWDQKESMEKINFQVKEINTGINDYN----- 267
Qy 200 DAQOQYDPT-----LLRIYRDNNTTISSTLSLSLYL 230
Db 268 --DQLDLDTPVTGAYAKQYKDKNEFTTLMANTWYL 301
RESULT 35
A71076
hypothetical protein PH0873 - *Pyrococcus horikoshii*
C:Species: *Pyrococcus horikoshii*
C:Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 05-Nov-1999
C:Accession: A71076
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: A71076
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-788 <KAW>
A:Cross-references: GB:AP000004; NID:G3236131; PIDN:BAA29967.1; PID:d1030910; PID:G32572
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH0873
Query Match 7.2%; Score 88; DB 2; Length 788;
Best Local Similarity 23.3%; Pred. No. 19;
Matches 48; Conservative 36; Mismatches 66; Indels 56; Gaps 10;
Qy 5 BEINEKLRKSELOQTALGNLKIYYNSKAINSSEKSDQFLNTLLFKGFTGHPWY 64
Db 180 EELNEENFRKLEQGG--IKTLLEVAYLKYYI---DKGENEYEinNKPK----- 225
Qy 65 NDLLVDLGSTAATSEYSGSSVDLYGAYGYOCAGTGNKTKACMYGGVTLHDNNRLTEBK 124
Db 226 NELKNLRSYLEASGYKYSQSIQFYVALTKG-----FVILSGLTSGTKYIAGEL- 278
Qy 125 VPINLWIDGKTTVPIDKVKTSKKEVTVQELDLQA-----RH-----YLHOK----- 166
Db 279 -----GELLDLPL--QVMSASGPNIVAKREIKSLQETINRHGFAYVGHPPGKISKIK 328
Qy 167 ----FGLYNS---DSFGGKVQORGLIV 185
Db 329 PPFIFWYDSDENDEYKKVPYGIIV 354
RESULT 36
AE1449
hypothetical protein lin0132 [imported] - *Listeria innocua* (strain Clip11262)
C:Species: *Listeria innocua*
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AE1449
R:Glaser, P.; Frangul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of *Listeria* species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AE1449
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1946 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC95365.1; PID:g16412551; GSPDB:GN00178
A:Experimental source: strain Clip11262

C:Genetics:
A:Gene: lin0132
Query Match 7.2%; Score 87.5; DB 2; Length 1946;
Best Local Similarity 22.0%; Pred. No. 69;
Matches 56; Conservative 30; Mismatches 98; Indels 71; Gaps 12;
Qy 4 SEEINEKLRKSELOQTALGNLKIYY-----YNSKAITSSBKSDQFLNTLL 53
Db 1198 TRNLNADYVRYVTGKPTDSEGNIAGVKFNWTKVIAYRGVMIWSNETADPF-----S 1252
Qy 54 FK-----GPTGHPWYNDLLDGLGSTAATSEYSGSSVDLYGAYGYOCAGGT-----P 101
Db 1253 FRQEDGSYVAE--LNGRYVDFSSGLVSTEAAGSKIDLYSAQEGVSQVSAITTKALVEP 1310
Qy 102 NTKACMYGGVTLHDNNRLTEKVKPINLWIDGKQTTVPIDKVKTSKKEVTVQ-----ELDIQ 158
Db 1311 NITA--EVSIVYDR-----VKLDVVGEDKDNNTTKKONENELF 1347
Qy 159 ARHYLHGKFGLYNSDSFGGKVQORGLIVFHS-----EGSTVSYDLFDAQGYDPTL 209
Db 1348 VNAYKEDGSTLVKSVRIDGLPRDIFVTDLSPPKVKVKEG---KYDLDGEG--PQN- 1401
Qy 210 LRIYRDNNTTISSTSL 224
Db 1402 -KYVYSETITTEKSL 1415
RESULT 37
T08081
probable myrosinase-binding protein - rape
N:Alternate names: jasmonate inducible protein
C:Species: *Brassica napus* (rape)
C:Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 11-May-2000
C:Accession: T08081
R:Geshi, N.; Brandt, A.
Planta 204, 295-304, 1998
A:Title: Two jasmonate-inducible myrosinase-binding proteins from *Brassica napus* L. seed
A:Reference number: Z16340; MUID:98192006; PMID:9530873
A:Accession: T08081
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-914 <GES>
A:Cross-references: EMBL:Y11482; NID:e1023100; PIDN:CAA72270.1; PID:e304149
A:Experimental source: cv. Global; isolate a4; seedlings
A:Note: jasmonate inducible
Query Match 7.1%; Score 87; DB 2; Length 914;
Best Local Similarity 20.1%; Pred. No. 28;
Matches 65; Conservative 35; Mismatches 89; Indels 134; Gaps 14;
Qy 2 EKSEINE-----KDLRKSELOQTALGNLKIYY-YS 34
Db 347 EKGEFNDYGFEGVKKITVGADQYSVTYIKIEYKDGKVEIREHGTSGELQEFSDVDPN 406
Qy 35 KAITSEKSDQFLT--NTLLFKGFTGHPWYNDLLDGLGSTAATSEY----- 81
Db 407 DSITEVGGYKHYNYVDTLITSLYFTTSKGTSPFLGINSKKGTEFEFKDENGKGLIG 466
Qy 82 -----GSSVDLYGAYGYOCAG-----TNKTCACMYGGVTLHDNNRLTEE 122
Db 467 LHGRGCGNAIDAGAYPDTGSGDGDVPSKDGPKTDVFGKGLG-----DKGEFFD 521
Qy 123 -----KKVPI---NLWIDGKQTTVPIDKVKTSKEV-----TVQ 153
Db 522 VGFEGVKKITVGADNLSI---TYIKIEYKDGKVEIREHGTARGKLKFEFSDVDPNDST 577
Qy 154 ELDLARH-----YLHGKFGLYN-----SDSFGGKVQORGLIV 185
Db 578 EVGTYKHYNYVDTLITSLYFTTSKGTSPFLGIDSEKKKGTEFEFKDENGK-----LIG 633
Qy 186 FHSSEGSTVSYDLFDAQGYDPT 208

Db 634 FHGRGNAL-----DAIGAYFDT 651

RESULT 38

T08102

myrosinase-binding protein (clone indmbp2) - rape

C;Species: Brassica napus (rape)

C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 21-Jul-2000

C;Accession: T08102

R;Taipaleensuu, J.; Eriksson, S.J.; Rask, L.

Eur. J. Biochem. 250, 680-688, 1997

A;Title: The myrosinase binding protein from Brassica napus seeds possesses lectin activity

A;Reference number: Z16355; MUID:98121188; PMID:9461290

A;Accession: T08102

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-988 <TAI>

A;Cross-references: EMBL:Y09437; NID:gl711295; PIDN:CAA70587.1; PID:gl711296

A;Experimental source: cv. Hanna; leaves

Query Match 7.1%; Score 87; DB 2; Length 988;

Best Local Similarity 20.5%; Pred. No. 31;

Matches 66; Conservative 35; Mismatches 89; Indels 132; Gaps 15;

QY 2 EKSEELNE-----KDLRKSELOGTALGNLAKIYY-YNS 34

Db 363 EKGEENDVGFEVKKITVGADQSYTYIKIEYVDGKVEIREHGTSGELQEFSDVDPN 422

QY 35 KAITSEKSADQFLT--NTLLFKGFTGHPWYNDLVDLGSTAATSEYE----- 81

Db 423 DSITEVGGTYKHNVTDTLLTSLYFTTSKGFTSPLFGINSEKKGTEFEFKDENGKLG 482

QY 82 -----GSSVDLYGAYGYOCAGG-----TPNKTACM-----YGGVTLHDNNRLTES- 122

Db 483 LHGRGNALDAIGAYFDTGSGDGDVPTKQVLADVPKKGPIGG-----DKGEFFDDV 538

QY 123 -----KKVPI---NLWDGKQTTVPIDKVKTSKKEY-----TVQEE 154

Db 539 GFGVKKITVGADNLSI---TVIKIEYVDGKVEVREHGTARGKLFSDVDYDPSITE 594

QY 155 LDLOARH-----YLGKGLYN-----SDSFGKVGQGLIVF 186

Db 595 VGTYKHNVTDTLLTSLYFTTSKGFTSPLFGIDSEKKGTEFEFKDENGK-----LIGF 650

QY 187 HSSEGSTSVYDLFDAQOQYPTD 208

Db 651 HGRGNAL-----DAIGAYFDT 667

RESULT 39

E71403

hypothetical protein - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

A;Variety: columbia

C;Date: 03-Aug-1998 #sequence_revision 03-Aug-1998 #text_change 05-Dec-1998

C;Accession: E71403

R;Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirks, P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Terryn, N.; Giel, vanagh, T.; Hempel, S.; Kottler, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.

Nature 391, 485-488, 1998

A;Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech, erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans, C.; Chludzisz, N.

A;Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal

A;Reference number: A71400; MUID:98121113; PMID:9461215

A;Accession: E71403

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-722 <BEV>

A;Cross-references: GB:Z97335; NID:G2244747; PID:e326875; PID:G2244776

C;Genetics:

A;Map position: 4C0P9-4G3845

Query Match 7.1%; Score 86.5; DB 2; Length 722;

Best Local Similarity 20.2%; Pred. No. 23;

Matches 47; Conservative 40; Mismatches 79; Indels 67; Gaps 10;

QY 6 EINEKDLRKSELOGTALGNLKOIYYNYSKAITSSSEKADQFLTNTLLFKGFTGHPWYN 65

Db 455 KINSEIDGMAEKGKSLGNAQTV---ESETLRVSLPAVD----- 491

QY 66 DLLVDLGSTAATSEYEGSSVDLYGAYGYOCAGTGNKTACMYGGVTLHDNNR-----LTE 121

Db 492 SVVVDSDNADSSRAANKTGLVDLAG-----NESELMQANVVAEKGKPKDTLSS 539

QY 122 EKKV---PINLWDGKQTTVPIDKVKTSKKEVTQVQLDLOARHLYHGKGLYNSDSFGGK 178

Db 540 ESSCYASPSVWFEKSDAS---DQIKSTSTSKDLSALQISAE-----SKDEVCRE 586

QY 179 VQRLIVFHSS---EGSTVSVDL---FDAQOQYPTDILLRIYRDNTTISSTLSLSI 226

Db 587 SNNGRIVEESFNEPNKTEYPISHFGSTGTA PDTV-----NTANQISLEI 632

RESULT 40

T30857

glucosyltransferase - Streptococcus salivarius

C;Species: Streptococcus salivarius

C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999

C;Accession: T30857

R;Simpson, C.L.; Giffard, P.M.; Jacques, N.A.

Infect. Immun. 63, 609-621, 1995

A;Title: Streptococcus salivarius ATCC 25975 possesses at least two genes coding for prin

A;Reference number: Z20909; MUID:95122197; PMID:7822030

A;Accession: T30857

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1449 <SIM>

A;Cross-references: EMBL:LJ5495; NID:G662378; PID:G662379; PIDN:AAC41412.1

C;Genetics:

A;Gene: gtfL

Query Match 7.1%; Score 86.5; DB 2; Length 1449;

Best Local Similarity 25.0%; Pred. No. 57;

Matches 46; Conservative 26; Mismatches 75; Indels 37; Gaps 9;

QY 23 LGNLKQIYYNYSKAITSSSEKADQFLTNTL-----LFGKFTGHPWY- 64

Db 245 LSNQKE-YRFDKNGGIGS---SADSTNTNTVNGDKNAFYGTTDKDIELVDGYFTANTWYR 301

QY 65 -NDLLVDLGSTAATSEYE-----GSSVDLYGAYGYOCAGT-PNKTACMYGGVTLH 114

Db 302 PKELKDGKWTASTENDKRPPLTVWMPKAIQASLYNMYKKEQGLGNTQTYTSFSSQTQM 361

QY 115 DNNRLTEKKVPINLWDGK---QTTVPIDKVKTSKKEVTQVQLDLOARHLYHGKFGLY 170

Db 362 DQALAEVQKRIEERAREGNTDMLRTIK-NFVKTPQGNWSTSE-NLDNNDHLQGGALLY 419

QY 171 NSDS 174

Db 420 NND5 423

RESULT 41

T38720

chromodomain helicase hrp3 - fission yeast (Schizosaccharomyces pombe)

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Dec-2002

C;Accession: T38720

R;Gentiles, S.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Wood, V.

submitted to the EMBL Data Library, September 1997

A;Reference number: Z21797

A;Accession: T38720

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-1388 <GEN>

A; Cross-references: EMBL:Z99167; PIDN:CAB1277.1; GSDB:GN00066; SPDB:SPAC3G6.01
A; Experimental source: strain 972h-; cosmid c3g6
C; Geneticals:
A; Gene: SPDB:SPAC3G6.01
A; Map position: 1
A; Introns: 64/3
C; Superfamily: chromodomain helicase CHD1; chromobox homology

```

Query Match      7.13; Score 86; DB 2; Length 1398;
Best Local Similarity 25.13; Pred. No. 60;
Matches 45; Conservative 27; Mismatches 69; Indels 38; Gaps 10;

Qy      35  KAITSSSEKSADQFLTNT-----LFLKGF-----FTGHPWYNLLDVLGCGSTAATSEYE 81
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1047 KAVSAAREKSLDNOSNNKSRKALLITFKGVNINAEFLVORLNDLDI-LVDAMPTSGYS 1105

Qy      82  GSSVDLY-GAYIGYCCAGGTENKTACMYGGVTLH-----DNNRLTEEEKVPINLWI 131
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1106 NFQIPMEHVRSHVHGSCQWG-PREDSMLLSGICKHGFGAWLEIRDDPELKMCKDIFLE-- 1161

Qy      132 DGKOT--TVPIDKVKTSKKEVTVOELDLQARHYL-----HGKFGLYNSD--SFGGKQV 180
      |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1162 DTKOTDINSVPDKENKEKKVPASVHLVRRGYYLLSALREHHQNGFIKSSPAISNGTKQ 1220

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RESULT 42
AH0340
putative autotransporter protein yapC [imported] - *Yersinia pestis* (strain CO92)
C:Species: *Yersinia pestis*
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001
C:Accession: AH0340
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentis,
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dou-
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.;
Nature 413, 523-527, 2001
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AH0340
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-638 <KUR>
A:Cross-references: GB:AL590842; PIDN:CA93031.1; PID:G15980769; GSPDB:GN00175
C:Genetics:
A:Gene: yapC

Query Match	7.0%;	Score 85.5;	DB 2;	Length 638;
Best Local Similarity	21.1%;	Pred. No. 24;		
Matches	43;	Conservative 20;	Mismatches 70;	Indels 71; Gaps 6;
Qy	68	LVDLIG--STAATSEYEGSSVDLYGAYGYOCAGGTENKTAQWGGVT-----	112	
Db	299	VVDLGVQYGYLQSENGSTDWYLATSTEEELPGITPNTVAPMLSSAAGVLNMAAAPPHI	358	
Qy	113	-----LHNNRLTEEEKVPINLWIDGKQTTPVDPDKV	143	
Db	359	LNABELSTLQRQGBLKADAEGTVGWAARYLTDLSRLSDNKNIAFNKTLUSGME--IGADK-	415	
Qy	144	KTSKKEVTVQBLDQARHLHGKFLGYNLSDSGGKVGQRLIVFHSSEGSTVSY-----	197	
Db	416	-----QGLNFRGNWLGAFTSYSSSDVKST-----HDANGDIRSYGGGLYLT	457	
Qy	198	LFDAQGGYPTLLRIYRDNTTSS	221	
Db	458	YLDQSGFYVDTVLKANRFNNKMT	481	

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RESULT 43
T30552
glucosyltransferase N - Streptococcus salivarius (fragment)
C:Species: Streptococcus salivarius
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
C:Accession: T30552
R:Jaffe, R.I.

```

submitted to the EMBL Data Library, February 1998
A;Description: Streptococcus salivarius V1477 gtfN.
A;Reference number: Z20854
A;Accession: T30552
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1449 <JAF>
A;Cross-references: EMBL:AF049609; NID:G2935545; PID:G2935546; PIDN:AAC05156.1
C;Genetics:
A;Gene: gtfN

Query Match	7.0%;	Score 85.5;	DB 2;	Length 1449;
Best Local Similarity	25.0%;	Pred. No. 70;		
Matches	46;	Conservative 26;	Mismatches 75;	Indels 37; Gaps 9;
Qy	23	LGNLKOIYYNSKAIPTSSEKSADQFLNTL-----LFXGFTTGHDPW-	64	
Db	245	LSNQKE-YRDKNGGTGS--SASTNTNTVINGDKNAFYCTTDKDELVDGYFTANTWYR	301	
Qy	65	-NDLLVDLGGTAATSYE-----GSSVDLYGAYGYQCAGT-PNKTACMYGGVTLH	114	
Db	302	PKBILDKGKEWTASTENDKRPLLTVWMPKSAIQASYLVNMYKEQGLGTNQTYTSPSSQTM	361	
Qy	115	DNNRLTEEKVPINLWLDGK---QTTVPIDKVKTSKKEVTVOELDLQARHYLHKGKGLY	170	
Db	362	DQAALEVQKRIEGRAREGNTDWIRTIK-NFVKTOPGWNSTSE-NLDNNDHLQGGALLY	419	
Qy	171	NSDS	174	

RESULT 44

glycosidase homolog lin2540 [imported] - *Listeria innocua* (strain Clifp11262)
 AG1749
 C:Species: *Listeria innocua*
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AG1749
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amand, A.; Baquero, F.; Berche, Y.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.F.; Jones, L.M.; Karst, U.; Science 294, 848-852, 2001
 A:Authors: Kreif, J.; Kuhn, M.; Kunst, F.; Kurapkut, G.; Machado, E.; Maitouk, C.; Schluter, T.; Smoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, A.; Title: Comparative genomics of *Listeria* species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AG1749
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1090 <GUA>
 A:Cross-references: GB:AL592022; PIDN:CAQ97767.1; PID:gl6415062; GSPDB:GNO01
 A:Experimental source: strain Clifp11262
 C:Genetics:
 A:Gene: lin2540

Query Match	7.0%;	Score 85;	DB 2;	Length 1090;
Best Local Similarity	21.5%;	Pred. No. 53;		
Matches 64;	Conservative 35;	Mismatches 100;	Indels 98;	Gaps 15;
Qy	8	NEXDLRKSELGQTALGNLK-----QIVYYSKALTSEKSAQDLTN	50	
Db	400	NEND--RESV-STALSNAKENEIPATGFLVLEQWSDEETYINWDATYTKANGPEPAYD	456	
Qy	51	TLAFKGFTGHPWYNDLLVLDGSTAA-----TSEYEGSSVDL-YGAYGYQCAGG	99	
Db	457	DFTFNGKWTNPFKAMVDVSHDAGMNIVLVQVPVLKDDNTVYEQRDNDDYIMISQGSADDD	516	
Qy	100	T--PNKTACMY---GGVTLHDNRLTEEKVPINLWDGKQ---TTVPIDKVKTSKEVT	151	
Db	517	TGAPYRVPASQWFGNGILLDFTN-----KDAVNWTSQREYLLTDVGIDGFKTDGGMV	570	
Qy	152	-----VOELDLQARHYLHG-----KFLGYS--	172	

Db 193 GHRLLGYGELPDRDRSHLWLGTF-----WGGIEGFTSSLYAELQ-----NWV----- 239
Qy 134 KQTTVPIDKVKTSKKEVTQVQELD-----LQARHYLHGKFGLYNSDSFGGKVGRLIVFHS 188
Db 240 KQYVADVD-----YTVIEDNWSLNPAGAHYK-----TVDSGDSLLGRIDNNTVSLHF 287
Qy 189 SEG---STVSVDLFDAGQVPTLLR-----IYRDNT 217
Db 288 AVGYRQHTVAVLKQVNGNTFFDYINQGSIFLDNS 323

RESULT 51
A64556
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 08-Oct-1999
C:Accession: A64556
R:Tomb, J.F.; White, O.; Kervatage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.; Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khaliak, H.G.; Glodek, A.; McKenney, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watthey, L.; Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpik, P.D.; Smith, H.O.; Fraser, C.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:9739467; PMID:9252185
A:Accession: A64556
A:Status: preliminary
A:Title: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-2893 <ROM>
A:Cross-references: GB:AE000547; GB:AE000511; NID:G2313377; PIDN:AAD07355.1; PID:G231338

Query Match 6.8%; Score 83; DB 2; Length 2893;
Best Local Similarity 20.9%; Pred. No. 2.8e+02;
Matches 49; Conservative 32; Mismatches 61; Indels 92; Gaps 12;

Qy 16 SELOGTALGNLKIYYNKAITS-----EKSADQFLTNLTKGFTGHPWYN 65
Db 2258 SKIKGSA--NIKNLNNYNAFOANLTISNOAVLEKNA-SFTVNNLNIQGAFFNN--- 2310
Qy 66 DLLVDLGSATSEYB-----GSSVDLYGAYGVQACAGTTPNKTACMYGGVTLHDNRR 118
Db 2311 -----ATQKIEVLNVLVNASLSTGYLGVGALNNSGA-----IHFN--- 2351
Qy 119 LTEKKVPINLWDGQTTVPIDKVKTSKKEVTQVQELDQARHYLHGKFGLYNSDSFGGK 178
Db 2352 -----LENTQTPTPL-----IQAE-----GIINLNT--- 2372
Qy 179 VQRLIVFHSSEGSTVSVDLFDAGQVPTLLR-----IYRDNTIISTSLISLYIT 232
Db 2373 TQPFMNVNNSMANNTTYTLKS-SRYD-----YINPNLSQSLNYIT 2416

RESULT 52
F64187
p-aminobenzoate synthase component I homolog - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
C:Accession: F64187
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kervatage, R.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fritchman, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: F64187
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-328 <TIG>
A:Cross-references: GB:U32797; GB:L42023; NID:G1574095; PIDN:AC22834.1; PID:G1574097; T

Query Match 6.8%; Score 82.5; DB 2; Length 328;
Best Local Similarity 27.3%; Pred. No. 18;
Matches 24; Conservative 16; Mismatches 35; Indels 13; Gaps 3;

Qy 136 TTVPIDKVKTSKKEVT---VQELDQARHYLHGKFGLYNSDSFGGKVGRLI-----V 185
Db 237 TLLPAGSISGAPKKTQIIQAEKQKRGYTGIFGFDGKTLQSAVAIRFISQVDEKEY 296
Qy 186 FHSSEGSTVSVDLFDAGQVPTLLR-----IYRDNT 213
Db 297 FHSGGGITH---SNAQDEYEELLEKRY 321

RESULT 53
S39663
aminopeptidase homolog ywad - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 07-Oct-1994 #sequence_revision 24-Feb-1995 #text_change 15-Oct-1999
C:Accession: S39663; S16427; D70050
R:Glaser, P.; Kunst, F.; Arnaud, M.; Coudart, M.P.; Gonzales, W.; Hullo, M.F.; Ionescu, N. A.; Rapoport, G.; Danchin, A.
Mol. Microbiol. 10, 371-384, 1993
A:Title: Bacillus subtilis genome project: cloning and sequencing of the 97 kb region for
A:Reference number: S39655; MUID:95020537; PMID:7934828
A:Accession: S39663
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-455 <GLA>
A:Cross-references: EMBL:X73124; NID:G413923; PIDN:CAAS1564.1; PID:G413932
R:Glaser, P.; Kunst, F.; Debarbouille, M.; Vertes, A.; Danchin, A.; Dedonder, R. DNA Seq. 1, 251-261, 1991
A:Title: A gene encoding a tyrosine tRNA synthetase is located near sacS in Bacillus subtilis
A:Reference number: S16421; MUID:92216127; PMID:1806041
A:Accession: S16427
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-68 <GL2>
A:Cross-references: EMBL:X52480; NID:G40236; PIDN:CAA36725.1; PID:G40243
R:Kunst, F.; Ogawara, K.; Moser, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertero, C.; Bron, S.; Brouillet, S.; Bruch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi, A.; Ehrlich, S.D.; Emerson, P.T.; Etian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallercio, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.; Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, Rieger, M.; Rivolta, C.; Rocha, B.; Roche, M.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Sekiguchi, J.; Sekowska, A.; Seror, A.; Authors: M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K. A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: D70050
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-455 <KUN>
A:Cross-references: GB:Z99123; GB:AL009126; NID:G2636240; PIDN:CAB15873.1; PID:G1186346;
A:Experimental source: strain 168
C:Genetics:
A:Gene: ywad

Query Match 6.8%; Score 82.5; DB 2; Length 455;
Best Local Similarity 22.0%; Pred. No. 28;
Matches 41; Conservative 25; Mismatches 67; Indels 53; Gaps 6;

Qy 1 SEKSEINEXDLRKSSELOQTALGNLKIYYNKAITSSEKSAQOF-----LTNTLLPK 55
Db 53 SQISEALGPR-----IAGTAEKKSALLIASSMRKLDVKVQFNPDRLEGLTSSA 105
Qy 56 GFTTGHFWYNDLVLGSLTAATSEYSGSSVDLYGAYGVQACAGTTPNKTACMYGGVTLHD 115
Db 106 G-----RDILQAASGSAPEEQGLTAPLYNAGLYQ-----KDFADAKGKIALIS 152
Qy 116 NNRLT-----EKKVPINLWDGQTTVPIDKVK-----TSK 147

Qy	188	SSEGSTVSY	196
		: :: ::	
Db	549	TSDGSTMYS	557
 RESULT 55			
B91025			
NADH dehydrogenase I chain			
C:Species: Escherichia coli			
C>Date: 18-Jul-2001	#sequence		
C:Accession: B91025			
R:Hayashi, T.; Makino, K.;			
gasawara, N.; Yasunaga, T.;			
DNA Res.	8,	11-22,	2001
A:Title: Complete genome se			
A:Reference number: A99629;			
A:Accession: B91025			
A>Status: preliminary			
A:Molecule type: DNA			
A:Residues: 1-600 <HAY>			
A:Cross-references: GB:BAO00			
A:Experimental source: stra			
C:Genetics:			
A:Gene: ECg3170			
C:Superfamily: Escherichia			
 Query Match			
Best Local Similarity	2		
Matches	51;	Conservati	
Qy	26	LKQIYYNNSKAITP	
	:	:::	
Db	380	LREFLDWMFKRLA	
Qy	85	VDLYGA--YGYQYQ	
	:	:::	
Db	436	FDRVKARPYSGYGE	
Qy	132	DGKQTTPIDKVKKV	
	:	:::	
Db	496	DHPLTTPP-----	
Qy	188	SSEGSTVSY	196
	:	:: ::	
Db	549	TSDGSTMYS	557
 RESULT 56			
C89869			
NADH dehydrogenase I chain			
C:Species: Escherichia coli			
C>Date: 16-Feb-2001	#sequen		
C:Accession: C95869			
R:Perna, N.T.; Plunkett III;			
iller, L.; Grotbeck, E.J.;			
Nature	409,	529-533,	2001
A:Title: Genome sequence of			
A:Reference number: A85480;			
A:Accession: C95869			
A>Status: preliminary			
A:Molecule type: DNA			
A:Residues: 1-600 <STO>			
A:Cross-references: GB:AEO00			
A:Experimental source: stra			
C:Genetics:			
A:Gene: nuoc			
C:Superfamily: Escherichia			
 Query Match			
Best Local Similarity	2		
Matches	51;	Conservati	

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F;1-33/Domain: signal sequence #status predicted <SIG>
F;34-466/Product: dep protein #status predicted <NAT>

Query Match          6.7%; Score 82; DB 2; Length 466;
Best Local Similarity 23.2%; Pred. No. 31;
Matches 48; Conservative 30; Mismatches 93; Indels 36; Gaps 8;

QY  29 IYYNSKATTSSEKADQELNTLL-----FKGFTHGPWNLLVDLGSTAATS--EY 80
DB 125 IFYPNGEPIETGETTIQDRLARTLKIKQKGAQFYG-----GVARAISTAKISLEDI 179
QY  81 EGGSSVD-----LYGAYGYQACAGTPTNCTACMYGGVTLHDNNRLTBEKKVPINLWIDGKQT 136
DB 180 KGKYKVEVRPKVNGMYGVDTAPP-----PMSGVTLQLMLKLAEKKEV----YKDV DHT 230
QY 137 TVPIDKVTSTKKEVTVQELDLQARHVLHGKFLGYNSSDFGGKVORGLIVFHSSSGSTVSY 196
DB 231 ATYMSKWE-----EISRIAYQDRKNIGDPNVYMDPNKQVSDKYIISTMKXNGDALSS- 283
QY 197 DLFDAGQGYPTLLRIYRDNTTISSTSS 223
DB 284 ---EAEHESSTHFVIIDRDGTWVSSTN 307

RESULT 59
S70908
transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB29)
C;Species: Haemophilus influenzae
A;Variety: strain 8929
C;Date: 10-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S70908; S73321
R;Cosmors: S.M.; Yang Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E.
Mol.; Microbiol. 19, 575-586, 1996
A;Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes.
A;Reference number: S70901; MUID:96228706; PMID:8830248
A;Accession: S70908
A;Molecule type: DNA

```

A;Residues: 1-631 <LOW>
A;Cross-references: EMBL:U15055
A;Experimental source: strain SB29, clone DS-1090-3-2
R;Icoosmore, S. M.
submitted to the EMBL Data Library, September 1994
A;Reference number: S73320
A;Accession: S73321
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-250, 'I', '252-349, 'RTDATN', 357-631 <LOW>
A;Cross-references: EMBL:U15055; NID:G1223948; PIDN:AAQ43931.1; PID:G1223949
A;Experimental source: strain SB29, clone DS-1090-3-2
C;Genetics:
A;Gene: tdp2
C;Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor an
F;1-17/Domain: signal sequence #status predicted <SIG>

```

Query Match      6.7%; Score 82; DB 2; Length 631;
Best Local Similarity 19.9%; Pred. No. 47;
Matches 54; Conservative 27; Mismatches 62; Indels 128; Gaps 12;

Qy      14 KXSEIQGTALG-----NLKQIYYNSKAITSSSEKSADQLTNTLLFKG 56
           ::          |||
Db      190 QVSYLFGSAFGAYNRRSRAISEDIDLENLTK-----EFTVNFGTKK- 237
                           |||
Qy      57 FRTGHWNDDL-----LVDLIGSTAATSEYEG-----SSVDL 87
           |||
Db      238 -LTGKIYYNERETNNNKQQRKHELYLDADIYSNFRGKVKTQKDSQEHPTSEGTL 296

Qy      88 YGAYGYQCAGGTPNKTCMTGGVTILHNNRL-----TEKKVPINLWDGKOTT 137
           ::|||
Db      297 EGGFYG-----PNGEE--LGGEKLADGNRVGVFSKAEETKDKKLSRETLIDGKLIT 347
                           |||
Qy      138 VPIDK-----VTSKKEVTVOELD-----LQARHYL 163
           :|||
```

Db 348 PKTKTDAKTAANKTDEKNTTDPISFGADYLLINYPVPLFPBENTNDFITSRHHK 407
QY 164 HG-----KFLGYNDSFGGK 178
Db 408 VGDKTYKVEACCKNLNVKFGMYEDPLNGE 438

RESULT 60
T33730
Hypothetical protein - Zymomonas mobilis
C:Species: Zymomonas mobilis
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 28-Jul-2003
C:Accession: T33730
R:Lee, J.S.; Jin, S.J.; Kang, H.L.; Kang, H.S.
Submitted to the EMBL Data Library, August 1998
A:Description: Sequence analysis of 67E10 cosmid clone of Zymomonas mobilis ZM4.
A:Reference number: T21392
A:Accession: T33730
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-644 <LE>
A:Cross-references: EMBL:AF086791; NID:G3820581; PID:G3820589; PIDN:AACT0368.1
C:Superfamily: glycol monoaminopeptidase

Query Match 6.7%; Score 82; DB 2; Length 644;
Best Local Similarity 20.8%; Pred. No. 48;
Matches 60; Conservative 27; Mismatches 76; Indels 126; Gaps 12;

QY 51 TLLFKGFTGH-----PWYND-----LLVDLGSTAAATSEY 80
Db 77 TLLYEWLPFGHSGPIEKLAGLIVTANNQIPQWDSVDVYAPHLDIPAGVTEITAY 136
QY 81 -----EGSSVDLYGAY-----GYOCA----- 97
Db 137 QYLSFTSQRIQSTPEWNLQWNTLALYAGYTRQIQPTVYPTGWSALEIS 196
QY 98 -----GGTPN-----CMYGGVTLHNNRLTEKKVPINLWIDGKQITVP 139
Db 197 GITPDGQTPNVQYKTTDFDTLIDSPVMAGRYTRTE-----TLAPGVLNLIADKPEDVMV 252
QY 140 IDKVTSTKEVTVQELDQ-ARHYLHGKFGLYNSDFG-----KVQGLIVFHSS 189
Db 253 TDQNLNAHQTLQTAQVLYGQHYSHYDPLLALSEKLGIGLEHHQSSDEGADYFSKW 312
QY 190 EGSTVSVDLFDQA-----GQV-----PDTLLRIYRDN 217
Db 313 DKSAGVGRDLAHEYNHNSWNGKVRPADLWTPDYKTPMDSLLWVYEGOT 361

RESULT 61
D82568
conserved hypothetical protein XF2349 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: D82568
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: D82568
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-745 <SIM>
A:Cross-references: GB:AE004045; GB:AE003849; NID:G9107517; PIDN:AAF85148.1; GSPDB:GN001
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briomes, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
Submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tsuchiko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A:Reference number: A59328
A:Status: annotation
A:Contents: annotation
C:Genetics:
A:Gene: XF2349

Query Match 6.7%; Score 82; DB 2; Length 745;
Best Local Similarity 22.3%; Pred. No. 58;
Matches 44; Conservative 37; Mismatches 86; Indels 30; Gaps 10;

QY 14 KSELGQTALGNLQKQIYYNNSKAITSEKAD--QFLTNTLLFKGF----FICHPYNDL 67
Db 113 KALSADGSIAGGYQYIRIHESSSANLEKASNGKFLANDGVSATFPIVWGSDSWENEV 172
QY 68 LVDLG--STAATSEYEGSSVDLYGAYGYQCAGGTENKATCMYGGVTLHNNRLTEKKV 125
Db 173 KLELGILESOVVALSGDGKTIGG--YGF-----STHLVPIWNGSHWIKHLDVPKE- 224
QY 126 PINLWIDGKQITVPID-KVK---TSKEVTVQELDQAR-----HYLHGKFGLYNSDSFG 177
Db 225 ---YYDAEVRALSTDGKVGAGYISSKNITRIGLEKSRNDTKNFTHA--FIWSGDGFGI 278
QY 178 KVQGLIVFHSSSEGSTV 194
Db 279 KTLGLTLNNESEGAEV 295

RESULT 62
H72204
pullulanase - Thermotoga maritima (strain MSB8)
C:Species: Thermotoga maritima
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 22-Jun-2003
C:Accession: H72204
R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey,
Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
C.M.
Nature 399, 323-329, 1999
A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A:Reference number: A72200; MUID:99287316; PMID:10360571
A:Accession: H72204
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-843 <ARN>
A:Cross-references: GB:AE001821; GB:AE000512; NID:G4982421; PIDN:AAD36907.1; PID:G498242
A:Experimental source: strain MSB8
C:Genetics:
A:Gene: TM1845
C:Superfamily: pullulanase type debranching enzyme

Query Match 6.7%; Score 82; DB 2; Length 843;
Best Local Similarity 28.3%; Pred. No. 68;
Matches 32; Conservative 15; Mismatches 36; Indels 30; Gaps 6;

QY 4 SEINERDLRKSGEL--QG-----TALGNLQIYYNNSK--AITSEKSGADQFLTNTLLF 54
Db 186 SESLKEEDLRKDVLEIEGYKPARVIMWEILDYDYGELGAVYSPEKT-----IF 236
QY 55 KGFTTGHFWNDLLVDLGS-----TAATSEYEGSSV-----DLGAYGYQ 95
Db 237 RVMSPVSKVKKVLLFKNGSDTEPYQVYNNMEYKNGVWEAVEGDLGVFLYQ 289

RESULT 63
C90595
Hypothetical protein MYPV_6670 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C:Accession: C90595
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, P.; Moszer, I.;

Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulmonis
A:Reference number: A99512; MUID:21287165; PMID:11353084
A:Accession: C90395

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-888 <KUR>
A:Cross-references: GB:AL445566; PID:gl14090082; PIDN:CAC13840.1; GSPDB:GN00153
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYP670
A:Genetic code: GSC3
C:Superfamily: isoleucine-tRNA ligase

Query Match 6.7%; Score 82; DB 2; Length 888;
Best Local Similarity 23.9%; Pred. No. 73;
Matches 56; Conservative 25; Mismatches 89; Indels 64; Gaps 11;

QY 41 EKADQFLNTLFGKFFTGHPWYNLLDLGSAATSEYEGSSV--DIY-----88
DB 501 EKSVDELLPEYKXKN-KTKETIMDVWFDGSGTSGVEIEGVSPFDLYLEIGIDQYRGW 559

QY 89 -----GAYGYQ-----CAGGTPNKTACMYGGVTLHDNNRLTEKKVPI-NL 129
DB 560 FNSIINSVAYWGSPYRLLSHGFLVDGGRKNSKOLGNV--DPQEIIOYKYGADILRL 617

QY 130 WIDG-----KQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSF 175
DB 618 WVANCEYADVSVSESIKQTVENYKIRN-----IKFLGLNQLQYDHSKKNL-----666

QY 176 GKGVQRLIVFHSEGSVSYDLPDAGQY--DTLLRYRDNNTTISSTLSIS 227
DB 667 --KLE-GIHELINERLKKVFDILOAYNDYDFNDVIKTLNPLTDLSSPYLSIS 717

RESULT 64
C89808
exotoxin 15 [imported] - Staphylococcus aureus (strain N315)

C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 14-Apr-2003
C:Accession: C89808

R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146

A:Accession: C89808
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-227 <KUR>
A:Cross-references: GB:BA000018; PID:gl13700324; PIDN:BA041622.1; GSPDB:GN00149

A:Experimental source: strain N315
C:Genetics:
A:Gene: set15
C:Superfamily: toxic shock syndrome toxin

Query Match 6.7%; Score 81.5; DB 2; Length 227;
Best Local Similarity 21.0%; Pred. No. 13;
Matches 46; Conservative 40; Mismatches 90; Indels 43; Gaps 8;

QY 10 KDLRKKSELOGTALGNLQKIYYNSKAITSSSEKSAQFLNTLLFKGFFTGHPWYNLLIV 69
DB 41 QDLSEYKGGFLTNVGTGKYGNKVTFFDINSQIDVLTG-----NEKL- 85

QY 70 DLGSAATSEYEGSSVDLYGAYGYQCAGTGNKTKACMGVTLHDNNRLTEKKVPI-NL 129
DB 86 -----TVKDDDEVSNVDVFFVREGSKSAITTS-----IGGIT-KTNGTQHKDTQVNNL 134

QY 130 WID--GKQTT-VPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGGKVGORGLIV 185
DB 135 SVKSTGCHTSTVTSSEYISYKEISLKDLPKLRKHLDKHDLKTEPKDSKIR-----189

QY 186 FHSSEGSVSYDLPDAGQYPTDRLRIYRDNNTTISSTLS 224
DB 190 ITMKNGGYTFEL-----NKKLQPHRMGDTIDSRNI 220

RESULT 65
AH1903
hypothetical protein all0778 [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120
A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C:Accession: AH1903
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi, R.; Kaneko, T.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.

DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena

A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AH1903

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-374 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA072735.1; PID:gl17130123; GSPDB:GN00179

A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: all0778

Query Match 6.7%; Score 81.5; DB 2; Length 374;
Best Local Similarity 21.4%; Pred. No. 26;
Matches 49; Conservative 35; Mismatches 88; Indels 57; Gaps 10;

QY 9 EKDLRKKSELOGTALGNLQKIYYNSKAITSSSEKSAQFLNTLLFKGFFTGHPWYNLL 68
DB 54 QKMAKTELEQGISLPELNSGYASLNKLLQNGENVOLTIANSL-----WVQ-- 101

QY 69 VDLGSAATSEYEGSSVDLYGAYGYQCAGTGNKTKACMGVTLHDNNRLTEKKVPI-NL 128
DB 102 -----DVSRLPDPFVQTTTRFYQA-----KVNLDLFQNVAVN--TIN 136

QY 129 LWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGGKVGORGLIV 188
DB 137 SWVQ-ENTKGRKIDIVNIE--FNQALFLINAIYFNGKW---SNAP-DKSTQTPQTFYT 188

QY 189 SEGTSVSYDLPDAGQYPTDRLRIYRDNNTTISSTLS-----SISLYLY 231
DB 189 ASGQKQHPMSQTEYR-----YETPQFQSVSLPYGQDGKVSLYIF 231

RESULT 66
A90267
proteinase related protein [imported] - Sulfolobus solfataricus

C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 24-May-2001

C:Accession: A90267
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-4

arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001

A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139

A:Accession: A90267
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-1269 <KUR>
A:Cross-references: GB:AE006641; NID:gl13814328; PIDN:AAK41392.1; GSPDB:GN00155

C:Genetics:
A:Gene: SS01141

Query Match 6.7%; Score 81.5; DB 2; Length 1269;
Best Local Similarity 23.7%; Pred. No. 1.3e+02;
Matches 50; Conservative 27; Mismatches 85; Indels 49; Gaps 10;

QY 33 NSKAITSEKSAQFLNTLLFKG---FFTGHPWYNLLVDLGSAATSEYEGSSVDLYG 89

Db 1032 NVKILNVSGNLLDPLTNVIVNSVKILNGN---ISNVIRNSTVLIMQSNANNITLY- 1087

Qy 90 AYYGYQCAGGTPNTACMYGVTWLDHNNRLTEEEKVPIINLWIDGKQTTVPIDKVKTSKKE 149

Db 1088 -----NSTLYAIGG-SINGLN-VYNSKWVPINTHIOGLYPDELPSISINLPSKN 1133

Qy 150 VT-----VQELDLQARHLYGKFGKGLYNSDSFGKQVQGLIVFHSSEGSTVSVDLFD 200

Db 1134 VTGTVNVTNVVIGEDVSRINYVNG--NLINSFTTNGT-----HIVINTQNY---- 1179

Qy 201 AQGQVPTDLLRIYRDNTTISSTLSISLYLY 231

Db 1180 PDGGYNLTVTATQSDGLSSNSS-----YLY 1205

RESULT 67

T29999

hypothetical protein ZC8.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 18-Feb-2000

C:Accession: T29999

R:Latreille, P.; Bradshaw, H.

submitted to the EMBL Data Library, July 1996

A:Description: The sequence of C. elegans cosmid ZC8.

A:Reference number: Z20719

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Accession: T29999

A:Molecule type: DNA

A:Residues: 1-228 <LAT>

A:Cross-references: EMBL:U64862; PIDN:AA52624.1; GSPDB:GN00028; CESP:ZC8.4

A:Experimental source: strain Bristol N2; clone ZC8

C:Genetics:

A:Gene: CESP:ZC8.4

A:Map position: X

A:Introns: 43/2; 80/3; 110/3; 153/2; 274/3; 738/2; 1249/1; 1392/3; 1454/1; 1602/1; 1686/

Query Match 6.7%; Score 81.5; DB 2; Length 2288;

Best Local Similarity 17.8%; Pred. No. 2.8e+02;

Matches 51; Conservative 44; Mismatches 103; Indels 89; Gaps 8;

Qy 8 NEKDLRKSELOQTALGN-----LKQIYYVNSKATTSSEKADQFLNTLPLPKGFFGHP 62

Db 93 NVEQOREVSEMM-AALQNKVHEYKRGHIAELSGRMVGARNMLDDPTSNVIMFDNYDQNT 151

Qy 63 WYNLLVLDGSTA-----ATSEYEGSSVDLYGAYGYQCAGGT 100

Db 152 YITHNVELWSPARGKRETIILGGGAPGLTTVNVHAGAGYSGSVAGYGG--GVQAMVGD 209

Qy 101 PNKTACMYG-----GVTLHDNN----- 117

Db 210 PNANYEMTARLDEERRRDEVRMQWENRQKSLSDENDLRREFRYANDSKDKETP 269

Qy 118 -----RLTEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHLYHGKFG 168

Db 270 INRRENLAQYLSDEQKMLDLWTELQVRKQFSDLKTH-----TEEDLKQKAEFTAIRN 325

Qy 169 LYN-----SDSPGKVGRLIVFHSSEGSTVSVDLFDACQCYPTLLRI 212

Db 326 VNNISRNAAFSAGAGDGLGLYGLEDDGVDNRNTNNYKVFETIKRM 372

RESULT 68

A1161

flagellar hook protein FlgB homolog lmo0697 [imported] - Listeria monocytogenes (strain

C:Species: Listeria monocytogenes

C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001

C:Accession: A1161

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, R.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat

ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A:Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: A1161

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-411 <GLA>

A:Cross-references: GB:NC_003210; PIDN:CAC98775.1; PID:G16410086; GSPDB:GN00177

A:Experimental source: strain EGD-e

C:Genetics:

A:Gene: lmo0697

Query Match 6.7%; Score 81; DB 2; Length 411;

Best Local Similarity 20.4%; Pred. No. 32;

Matches 43; Conservative 32; Mismatches 64; Indels 72; Gaps 9;

Qy 72 GSTAATSEYEGSSVDLYGAYGYQCAGGTPNTACMYGVTWLDHNNRLTEEK----- 123

Db 82 GSPTSTGRNKDAALQGRGFFIAGDNAGG--NIVYTRDGSFAVSDNNYLTQQQKGYVMGYA 139

Qy 124 -----KVPINLWIDGKQT-----TVPIDKVKTSKKEVTVQELDLQARH 161

Db 140 TDKNGVNLNGNLQPIQIPLNSALPGBATKNGSLSGNIPLD---WGEKDTISSELSVY--- 193

Qy 162 YLHGKFGLYNSDFGG--KVQRLIVFHSSEGSTVSVDL-----FDA 201

Db 194 -----DNAGGKHKLQVNMKAATPDASGNVSVEYEQMDGKALTPPVTGTLNLYNA 242

Qy 202 QGOY--PDTLLRIYRDNTTISSTLSISLYL 230

Db 243 QGELTNPDAKNI-QINSIVNGKQVNMGLNL 272

RESULT 69

A11520

flagellar hook protein FlgE homolog lin0705 [imported] - Listeria innocua (strain Clip11;

C:Species: Listeria innocua

C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001

C:Accession: A11520

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, R.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat

ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A:Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: A11520

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-411 <GLA>

A:Cross-references: GB:AL592022; PIDN:CAC95937.1; PID:G16413157; GSPDB:GN00178

A:Experimental source: strain Clip11262

C:Genetics:

A:Gene: lin0705

Query Match 6.7%; Score 81; DB 2; Length 411;

Best Local Similarity 20.4%; Pred. No. 32;

Matches 43; Conservative 32; Mismatches 64; Indels 72; Gaps 9;

Qy 72 GSTAATSEYEGSSVDLYGAYGYQCAGGTPNTACMYGVTWLDHNNRLTEEK----- 123

Db 82 GSPTSTGRNKDAALQGRGFFIAGDNAGG--NIVYTRDGSFAVSDNNYLTQQQKGYVMGYA 139

Qy 124 -----KVPINLWIDGKQT-----TVPIDKVKTSKKEVTVQELDLQARH 161

Db 140 TDKNGVNLNGNLQPIQIPLNSALPGBATKNGSLSGNIPLD---WGEKDTISSELSVY--- 193

Qy 162 YLHGKFGLYNSDFGG--KVQRLIVFHSSEGSTVSVDL-----FDA 201

Db 194 -----DNAGGKHKLQVNMKAATPDASGNVSVEYEQMDGKALTPPVTGTLNLYNA 242

Qy 202 QGOY--PDTLLRIYRDNTTISSTLSISLYL 230

Db 243 QGELTPDALXNI-QINSTVNGKQVNMGLNL 272

RESULT 70

T15410

hypothetical protein C04F6.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 26-May-2000

C:Accession: T15410

R:Nhan, M.

submitted to the EMBL Data Library, December 1995

A:Description: The sequence of C. elegans cosmid C04F6.

A:Reference number: Z18346

A:Accession: T15410

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-611 <NHA>

A:Cross-references: EMBL:U42835; NID:g1125760; PID:g1125764; PIDN:AAA83588.1; CESP:C04F6

C:Genetics:

A:Gene: CESP:C04F6.4

A:Introns: 25/1; 184/3; 349/1; 514/3; 577/1

C:Superfamily: unassigned WD repeat proteins; WD repeat homology

Query Match 6.7%; Score 81; DB 2; Length 611;

Best Local Similarity 18.7%; Pred. No. 55;

Matches 53; Conservative 46; Mismatches 78; Indels 106; Gaps 12;

QY 23 LGNLEKQIYYNSKAITSSSEKADQFLNTLLPKGFTGH--PW-----YNDLLVDLGST 74

DB 313 LGSIDQVRVGHNKAITALSSAD-----GKTLFSADAEGHINSWDISTGISNRVFPDVHAT 368

QY 75 AATSEYEGSSVDLYGAY-----GYQCAGGTENK-----TA 105

DB 369 MITGIKTSKGLFTVSWDHLKVPAGSGVDSSKAVANKLSSQPLGLAVSADGDIIVA 428

QY 106 CMYGGVTLHNNRLTEKKVPIN-----LWIDGQTTVPIDKV---KTSKK 148

DB 429 ACYKHAIYVSHGKLT-----VPISYNSCVALSNDKQFVAVGGQDKVHVYKLSGASVSEV 485

QY 149 EVTVQELDL-----QAR-----HYLHGKFLYNSDSFGSKVQGLIVFHS 188

DB 486 KTIHFAEITSVAFSNGAFVATDQSRKVIPIYVANFELAHINSW-----TFHT 536

QY 189 SEGTSVSYDLFDAGQGPPTLLRIYRDNTTISTSLISLYLY 231

DB 537 AKVACVSW-----PDNVRLATGSLDINSVIVW 563

RESULT 71

T28421

probable DNA-directed RNA polymerase (EC 2.7.7.6) - Pichia kluyveri mitochondrion linear

N:Alternate names: RNA polymerase

C:Species: Mitochondrion Pichia kluyveri

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000

C:Accession: T28421

R:Nosek, J.

submitted to the EMBL Data Library, March 1997

A:Reference number: Z20485

A:Accession: T28421

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-992 <NOS>

A:Cross-references: EMBL:Y11606; PIN:CAA72339.1

A:Experimental source: strain CBS 7907

C:Genetics:

A:Genome: Mitochondrion linear plasmid

C:Superfamily: phage T7 DNA-directed RNA polymerase

C:Keywords: mitochondrion; nucleotidyltransferase; transcription

Query Match 6.7%; Score 81; DB 2; Length 992;

Best Local Similarity 24.5%; Pred. No. 16+02;

Matches 37; Conservative 28; Mismatches 62; Indels 24; Gaps 8;

QY 4 SEBINEKDLRKKSELOGTALGNLKOIYYNSKAITSSSEKADQFLNTLLPKGFTGH 63

DB 598 SKDMSPRDF--YTFIKDSVLDNKKDM---NMNKNVSVERTEMLGLTRQMW-KTMVIMF 651

QY 64 YNDLLVDLGSTAAITSEYEGSSVDLYGAYGYQ-----CAGGTPNKTCACMGVTLHDNN 117

DB 652 -----NAGVTTMT-KYLEDLSLVNMGYYTADKDLVCCCKSENKDSCHY-YKSLN 703

QY 118 RLTEKKVP-----INLWIDGQTTVPIDKV 144

DB 704 ARSPESKVPENNLNMTLTSKYSKSLCKCK 734

RESULT 72

AP1489

cell wall-associated protein precursor wapA (B. subtilis) homolog lin0454 [imported] - Lj

C:Species: Listeria innocua

C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001

C:Accession: AP1489

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.

Science 294, 849-852, 2001

A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Matok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AP1489

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2167 <GLA>

A:Cross-references: GB:AL592022; PIDN:CAC95686.1; PID:g16412895; GSPDB:GN00178

A:Experimental source: strain Clp11362

C:Genetics:

A:Gene: lin0454

Query Match 6.7%; Score 81; DB 2; Length 2167;

Best Local Similarity 21.7%; Pred. No. 2.9e+02;

Matches 41; Conservative 23; Mismatches 81; Indels 44; Gaps 8;

QY 32 YNSKAITSSSEKADQFLNTLLPKGFTGHWPYNDLLVDLGSTAAITSEYEGSSVDLYGAY 91

DB 1432 WNRSAVVVKTKPVKMLKVTMPFRNGLTGKAWFDDVRVEGEVLTKEVDAS-----GNY 1486

QY 92 Y--GYQCAGGTPNKTCACMGVTLHDNNRLTEKKVPINLWIDGQTTVP----- 140

DB 1487 VTASYDEGRKISFTYDIYGNKTSE-----TDEKGNKKTLYTDADNALIDTKLANGTSA 1541

QY 141 ----DKVTKSKVETVQVELDQARHYLHGKFG--GLYNSDSFGKVGQGLIVFHSSSGSTV 194

DB 1542 KYDDNNGNITTEKVTAS-----GKTQKNIEYD-----VDNKITAFDTALNRTI 1585

QY 195 SYDLFDPAQG 203

DB 1586 KYE-YDAAG 1593

RESULT 73

S25997

gene atpA intron 1 protein - liverwort (Marchantia polymorpha) mitochondrion

C:Species: Mitochondrion Marchantia polymorpha

C>Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 19-Jan-2001

C:Accession: S25997

R:Oda, K.; Yamato, K.; Ohta, E.; Nakamura, Y.; Takemura, M.; Nozato, N.; Akashi, K.; Kane J. Mol. Biol. 223, 1-7, 1992

A:Title: Gene organization deduced from the complete sequence of liverwort Marchantia po

A:Reference number: S25941; MUID:92114051; PMID:1731062

A:Accession: S25997

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-1395 <ODA>

A:Cross-references: EMBL:MG8929; NID:g786182; PIDN:AA09444.1; PID:g786230

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1992

C;Genetics:

A;Genome: mitochondrion
C;Superfamily: gene atpA intron protein; H+-transporting ATP synthase alpha chain homol
C;Keywords: mitochondrion; nucleotide binding; P-loop
F;1-329/Region: atpA exon 1 encoded
F;170-177/Region: nucleotide-binding motif A (P-loop)
F;331-1395/Region: atpA intron encoded

Query Match 6.6%; Score 80.5; DB 2; Length 1395;

Best Local Similarity 18.9%; Pred. No. 1.8e+02;
Matches 42; Conservative 41; Mismatches 92; Indels 47; Gaps 10;

Qy 29 IYNNKAITSEKADQFLNTLLFKGFTGHWPYNDLLVDLSTAAATSEYEGSSVDLY 88

Db 300 VFYLSRLLEAAKMSDQ-----TGAGSLTALP-----VIECAPTGRSMIQTWVGGEVA 348

Qy 89 GAYGYQCAGTTPNKTACMYGVTLHNNRLTEKKVP-INL--WIDGQTT----- 137

Db 349 GRYQTTRSPKQDSARRIGRADLHGQKINPSSGVINLVQVNAASKYDESSGYK 408

Qy 138 -VPIDKVKTSKEVT-----VOELDQARHYLHGKFLYNSDSFGKQVQRLIV 185

Db 409 HIPVPIHSGSAHLTRQGLLRPSGVVTEGD-KPKAYALGTRN-YSKDSFQPLTEGV-- 464

Qy 186 FHSSEGSTVSYDLFDA-----QGQYPTDLLRIYRDNTTI 219

Db 465 -HTNEGTTGTFELLTGLNRWVKVTKGYEDIFSLIAREDNLI 505

RESULT 74

A55426
Gingipain R (EC 3.4.22.37) precursor - Porphyromonas gingivalis
N;Alternate names: 50K high molecular mass arginine-specific cysteine proteinase; HGP; R
C;Species: Porphyromonas gingivalis
C;Date: 10-Feb-1995 #sequence_revision 10-Feb-1995 #text_change 08-Oct-1999
C;Accession: A55426; D53113
R;Payloff, N.; Potempa, J.; Pike, R.N.; Prochazka, V.; Kiefer, M.C.; Travis, J.; Barr, P
J. Biol. Chem. 270, 1007-1010, 1995
A;Title: Molecular cloning and structural characterization of the Arg-gingipain protein
A;Reference number: A55426; MUID:95138080; PMID:7836351
A;Accession: A55426
A;Status: preliminary
A;Molecule type: DNA

A;Residues: 1-1704 <PAV>
A;Cross-references: GB:U15282; NID:9557067; PIDN:AAA69539.1; PID:G557068
R;Pike, R.; McGraw, W.; Potempa, J.; Travis, J.
J. Biol. Chem. 269, 406-411, 1994
A;Title: Lysine- and arginine-specific proteinases from Porphyromonas gingivalis. Isolac
A;Reference number: A53113; MUID:94103245; PMID:8276827
A;Accession: D53113
A;Status: preliminary
A;Molecule type: protein
A;Residues: 228-249 <PIK>
A;Experimental source: H66
A;Note: sequence extracted from NCBI backbone (NCBIP:141694)
C;Keywords: cysteine proteinase; hydrolase

Query Match 6.6%; Score 80.5; DB 2; Length 1704;

Best Local Similarity 22.4%; Pred. No. 2.3e+02;
Matches 61; Conservative 33; Mismatches 107; Indels 71; Gaps 12;

Qy 5 BEINERDLRKKSELOQTALGNLQIYYNNKAITSEKAD-QFLTNLLFKGFTGHWP 63

Db 1075 EPIITAKGVSPPAIRGIQGTWRQ-----KTVDLPAGTKYVAFRHFSQDMF 1121

Qy 64 YNDL-----LVDLGSTAAATSEY-----EGSSVDLYGAYGYQCA----- 97

Db 1122 YIDLDEVEIKANGKRADETTFETSTHGEAPAEWTTIDADGGQGLCLSLGQLDLTAH 1181

Qy 98 GGTPTNKTACMYGVTLHNNRL-----TEKKV-----PINLWIDGQTTVPIDKVKTSK 148

Db 1182 GGTNVVAFSFWNGMALNPENYLISKDVTGATKYKYIYVNDGFFGCHYAVMISKITINAG 1241

Qy 149 ETVQV-ELDLQARHYLHGKFLYNSDSFGKQVQ-----RGLIVFHSSEGSTV 194

Db 1242 DFTVVFEETPNCINGKARFGL-STEANGAKQSPQSWIERTVDLPAGTKYVAFRHYNCSDL 1300

Qy 195 SYDLFP-----AQGYP-----DTLLRIYRDNTTI 219

Db 1301 NVILLDDIOFTWGGSPPTDYTYTVYRDGTGI 1332

RESULT 75

G82875

hypothetical protein UU558 [imported] - Ureaplasma urealyticum

C;Species: Ureaplasma urealyticum

C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C;Accession: G82875

R;Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.

submitted to GenBank, February 2000

A;Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mini

A;Reference number: A82870

A;Accession: G82875

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-1883 <GLA>

A;Cross-references: GB:AE002154; GB:AF222894; NID:G6899557; PIDN:AAF30971.1; GSPDB:GN001;

A;Experimental source: serovar 3; biovar 1

C;Genetics:

A;Gene: UU558

A;Genetic code: SGC3

Query Match 6.6%; Score 80.5; DB 2; Length 1883;

Best Local Similarity 22.4%; Pred. No. 2.6e+02;

Matches 49; Conservative 29; Mismatches 76; Indels 65; Gaps 10;

Qy 11 DLKKSELOQTALGNLQIYYNNKAITSEKADQFLTNLLFKGFTGHWPYNDLLVD 70

Db 814 DIKPSRLKA-----EYFYNDQ--NSQEQKNDNFKFGSVIEK----- 849

Qy 71 LGSTAAITSEYEGSSVDLYGAYGYQCAGTTPNK-----TACMYGVTLHNNRLTEKKV 125

Db 850 -----PGLSKYDGLIKD-----GMGPIKFKDGRIVY---KLHKKKH--PYKDD 890

Qy 126 PINLWIDGQTTVPID-----KVKTSKKEVTVOEL-----DLQARHYLHGKF---G 168

Db 891 DIEILIKTKNTPVIDLSTCLKSDGTINTRKLNKVKREIQDSINSLIVKRYNGGWDENG 950

Qy 169 LYNDSFGGKQVQGLIVFHSSEGSTVSYDLFDAQGGYPD 207

Db 951 NFDTSMFNLTYPDHPMFTSNEKRKWAERITDAMFKYPD 989

Search completed: August 12, 2004, 13:33:09

Job time : 11.3708 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 12, 2004, 13:22:49 ; Search time 5.11863 Seconds
(without alignments)
2370.233 Million cell updates/sec

Title: US-09-900-766-2

Perfect score: 1218

Sequence: 1 SEKSEINEKDLRKSELOG.....RDNTTISTSLISLYLYTT 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1107	90.9	257	1	ETXE STAAU
2	948	77.8	257	1	ETXA STAAW
3	611	50.2	258	1	ETXD STAAU
4	308	25.3	241	1	ETXH STAAW
5	284.5	23.4	266	1	ETC1 STAAU
6	277.5	22.8	266	1	ETC2 STAAU
7	269.5	22.1	251	1	SPEA STRPY
8	268.5	22.0	266	1	ETXB STAAU
9	263.5	21.6	266	1	ETC1 STAAU
10	241	19.8	258	1	ETXG STAAW
11	185	15.2	236	1	SPRH STRPY
12	183.5	15.1	234	1	SPBG STRPY
13	148.5	12.2	235	1	SPEC STRPY
14	100	8.2	234	1	TSST STAAU
15	95.5	7.8	150	1	R19E THEVO
16	93	7.6	979	1	P115 MYCHR
17	91	7.5	1634	1	DPOL NETUA
18	90	7.4	447	1	LEC PARPC
19	88.5	7.3	150	1	R19E THEAC
20	88	7.2	419	1	TYPH MYCPI
21	86	7.1	1388	1	HRP3 SCHPO
22	84.5	6.9	443	1	PORD PSEAE
23	84	6.9	1050	1	ITA5 XENLA
24	83.5	6.9	282	1	PRTA ASPNG
25	83	6.8	612	1	DNAX STRMU
26	82.5	6.8	308	1	TX30 CAEEL
27	82.5	6.8	314	1	RPOA LACPL
28	82.5	6.8	328	1	YB70 HAEIN
29	82.5	6.8	455	1	YWAD BACSU
30	82.5	6.8	600	1	NUCD ECOLI
31	82	6.7	607	1	DNAX STRPY
32	82	6.7	843	1	PULA THEMA
33	82	6.7	3718	1	LMA5 MOUSE

34	81	6.7	607	1	DNAX STRP3
35	81	6.7	609	1	DNAX STRA3
36	81	6.7	611	1	WDRI CAEEL
37	80.5	6.6	943	1	UPRA STRMU
38	80	6.6	345	1	PURA METJA
39	80	6.6	411	1	PGK METIH
40	80	6.6	1151	1	ITAI HUMAN
41	79.5	6.5	324	1	YB64 PASMU
42	79.5	6.5	637	1	VE1 HPV35
43	79.5	6.5	692	1	Y650 METJA
44	79	6.5	551	1	CHIT NPVAC
45	79	6.5	862	1	SLA2 BACAA
46	79	6.5	3695	1	LMA5 HUMAN
47	78.5	6.4	396	1	YJR1 YEAST
48	78.5	6.4	413	1	SP74 YEAST
49	78.5	6.4	509	1	CLS1 BACAA
50	78.5	6.4	762	1	SLAP ACEKI
51	78	6.4	376	1	ADH1 ORYSA
52	78	6.4	607	1	DNAX STRPN
53	78	6.4	607	1	DNAX STRR6
54	78	6.4	683	1	BGH3 RABIT
55	78	6.4	1157	1	XYNA THESA
56	78	6.4	1592	1	GTF2 STRDO
57	78	6.4	1914	1	RLF HUMAN
58	77.5	6.4	254	1	Y663 HAEIN
59	77.5	6.4	985	1	Y786 CORGL
60	77.5	6.4	1419	1	MDR PLAFF
61	77.5	6.4	2352	1	MOKC SCHPO
62	77	6.3	351	1	FEN AERPE
63	77	6.3	704	1	MSN2 YEAST
64	77	6.3	1597	1	GTF1 STRDO
65	76.5	6.3	284	1	YPV2 METTF
66	76.5	6.3	428	1	YQPI CAEEL
67	76.5	6.3	600	1	NUCD SALTY
68	76.5	6.3	635	1	ETFL YABAM
69	76.5	6.3	1689	1	RPAL SCHPO
70	76.5	6.3	2971	1	YCX9 CHLRE
71	76	6.2	247	1	PCNA HALMA
72	76	6.2	449	1	G6PI STRTR
73	76	6.2	509	1	YF08 MYCPN
74	76	6.2	670	1	PBP STAAU
75	76	6.2	704	1	NEUL HUMAN
76	76	6.2	1165	1	PEX6 PICPA
77	76	6.2	1902	1	P2P LACPA
78	75.5	6.2	420	1	ALA9 HUMAN
79	75.5	6.2	457	1	GALS KUULA
80	75.5	6.2	814	1	SYL STAEF
81	75	6.2	316	1	MIAA TREPA
82	75	6.2	343	1	FEN PYRHO
83	75	6.2	349	1	FEN SULSO
84	75	6.2	445	1	SLP2 DROME
85	75	6.2	455	1	EPIC STAEF
86	75	6.2	479	1	CBSP SULSO
87	75	6.2	506	1	SYE BIFLO
88	75	6.2	536	1	TRX1 DROME
89	75	6.2	695	1	CICA PAEPP
90	75	6.2	808	1	DHG GLUOX
91	74.5	6.1	171	1	LACB STAEF
92	74.5	6.1	654	1	MCPC BACSU
93	74.5	6.1	676	1	HS70 BRELC
94	74.5	6.1	1887	1	FAS2 YEAST
95	74	6.1	380	1	ADH WALDO
96	74	6.1	406	1	G6PI CAMJE
97	74	6.1	449	1	G6PI STRA3
98	74	6.1	485	1	HOXA BRAJA
99	74	6.1	504	1	FLIC SALEN
100	74	6.1	507	1	FLGX BACSU

ALIGNMENTS

RESULT 1

RL Lancet 359:1819-1827(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=PR1337.
 RA MEDLINE=68068692; PubMed=3335483;
 RX Bailey M.J., Mekalanos J.J.;
 RT "Nucleotide sequence of the type A staphylococcal enterotoxin gene.";
 RL J. Bacteriol. 170:34-41(1988).
 RN [3]
 RP SEQUENCE OF 25-257.
 RX MEDLINE=97222293; PubMed=3584106;
 RA Huang I.-Y., Hughes J.L., Bergdoll M.S., Schantz E.J.;
 RT "Complete amino acid sequence of staphylococcal enterotoxin A.";
 RL J. Biol. Chem. 262:7006-7013(1987).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=95354648; PubMed=7628431;
 RA Schad E.M., Zaitseva I., Zaitsev V.N., Dohlisten M., Kalland T.,
 RT Schlievert P.M., Ohlendorf D.H., Svensson L.A.;
 RL "Crystal structure of the superantigen staphylococcal enterotoxin
 type A.";
 RN EMBO J. 14:3292-3301(1995).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=97113025; PubMed=8943278;
 RA Sundstroem M., Hallen D., Svensson A., Schad E., Dohlisten M.,
 RA Abrahmsen L.;
 RT "The Co-crystal structure of staphylococcal enterotoxin type A with
 Zn2+ at 2.7-A resolution. Implications for major histocompatibility
 complex class II binding.";
 RL J. Biol. Chem. 271:32212-32216(1996).
 RN [6]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=96022987; PubMed=7552730;
 RA Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
 RT "Residues defining V beta specificity in staphylococcal
 enterotoxins.";
 RL Nat. Struct. Biol. 2:680-686(1995).
 RN [7]
 RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
 RX MEDLINE=97334373; PubMed=9191070;
 RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
 RT "A structural and functional comparison of staphylococcal
 enterotoxins A and C2 reveals remarkable similarity and
 dissimilarity.";
 RL J. Mol. Biol. 269:270-280(1997).
 CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
 CC staphylococcal food poisoning syndrome. The illness characterized
 CC by high fever, hypotension, diarrhea, shock, and in some cases
 CC death.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
 CC for the toxin interaction with MAC class II.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
 CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
 CC family.
 CC -----
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 CC -----
 DR EMBL; AF004826; BAB95754.1; -;
 DR EMBL; M18970; AAA26681.1; -;
 DR PIR; A28664; A28664.
 DR PDB; 1BSF; 11-JUL-96.
 DR PDB; 1SXT; 19-NOV-97.
 DR PDB; 1DYO; 21-FEB-02.
 DR PDB; 1I4G; 21-MAR-01.

DR PDB; 1I4H; 21-MAR-01.
 DR PDB; 1LO5; 18-DEC-02.
 DR PDB; 1SEA; 15-OCT-95.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bctrl_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF02876; Staph_strep_tox_C; 1.
 DR Pfam; PF01123; Staph_strep_toxin; 1.
 DR PRINTS; PR00279; BACTRL_TOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 DR Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
 KW 3D-structure; Complete proteome.
 FT SIGNAL 1 24
 FT CHAIN 25 257 ENTEROTOXIN TYPE A.
 FT DISULFID 120 130
 FT METAL 211 211 ZINC.
 FT METAL 249 249 ZINC.
 FT METAL 251 251 ZINC.
 FT CONFLICT 242 242
 FT HELIX 28 31
 FT TURN 32 33
 FT HELIX 39 41
 FT TURN 44 45
 FT HELIX 46 53
 FT TURN 56 56
 FT STRAND 59 65
 FT STRAND 69 69
 FT TURN 73 74
 FT STRAND 75 78
 FT TURN 79 80
 FT STRAND 90 94
 FT HELIX 98 104
 FT TURN 105 106
 FT STRAND 108 116
 FT TURN 118 119
 FT TURN 125 126
 FT STRAND 128 132
 FT STRAND 135 137
 FT TURN 139 140
 FT STRAND 142 149
 FT STRAND 151 155
 FT TURN 156 157
 FT STRAND 158 160
 FT HELIX 164 166
 FT STRAND 167 171
 FT STRAND 173 175
 FT HELIX 176 191
 FT TURN 193 194
 FT HELIX 197 199
 FT TURN 200 200
 FT STRAND 205 212
 FT STRAND 218 221
 FT TURN 222 223
 FT HELIX 230 233
 FT HELIX 234 237
 FT TURN 238 239
 FT STRAND 242 244
 FT STRAND 248 255
 SQ SEQUENCE 257 AA; ADEBFSBCALF14577 CRC64;
 Query Match 77.8%; Score 948; DB 1; Length 257;
 Best Local Similarity 76.4%; Pred. No. 1.3e-75;
 Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKSDQFLNTLLFKGFFTC 60
 DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHDFLOHTILFKGFFTD 84
 QY 61 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCWYGGVTLHDNNRLT 120

Db 85 HSWYNDLLVDFDSKIDVYKGRKVDLYGAYGYQCAGTGNKTCACMYGGVTLHDNNRLT 144

QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGIYNSDSFGKQV 180

Db 145 EEKVPINLWIDGKQNTVPIDKVTSKKEVTVOELDLQARHYLHGKFGIYNSDSFGKQV 204

QY 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTDILLRIYRDNNTTSSISLSLYLT 233

Db 205 RGLIVFHSSEGSTVSYDLFDAQOQYPTDILLRIYRDNNTTSSISLSLYLT 257

RESULT 3

ETXD STAAU STANDARD; PRT; 258 AA.

ID ETXH STAAU STANDARD; PRT; 241 AA.

AC Q53585;

DT 15-MAR-2004 (Rel. 43, Created)

DT 15-MAR-2004 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Enterotoxin type D precursor (SED).

GN ENT.

OS Staphylococcus aureus.

OC Bacteria; Firmicutes; Bacilliales; Staphylococcus.

OX NCBI_TaxID=1280;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=89359112; PubMed=2549000;

RA Bayles K.W., Iandolo J.J.;

RT "Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin D.";

RL J. Bacteriol. 171:4799-4806(1989).

RN [2]

RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).

RC STRAIN=AFCC 23235;

RX MEDLINE=97157473; PubMed=9003758;

RA Sundstroem M., Abrahamson L., Antonsson P., Mehindate K., Mourad W., Dohlsten M.;

RT "The crystal structure of staphylococcal enterotoxin type D reveals Zn2+-mediated homodimerization.";

RL EMBO J. 15:6832-6840(1996).

CC -1- FUNCTION: Staphylococcal enterotoxins cause the intoxication by high fever, hypotension, diarrhea, shock, and in some cases death.

CC -1- SUBUNIT: Homodimer; zinc-dependent.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.

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CC EMBL; M28521; AAB06195.1; .

CC PIR; A33953; A33953.

CC HSSP; P13163; LSXT.

CC InterPro; IPR008952; Bact_endotox.

CC InterPro; IPR006177; Bctrl_tox.

CC InterPro; IPR006123; Staph/Strep_toxin.

CC InterPro; IPR006126; Staph/Strep_tox.

CC InterPro; IPR006173; Staph_tox_OB.

CC Pfam; PF02876; Staph_Strep_tox_C7_1.

CC Pfam; PF01123; Staph_Strep_toxin; 1.

CC PRINTS; PR00279; BACTETOXIN.

CC PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.

CC PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

CC Enterotoxin; Toxin; Signal; Superantigen; Zinc.

CC SIGNAL 1 25

CC CHAIN 26 258 ENTEROTOXIN TYPE D.

CC METAL 212 212 ZINC.

FT METAL 250 250 ZINC.

FT METAL 252 252 ZINC.

FT VARIANT 114 114 P -> A (IN STRAIN ATCC 23235).

SQ SEQUENCE 258 AA; 29746 MW; 47766A28D42597FD CRC64;

Query Match 50.2%; Score 611; DB 1; Length 258;

Best Local Similarity 51.1%; Pred. No. 3.6e-46;

Matches 118; Conservative 35; Mismatches 78; Indels 0; Gaps 0;

QY 1 SEKSEENEDLRKSKELQGTALGNLKIYYVNSKAITSEKSDADQFLNTLLFKGFFTC 60

Db 26 NENIDSVKRELHKSKSELSTALNNMKSHVADKNPIGENKSTGDFLENTLYKKFFTD 85

QY 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYQCAGTGNKTCACMYGGVTLHDNNRLT 120

Db 86 LINFEDLLINFNSKEMAKHFKSKNDVVPYRISYVGVGIBIDRTACTYGGVTPHEGKCLK 145

QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGIYNSDSFGKQV 180

Db 146 ERKIPINLWINGVQKESVLDKVTQDKNVTYVQELDAQARYLQKDLKLYNNDTLGGKIQ 205

QY 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTDILLRIYRDNNTTSSISLSLYLT 231

Db 206 RGKIEFDSGSKSVYDLFDVKGDFPEKQLRIYSDNKLSTELHLDIYLY 256

RESULT 4

ETXH STAAU STANDARD; PRT; 241 AA.

AC Q53585;

DT 15-MAR-2004 (Rel. 43, Created)

DT 15-MAR-2004 (Rel. 43, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Enterotoxin type H precursor (SEH).

GN ENTH OR SEH OR MW0051.

OS Staphylococcus aureus (strain MW2), and Staphylococcus aureus.

OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI_TaxID=196620, 1280;

RN [1]

RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.

RC STRAIN=D4508;

RX MEDLINE=95053699; PubMed=7964453;

RA Ren K., Bannan J.D., Pancholi V., Cheung A.L., Robbins J.C., Fischetti V.A., Zabriskie J.B.;

RT "Characterization and biological properties of a new staphylococcal exotoxin.";

RT J. Exp. Med. 180:1675-1683(1994).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=MW2;

RX MEDLINE=22040717; PubMed=12044378;

RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A., Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L., Yamamoto K., Hiramatsu K.;

RT "Genome and virulence determinants of high virulence community-acquired MRSA.";

RT Lancet 359:1819-1827(2002).

RN [3]

RP X-RAY CRYSTALLOGRAPHY (1.69 ANGSTROMS).

RX MEDLINE=20444256; PubMed=10986116;

RA Haekansson M., Petersson K., Nilsson H., Forsberg G., Bjoerk P., Antonsson P., Svensson L.A.;

RT "The crystal structure of staphylococcal enterotoxin H: implications for binding properties to MHC class II and TCR molecules.";

RL J. Mol. Biol. 302:527-537(2000).

CC -1- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases death.

CC -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary for the toxin interaction with MHC class II.

CC -1- SUBCELLULAR LOCATION: Secreted.

```

CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC -----
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CC -----
CC EMBL; U11702; AAA19777.1; -.
CC DR EMBL; AF004822; BAB93916.1; -.
CC DR PDB; 1ENF; 10-JAN-01.
CC DR PDB; 1EWC; 10-JAN-01.
CC DR PDB; 1F77; 10-JAN-01.
CC DR PDB; 1HXV; 27-JUN-01.
CC DR InterPro; IPR008992; Bact_endotox.
CC DR InterPro; IPR006177; Bctrl_tox.
CC DR InterPro; IPR006173; Staph/Strep_toxin.
CC DR Pfam; PF01123; Staph_Strep_toxin; 1.
CC DR Pfam; PF02876; Staph_Strep_tox_C; 1.
CC DR PRINTS; PR00279; BACTRTOXIN.
CC DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
CC DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
CC KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
CC 3D-structure; Complete proteome.
CC FT SIGNAL 1 24
CC FT CHAIN 25 241 ENTEROTOXIN TYPE H.
CC FT METAL 230 230 ZINC.
CC FT METAL 232 232 ZINC.
CC FT DISULFID 106 116
CC SQ SEQUENCE 241 AA; 27858 MW; 70F77985977616CE CRC64;

Query Match 25.3%; Score 308; DB 1; Length 241;
Best Local Similarity 33.9%; Pred. No. 9.7e-20;
Matches 76; Conservative 46; Mismatches 90; Indels 12; Gaps 7;

Qy 10 KDLRRKSELOGTALGNLKKQIYYNSKAITSEKSDAQPLNTLLFKGFTGHPWYNDLV 69
Db 25 EDLHDKSELTLALAN--AYQYNHPFIKENIKDEISGERKDLFRN--QGDSG-NDLRV 79

Qy 70 DLGSTATSEVGSVDLYGAYVQACGGTPNKTACMYGVTLDHNNRLTEKKVPINL 129
Db 80 KFATADLAQKFNKNDYIGASFYKCEKISGENISECLYGGTTL-NSEKLAQERVIGANV 138

Qy 130 WIDGQOTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGSKVQVORGLVPHSS 189
Db 139 WVDGIQKTEL--ITFNKNVTLQELDIKIRKILSDKVIYKDS---EISKGLIEFDMK 193

Qy 190 EGSTVSYDLFDAQQYPTLLRIYRDNNTTISSTLS-ISLYLYT 232
Db 194 TPRDYSFDIYDLKGENDYEIDKIYEDNKTLSDDIISHIDVNLVT 237

RESULT 5
ETC3_STAAM STANDARD; PRT; 266 AA.
AC P23313;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Enterotoxin type C-3 precursor (SEC3).
GN ETC3 OR SAV2009 OR SA1817.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315), and
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=158878, 158879, 1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699, and N315;

```

```

RX MEDLINE=21311192; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Chui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekinizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Ogasawara N., Hayashi H., Hiramatsu K.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT aureus.;
RT Lancet 357:1225-1240 (2001).
RL [2]
RN SEQUENCE FROM N.A.
RP MEDLINE=90220508; PubMed=2325627;
RX Hovde C.J., Hackett S.P., Bohach G.A.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C3 gene:
RT sequence comparison of all three type C staphylococcal
RT enterotoxins.";
RT Mol. Gen. Genet. 220:329-333 (1990).
RN [3]
RX MEDLINE=97064178; PubMed=8906797;
RA Fields B.A., Malchioldi E.L., Li H., Ysern X., Stauffacher C.V.,
RA Schlievert P.M., Karjalainen K., Mariuzza R.A.;
RT "Crystal structure of a T-cell receptor beta-chain complexed with a
RT superantigen.";
RT Nature 384:188-192 (1996).
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases
CC death.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AP003364; BAB58171.1; -.
CC DR EMBL; AP003364; BAB58171.1; -.
CC DR EMBL; X51661; CAA35972.1; -.
CC DR PIR; S11885; S11885.
CC DR PDB; 1JCK; 12-NOV-97.
CC DR PDB; 1KLJ; 02-AUG-02.
CC DR PDB; 1KLU; 14-AUG-02.
CC DR InterPro; IPR008992; Bact_endotox.
CC DR InterPro; IPR006177; Bctrl_tox.
CC DR InterPro; IPR006123; Staph/Strep_toxin.
CC DR InterPro; IPR006126; Staph/Strep_tox.
CC DR InterPro; IPR006173; Staph_tox_OB.
CC DR Pfam; PF02876; Staph_Strep_tox_C; 1.
CC DR Pfam; PF01123; Staph_Strep_toxin; 1.
CC DR PRINTS; PR00279; BACTRTOXIN.
CC DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
CC DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
CC KW Enterotoxin; Toxin; Signal; Superantigen; 3D-structure;
CC Complete proteome.
CC FT SIGNAL 1 27
CC FT CHAIN 28 266 ENTEROTOXIN TYPE C-3.
CC FT DISULFID 120 137
CC SQ SEQUENCE 266 AA; 30671 MW; 5ED9A32D11FFCA59 CRC64;

Query Match 23.4%; Score 284.5; DB 1; Length 266;
Best Local Similarity 32.5%; Pred. No. 1.2e-17;
Matches 76; Conservative 45; Mismatches 94; Indels 19; Gaps 9;

Qy 11 DLRRKSELOGTALGNLKKQIYYNSKAITSEKSDAQPLNTLLFKGFTGHPWYNDLV 69
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Mu50 / ATCC 700699, and N315;

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Db 37 DLHKSSEFTCT-MGNMK--YLYDDHYVSATKVSVDKFLAHLDIYINISDKLKNYDKVKT 93
 Qy 70 DLGSTAATSEYSGSSVDLYGAYGYOC-----AGGTENKTAQMYGGVTLHDNNRLTEE 122
 Db 94 ELLNEDLAKYKDEVDVYGSNNYVNCYFSSKDNVGVTKGTCMYGGITKHEGNHFDNG 153
 Qy 123 --KKVPINLWIDGQTVTPIDKVTSEKVEVTVQELDLQARHYLHGKFLYNSDSFGGKVQ 180
 Db 154 NLQNLVRVY-ENKRTISFE-VQTDKSVTAQELDIKARNFINKNLYEFNS--SPYE 209
 Qy 181 RGLIVSHSSGSSVSYDLFDAQQYDP--TLRIYRDNTTISTSLISLYLT 232
 Db 210 TGVYKFIENNGNFWYDMMPAPGDKFDQSKYLMWYNDKTVDSKVKIEVHLT 263

RESULT 6
 ETC2 STAAU STANDARD; PRT; 266 AA.
 AC P34071;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Enterotoxin type C-2 precursor (SEC2).
 GN ETC2.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.
 RX MEDLINE=89277549; PubMed=2543637;
 RA Bohach G.A., Schlievert P.M.;
 RT "Conservation of the biologically active portions of staphylococcal
 enterotoxins C1 and C2."
 RL Infect. Immun. 57:2249-2252(1989).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=96027099; PubMed=7582894;
 RA Papageorgiou A.C., Acharya K.R., Shapiro R., Passalacqua E.F.,
 RA Brehm R.D., Tranter H.S.;
 RT "Crystal structure of the superantigen enterotoxin C2 from
 Staphylococcus aureus reveals a zinc-binding site."
 RL Structure 3:769-779(1995).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=96022987; PubMed=7552730;
 RA Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
 RT "Residues defining V beta specificity in staphylococcal
 enterotoxins."
 RL Nat. Struct. Biol. 2:680-686(1995).
 RN [4]
 RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
 RX MEDLINE=97334373; PubMed=9191070;
 RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
 RT "A structural and functional comparison of staphylococcal
 enterotoxins A and C2 reveals remarkable similarity and
 dissimilarity."
 RL J. Mol. Biol. 269:270-280(1997).
 CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
 staphylococcal food poisoning syndrome. The illness characterized
 by high fever, hypotension, diarrhea, shock, and in some cases
 death.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
 for the toxin interaction with MHC class II.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
 family.
 CC PIR; A60114;
 DR PDB; 1STE; 23-DEC-96.
 DR PDB; 1SE2; 08-MAR-96.
 DR PDB; 1CQV; 19-SEP-01.
 DR PDB; 1I4P; 19-SEP-01.
 DR PDB; 1I4Q; 19-SEP-01.
 DR PDB; 1I4R; 19-SEP-01.

PDB; 1I4X; 19-SEP-01.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bctrl_tox.
 DR InterPro; IPR006123; Staph/Strep toxin.
 DR InterPro; IPR006126; Staph/Strep tox.
 DR InterPro; IPR006173; Staph_tox_08.
 DR Pfam; PF02876; Staph_strep_tox_C7; 1.
 DR Pfam; PF01123; Staph_strep_coxin; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
 KW 3D-structure.
 FT SIGNAL 1 27 ENTEROTOXIN TYPE C-2.
 FT CHAIN 28 266
 FT DISULFID 120 137
 FT METAL 36 36 ZINC.
 FT METAL 110 110 ZINC.
 FT METAL 145 145 ZINC.
 FT METAL 149 149 ZINC.
 FT METAL 149 149 ZINC.
 FT HELIX 35 37
 FT HELIX 41 43
 FT STRAND 44 44
 FT TURN 48 48
 FT TURN 49 55
 FT STRAND 60 65
 FT STRAND 69 69
 FT TURN 73 74
 FT STRAND 75 79
 FT TURN 83 86
 FT STRAND 90 94
 FT HELIX 98 104
 FT TURN 105 106
 FT STRAND 109 113
 FT STRAND 116 116
 FT TURN 118 119
 FT TURN 128 129
 FT STRAND 136 139
 FT STRAND 142 144
 FT TURN 146 147
 FT STRAND 149 149
 FT HELIX 151 153
 FT STRAND 156 164
 FT TURN 165 166
 FT STRAND 167 176
 FT STRAND 178 178
 FT STRAND 180 182
 FT HELIX 183 198
 FT STRAND 208 216
 FT TURN 218 219
 FT STRAND 222 226
 FT STRAND 232 232
 FT HELIX 237 241
 FT HELIX 242 246
 FT STRAND 249 251
 FT TURN 252 254
 FT STRAND 256 263
 SQ SEQUENCE 266 AA; 30604 MW; 8407FBI8536FAC08 CRC64;
 Query Match 22.8%; Score 277.5; DB 1; Length 266;
 Best Local Similarity 31.1%; Pred. No. 51e-17;
 Matches 76; Conservative 47; Mismatches 102; Indels 19; Gaps 9;
 Qy 1 SEKSEENKDLKKSELOQTALGNLKIYYNKAITSSE-KSADQFLTNLLFKGFFT 59
 Db 27 AESQPDTPDELHKSSSEFTCT-MGNMK--YLYDDHYVSATKVSVDKFLAHLDIYINISDK 83
 Qy 60 GHPWYNDLLVDLGLSTAATSEYSGSSVDLYGAYGYOC-----AGGTENKTAQMYGGVT 112
 Db 84 KLRNYDKVKTLELLEDLAKYKDEVDVYGSNNYVNCYFSSKDNVGVTKGTCMYGGIT 143
 Qy 113 LHDNNRLTEE--KKVPINLWIDGQTVTPIDKVTSEKVEVTVQELDLQARHYLHGKFLY 170

Db 144 KHEGNFDNGNLQNLVIRV-ENKRTISFE-VQTDKSKVTAQELDIKARNFLINKKNLY 201
Qy 171 NSDSFGKQVQGLVIFHSSEGSTVSYDLFQAQGYD--TLRIYRNTTISSTLSISL 228
Db 202 EFNS--SPYETGYIKFIENNGNTFWYDMPAGDKFDQSKYLMYNDKNTVDSKVKIEV 259
Qy 229 YLYT 232
Db 260 HLTT 263

RESULT 7
SPEA STRPY STANDARD; PRT; 251 AA.
AC P08035;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin) (SPE A).
DE SPEA OR SPYMI8 0393.
GN Streptococcus pyogenes, and
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
CX NCBI_TaxID=1314, 186103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86166804; PubMed=3514452;
RA Weeks C.R., Ferretti J.J.;
RT "Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage T12.";
RL Infect. Immun. 52:144-150(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86284313; PubMed=3526093;
RA Johnson L.P., L'Italian J.J., Schlievert P.M.;
RT "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to Staphylococcus aureus enterotoxin B";
RL Mol. Gen. Genet. 203:354-356(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX STRAIN=MGAS8232 / Serotype M18;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S., Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F., Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q., Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18 group A Streptococcus strains associated with acute rheumatic fever outbreaks.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).
RX MEDLINE=99094887; PubMed=9878045;
RA Papageorgiou A.C., Collins C.M., Gutman D.M., Kline J.B., O'Brien S.M., Tranter H.S., Acharya K.R.;
RT "Structural basis for the recognition of superantigen streptococcal pyrogenic exotoxin A (SpeA) by MHC class II molecules and T-cell receptors.";
RL EMBO J. 18:9-21(1999).
CC -!- FUNCTION: Causative agent of the symptoms associated with scarlet fever, have been associated with streptococcal toxic shock-like disease and may play a role in the early events of rheumatic fever.
CC -!- SUBUNIT: Binds to major histocompatibility complex class II beta chain.
CC -!- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE T12.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.

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CC or send an email to license@isb-sib.ch).

CC EMBL; U40453; AAC48868.1; -;
CC EMBL; X03929; CAA27568.1; -;
CC EMBL; AE009982; AAL97141.1; -;
CC F1R; A26152; A26152.
CC PDB; 1B12; 24-NOV-99.
CC PDB; 1FNU; 17-NOV-00.
CC PDB; 1FNV; 17-NOV-00.
CC PDB; 1FNU; 17-NOV-00.
CC PDB; 1HAS; 03-APR-02.
CC PDB; 1LOX; 03-APR-02.
CC InterPro; IPR008982; Bact_endotox.
CC InterPro; IPR006177; Bctrl_tox.
CC InterPro; IPR006123; Stap/Strep_toxin.
CC InterPro; IPR006126; Staph/Strep_tox.
CC InterPro; IPR006173; Staph_tox_OB_
CC Pfam; PF02876; Stap_strp_tox_C_1.
CC Pfam; PF01123; Stap_strp_toxin; 1.
CC PRINTS; PR00279; BACTRIOTOXIN.
CC DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
CC DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
CC KW Toxin; Signal; 3D-structure; Complete proteome.
CC FT SIGNAL 1 30 EXOTOXIN TYPE A.
CC FT CHAIN 31 251
CC FT DISULFID 117 128
CC FT CONFLICT 6 6 K -> E (IN REF. 2).
CC FT CONFLICT 17 18 VT -> MK (IN REF. 2).
CC FT CONFLICT 25 35 SOEVFAQDDP -> LPKGICSTRPK (IN REF. 2).
CC FT CONFLICT 40 40 H -> Q (IN REF. 2).
CC FT CONFLICT 43 43 S -> N (IN REF. 2).
CC FT CONFLICT 47 59 NQNTLYFLYEGDP -> TEKIYFFMRVTL (IN REF. 2).
CC FT CONFLICT 129 129 I -> L (IN REF. 2).
CC FT CONFLICT 165 178 TNKQMTAQELDYK -> QIKNGCSRSISYT (IN REF. 2).
CC FT HELIX 36 38
CC FT HELIX 42 44
CC FT TURN 48 48
CC FT HELIX 49 56
CC FT STRAND 60 66
CC FT STRAND 69 69
CC FT TURN 73 74
CC FT STRAND 75 78
CC FT STRAND 82 82
CC FT TURN 83 84
CC FT STRAND 85 85
CC FT STRAND 87 91
CC FT HELIX 95 101
CC FT TURN 102 103
CC FT STRAND 105 110
CC FT STRAND 113 113
CC FT TURN 115 116
CC FT STRAND 126 130
CC FT STRAND 133 135
CC FT TURN 137 138
CC FT STRAND 140 153
CC FT TURN 154 155
CC FT STRAND 156 167
CC FT STRAND 169 171
CC FT HELIX 172 187
CC FT STRAND 199 205
CC FT STRAND 212 215
CC FT STRAND 224 227
CC FT HELIX 228 231
CC FT TURN 232 233
CC FT STRAND 236 238
CC FT TURN 239 241


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RT relatedness to other pyrogenic toxins.";
RL Mol. Gen. Genet. 209:15-20(1987).
RN [2]
RR SEQUENCE OF 28-266.
RX MEDLINE=83213327; PubMed=6189824;
RA Schmidt J.J., Spero L.;
RT "The complete amino acid sequence of staphylococcal enterotoxin C1.";
RL J. Biol. Chem. 258:6300-6306(1983).
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC of staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases
CC death.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC -----
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CC -----
CC EMBL; X05815; CAA29260.1; -.
CC PIR; S06356; ENGAC1.
CC DR HSP; P34071; 1SE2.
CC DR InterPro; IPR008992; Bact_endotox.
CC DR InterPro; IPR006177; BctI_tox.
CC DR InterPro; IPR006123; Staph/Strep_toxin.
CC DR InterPro; IPR006126; Staph/Strep_tox.
CC DR InterPro; IPR006173; Staph_tox_OB.
CC DR Pfam; PF02876; Staph_Strep_tox_C; 1.
CC DR Pfam; PF01123; Staph_Strep_toxin; 1.
CC DR PRINTS; PS00279; BACTRLTOXIN.
CC DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
CC DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
CC DR Enterotoxin; Toxin; Signal; Superantigen.
CC KW SIGNAL
CC FT 1 27
CC FT CHAIN 28 266 ENTEROTOXIN TYPE C-1.
CC FT DISULFD 120 137
CC FT CONFLICT 177 177 D -> N (IN REF. 2).
CC FT SEQUENCE 266 AA; 30546 MW; 3A7AB59A8966853B CRC64;
CC -----
CC Query Match 21.6%; Score 263.5; DB 1; Length 266;
CC Best Local Similarity 30.6%; Pred. No. 8.5e-16;
CC Matches 75; Conservative 45; Mismatches 104; Indels 21; Gaps 9;
CC -----
CC QY 1 SEKSEENEXDLKPKSELGTALGNLQIYV--VYNSKAITSEKSAOFLNTLLKGF 58
CC Db 27 AESQFDTPDELHAKSKFTG-LMNNKVLVDHYVS---ATKVASVDRFLAHLIYV 82
CC QY 59 TCHPWYNDLVLDCGAATSEYEGSSVDLYGAYGYQC-----AGGTPNKTACTMYGGV 111
CC Db 83 KKLKNYDKVKTLLNEGLAKKYKDEVDVYGSNYVNCVFSSKONVGVKVGKTCMYGGI 142
CC QY 112 TLHNNRLTEE--KKVPINLWIDCKQTTPIDKVKTSKEVTVQELDQARHYLHGKFL 169
CC Db 143 TKHEGNHFDNGLNQNLIRIYV-ENKNTTISFE-VQTDKKSVAQELDKARNFINKNL 200
CC QY 170 YNSDFGKGVQRGILVPHSSEGTVSYDLFDAQGVDP--TLIRIYRNTTISSTLSIS 227
CC Db 201 YEFNS--SPYETGYIKIEIENNGNTFWYDMWPAFGKFDQSKLYMYNDKIVDSKV 258
CC QY 228 LYLVT 232
CC Db 259 VELAT 263
CC -----
CC RESULT 10
CC ETXG_STAAM
CC ID ETXG_STAAM PRT; 258 AA.
CC AC O85382;

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Qy	3	KSEINEKDLRKSELQCTALGNLKKQIYY---YNSKAITSSEKSADQFLTNLLFKGFTT	59
Dd	30	KLELDNKVSDYKN--KGT-NGRYNMNLYTFPPVEGRGVINSR---QFLSHDLIFP---I	79
Qy	60	GHPWNVDLLDVGSTAASTSEYEGSSVDLYGAYYGQCA-----GGTPENKTACM	107
Dd	80	EYKSYNEVKTELENTELANNYKDKVLDFVPFYTCIIIPKSPEDINQFPG-----CCM	134
Qy	108	YGVVTLLH--DNNRLTEEEKVPINLIWDKGTTVIDPKVTKTSKEVTVQVELDLQARHYLHG	165
Dd	135	YGLGLFNSSENER---DKLITVQTIDNRQSLG--FTITTNNKVITIQEILDYKAREHLTK	189
Qy	166	KFGLYNYSFGCKYQRGILIVPHSSEGSTVSVDLFDAQGYPDIT---LLRIYRDNTTIST	222
Dd	190	EKKLVFFD--GSAFESGYIKETKNITSFWFDLPFKKELVFVPYKPLNIYGDNVDSK	247
Qy	223	SLSISLIYLTY 232	
Dd	248	SIKMEVFLNT 257	

RESULT 11

ID	SPEH_STRPY	STANDARD;	PRT;	236 AA.
Qy	Q9X5C8;			
Dt	16-OCT-2001 (Rel. 40, Created)			
Dt	16-OCT-2001 (Rel. 40, Last sequence update)			
Dt	10-OCT-2003 (Rel. 42, Last annotation update)			
De	Exotoxin type H precursor (SPE H).			
Gn	SPEH OR SPY1008.			
Oc	Streptococcus pyogenes.			
Oc	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;			
Oc	Streptococcus.			
Ox	NCBI_TaxId=1314;			
Rn	[1]			
Rn	SEQUENCE FROM N.A.			
Rc	MEDLINE=M15;			
Rx	MEDLINE=99093428; PubMed=9874566;			
Rx	Proft T., Moffatt S.L., Berkahn C.J., Fraser J.D.;			
Rt	"Identification and characterization of novel superantigens from			
Rt	Streptococcus pyogenes";			
Rl	J. Exp. Med. 189:189-192(1999).			
Rn	[2]			
Rn	SEQUENCE FROM N.A.			
Rc	STRAIN-SF370 / ATCC 700294 / Serotype M1;			
Rx	MEDLINE=21192684; PubMed=11296296;			
Rx	Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,			
Ra	Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,			
Ra	Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,			
Ra	Xuan X., Clifton S.W., Roe B.A., McLoughlin R.;			
Rl	"Complete genome sequence of an M1 strain of Streptococcus pyogenes.";			
Rt	Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).			
Cc	-!- FUNCTION: Mitogenic for human peripheral blood lymphocytes.			
Cc	-!- SUBUNIT: Binds to major histocompatibility complex class II beta			
Cc	chain.			
Cc	-!- SUBCELLULAR LOCATION: Secreted.			
Cc	-!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin			
Cc	family.			

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Dd	EMBL; AF124500; AAD30989.1; -	
Dr	EMBL; AE006546; AK333907.1; -	
Dd	FDB; IET9; 24-MAY-00.	
Dr	PDB; 1EU4; 24-MAY-00.	
Dr	InterPro; IPR008992; Bact_endotox.	
Dr	InterPro; IPR006123; Strep/Strep toxin.	

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DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF02876; Staph_Strp_tox_C; 1.
DR Pfam: PF01123; Staph_Strp_toxin; 1.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR Toxin; Signal; Complete proteome; 3D-structure.
KW SIGNAL; 1 32 POTENTIAL.
FT CHAIN 33 236 EXOTOXIN TYPE H.
SQ SEQUENCE 236 AA; 27485 MW; 16352923907AD40D CRC64;

Query Match 15.2%; Score 185; DB 1; Length 236;
Best Local Similarity 26.7%; Pred. No. 5.3e-09;
Matches 56; Conservative 46; Mismatches 84; Indels 24; Gaps 9;

Qy 25 NLKQIYYNSKAI-TSSEKADQFLNTLLFKGFTGHPWYN-----DLLVDLGSSTAATSE 79
Db 42 NLESYKHDSNLIBADSIKNSPDIVTSHML-----KYSVKDKNLSVFFKDWISQE 92
Qy 80 YEGSSVDLYGAYGYQCAGGTPNKTCMVGVTLDHNNRLTEEEKKVPINLWIDGKQTTP 139
Db 93 FXDKEDVIYALSAQEVCE--CPGRYEAFGGITLTNSEK--KEIKVPVNVWDRSKQO--P 146
Qy 140 IDKVKTSKKEVTVQELDLQARHYLHGKFLGNSDFGKVGQVGLIVFHSSEGSTVSDYL- 198
Db 147 PMFITVNRKPKVTAGEDIKVRKLLIKKYDIYNNRE--QKYSKGTVTLLDLSGDKDIVFDLY 204
Qy 199 FDAQGVPTLLRIYRDNTTISSTLSLSL 228
Db 205 YFGNGDP-NSMLKYSNNERIDSTQFHVQV 233

RESULT 12
SPEC_STRPY STANDARD; PRT; 234 AA.
AC Q9X5C7;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Exotoxin type G precursor (SPE G).
GN SPEC OR SPY0212.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M1;
RX MEDLINE=98093428; PubMed=9874556;
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Proft T., Moffatt S.L., Berkahn C.J., Fraser J.D.;
RT "Identification and characterization of novel superantigens from
RT Streptococcus pyogenes."
RL J. Exp. Med. 189:189-192(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes."
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
CC -!- FUNCTION: Mitogenic for human peripheral blood lymphocytes.
CC -!- SUBUNIT: Binds to major histocompatibility complex class II beta
CC chain.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC
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CC
CC EMBL: AF124499; RAD30988.1; -.
CC EMBL: AE006489; RAK33303.1; -.
CC HSSP: PI3380; 1AN8.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bctrl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF02876; Staph_Strp_tox_C; 1.
DR Pfam: PF01123; Staph_Strp_toxin; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR Toxin; Signal; Complete proteome.
KW SIGNAL; 1 24 POTENTIAL.
FT CHAIN 25 234 EXOTOXIN TYPE G.
SQ SEQUENCE 234 AA; 27262 MW; 49525C49E4BA2052 CRC64;

Query Match 15.1%; Score 183.5; DB 1; Length 234;
Best Local Similarity 27.6%; Pred. No. 7e-09;
Matches 56; Conservative 37; Mismatches 81; Indels 29; Gaps 7;

Qy 33 NSKAITSSKSDAQFLNTLLFKGFTGHPWYNLDLGLSTAATSEYEGSSVDLYGAYY 92
Db 57 NSIHINTKQRSECL-----YVDSIVSLGIT--DQFIKDKVDVFGLPY 99
Qy 93 GYQCAGGTPNKTCMVGVTLDHNNRLTEEEKKVPINLWIDGKQTTPIDKVKTSKEVTV 152
Db 100 NF-----SPYVDNTYGGIVKHSNQGKSLQFVGI-LNQDQKETYLPSEAVIKKKQFTL 153
Qy 153 QELDLQARHYLHGKFLGNSDFGKVGQVGLIVFHSSEGSTVSDYLFAQGOY--PDTLL 210
Db 154 QEFDFKIRKFLMEKYNIVDSSES---RYTSGSLFLATKSKHYEVDLFNKDKLLSRDSFF 210
Qy 211 RIYRDNTTISSTLS-LSLYLT 232
Db 211 KRYKDKNFENSEISHFDIYLT 233

RESULT 13
SPEC_STRPY STANDARD; PRT; 235 AA.
AC PI3380;
DT 01-JAN-1990 (Rel. 13, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Exotoxin type C precursor (SPE C).
GN SPEC OR SPY0711.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-52.
RC STRAIN=T18P / MGAS 1585;
RX MEDLINE=88314303; PubMed=3045005;
RA Goshorn S.C., Schlievert P.M.;
RT "Nucleotide sequence of streptococcal pyrogenic exotoxin type C."
RL Infect. Immun. 56:2518-2520(1988).
RN [2]
RP REVISIONS TO 21-26.
RC STRAIN=T18P / MGAS 1585;
RX MEDLINE=92363541; PubMed=1500157;
RA Kapur V., Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
RT "Molecular population genetic evidence of horizontal spread of two
RT alleles of the pyrogenic exotoxin C gene (speC) among pathogenic
RT clones of Streptococcus pyogenes."
RL Infect. Immun. 60:3513-3517(1992).
RN [3]
```

SEQUENCE FROM N.A.
 RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
 RX MEDLINE=21192684; PubMed=11296296;
 RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
 RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
 RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
 RA "Complete genome sequence of an M1 strain of *Streptococcus*
 RT *pyogenes*.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 30-235.
 RX MEDLINE=97397352; PubMed=9253413; Baker E.N.;
 RA Rousset A., Anderson B.F., Baker H.M., Fraser J.D., Baker E.N.;
 RA "Crystal structure of the streptococcal superantigen SPE-C:
 RT dimerization and zinc binding suggest a novel mode of interaction
 RT with MHC class II molecules.";
 RL Nat. Struct. Biol. 4:635-643(1997).
 CC -!- FUNCTION: Causative agent of the symptoms associated with scarlet
 CC fever, have been associated with streptococcal toxic shock-like
 CC disease and may play a role in the early events of rheumatic
 CC fever.
 CC -!- SUBUNIT: Binds to major histocompatibility complex class II beta
 CC chain.
 CC -!- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
 CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
 CC family.
 CC -----
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 CC -----
 DR EMBL: M35514; AAA27017.1; ALT SEQ.
 DR EMBL: M97156; AAB59091.1; -.
 DR EMBL: M97157; AAB59092.1; -.
 DR EMBL: AE006523; AK33664.1; -.
 DR EIR: A30509; A30509.
 DR EIR: A44799; A44799.
 DR PDB: 1AN8; 29-APR-98.
 DR PDB: 1KTK; 07-JUN-02.
 DR InterPro: IPR008992; Bact endotox.
 DR InterPro: IPR006177; Bctr1 tox.
 DR InterPro: IPR006123; Staph/Strep toxin.
 DR InterPro: IPR006126; Staph/Strep tox.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR Pfam: PF02876; Staph_Strep_tox_C; 1.
 DR Pfam: PF01123; Staph_Strep_toxin; 1.
 DR PRINTS: PR00279; BACTRLTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Toxin; Signal; 3D-structure; Complete proteome.
 FT SIGNAL 1 27
 FT CHAIN 28 235 EXOTOXIN TYPE C.
 FT CONFLICT 53 53 N -> D (IN REF. 1).
 FT HELIX 33 44
 FT STRAND 49 59
 FT STRAND 63 67
 FT HELIX 69 72
 FT TURN 74 75
 FT STRAND 77 81
 FT HELIX 84 87
 FT TURN 88 89
 FT TURN 92 93
 FT STRAND 95 100
 FT TURN 108 109
 FT STRAND 110 114
 FT STRAND 117 119
 FT STRAND 127 128
 FT STRAND 131 135

FT TURN 136 137
 FT STRAND 141 142
 FT TURN 144 145
 FT STRAND 148 149
 FT STRAND 153 155
 FT HELIX 156 171
 FT TURN 173 174
 FT TURN 176 177
 FT STRAND 182 189
 FT TURN 190 191
 FT STRAND 194 198
 FT TURN 204 205
 FT HELIX 208 212
 FT STRAND 213 217
 FT STRAND 220 222
 FT HELIX 223 225
 FT STRAND 226 235
 SQ SEQUENCE 235 AA; 27371 MW; 070534ABB952C1E0 CRC64;
 Query Match 12.2%; Score 148.5; DB 1; Length 235;
 Best Local Similarity 25.8%; Pred. No. 8.1e-06;
 Matches 58; Conservative 39; Mismatches 85; Indels 45; Gaps 11;
 QY 34 SKAITSEKSADQFLNTLLFKGFFTGHPW-VNDLLVDLGSTAA-----TSEYEGSS---- 84
 DB 22 SPIIKSDSKDISNVKSDLLYA--YITPDYKNCRVNFTTHTLNIDTQYRGKDYIS 79
 QY 85 -----VDLYGAYGYQCAGGTPTKACMYGGVTLDHNRRLTEKKVPIN 128
 DB 80 SEMSEYASQKFKEDHVDVDFGLFYILNHTG-----EYTGITPAQNNKVNH--KLLGN 132
 QY 129 LWIDGQTTVPIDKVTSKKEVTVOQLDLQARHLHGKFLYNSDS--FGKVKVQGLIVF 186
 DB 133 LFTSGSQQLNNKILKIDKIVTFQIDFKIRKLYMDNYKIYDATSPYVSGRIEIG---- 188
 QY 187 HSSEGSTVSVLDLPA--QGQYPTLLRIYRDNNTTISTSLIS-LSLYL 230
 DB 189 -TKDGKHEQIDLPSPNEGSTRSDIFAK-YKDNRIINMKNFHFDIYL 233
 RESULT 14
 TSST STAAU STANDARD; PRT; 234 AA.
 AC P06886;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Toxic shock syndrome toxin-1 precursor (TSSST-1).
 GN TST.
 OS *Staphylococcus aureus*.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OC NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
 RX MEDLINE=87057222; PubMed=3782090;
 RA Blomster-Hautamaa D.A., Kreiswirth B.N., Kornblum J.S., Novick R.P.,
 RA Schlievert P.M.;
 RT "The nucleotide and partial amino acid sequence of toxic shock
 RL syndrome toxin-1.";
 RN J. Biol. Chem. 261:15783-15786(1986).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=94150598; PubMed=8107781;
 RA Acharya K.R., Passalacqua E.F., Jones E.Y., Harlos K., Stuart D.I.,
 RA Brehm R.D., Tranter H.S.;
 RT "Structural basis of superantigen action inferred from crystal
 RT structure of toxic-shock syndrome toxin-1.";
 RL Nature 367:94-97(1994).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=94092653; PubMed=8268150;
 RA Prasad G.S., Earhart C.A., Murray D.L., Novick R.P., Schlivert P.M.,
 RA Ohlendorf D.H.;

RT "Structure of toxic shock syndrome toxin 1.";
RL Biochemistry 32:13761-13766(1993).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.07 ANGSTROMS).
RX MEDLINE=96319751; PubMed=8759320;
RA Papageorgiou A.C., Brehm R.D., Leonidas D.D., Tranter H.S.,
RA Acharya K.R.;
RT "The refined crystal structure of toxic shock syndrome toxin-1 at
RT 2.07-A resolution.";
RL J. Mol. Biol. 260:553-569(1996).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).
RX MEDLINE=97337442; PubMed=9194182;
RA Prasad G.S., Radhakrishnan R., Mitchell D.T., Earhart C.A.,
RA Dinges M.W., Cook W.J., Schlvert P.M., Ohlendorf D.H.;
RT "Refined structures of three crystal forms of toxic shock syndrome
RT toxin-1 and of a tetramutant with reduced activity.";
RL Protein Sci. 6:1220-1227(1997).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF MUTANTS.
RX MEDLINE=98254504; PubMed=9585531;
RA Earhart C.A., Mitchell D.T., Murray D.L., Pinheiro D.M., Matsumura M.,
RA Schlvert P.M., Ohlendorf D.H.;
RT "Structures of five mutants of toxic shock syndrome toxin-1 with
RT reduced biological activity.";
RL Biochemistry 37:7194-7202(1998).
RN [7]
CC -!- FUNCTION: Responsible for the symptoms of toxic shock syndrome.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC
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CC
CC EMBL: J02615; AAA26682.1; --
DR PIR: A24606; XCSAS1.
DR PDB: 2TSS; 24-DEC-97.
DR PDB: 3TSS; 24-DEC-97.
DR PDB: 4TSS; 24-DEC-97.
DR PDB: 5TSS; 24-DEC-97.
DR PDB: 1QIL; 12-AUG-97.
DR PDB: 2QIL; 12-AUG-97.
DR PDB: 1AW7; 18-NOV-98.
DR PDB: 1TS2; 16-DEC-98.
DR PDB: 1TS3; 16-DEC-98.
DR PDB: 1TS4; 16-DEC-98.
DR PDB: 1TS5; 16-DEC-98.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR008375; Staph_exotoxin.
DR InterPro: IPR006173; Staph_tox OB.
DR InterPro: IPR006125; Staph_toxin.
DR Pfam: PF02876; Staph_Strep_tox C; 1.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR PRINTS: PR01800; STAPHSTREPTOXIN.
DR PRINTS: PR01501; TOXICSHOCKTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Toxin; Superantigen; Signal; 3D-structure.
FT SIGNAL 1 40
FT CHAIN 41 234 TOXIC SHOCK SYNDROME TOXIN-1.
FT HELIX 46 54
FT STRAND 58 69
FT TURN 70 71
FT STRAND 72 76
FT TURN 78 79
FT STRAND 82 86

FT TURN 90 91
FT TURN 98 99
FT STRAND 101 108
FT STRAND 113 114
FT TURN 116 117
FT STRAND 120 125
FT STRAND 128 129
FT STRAND 133 138
FT STRAND 142 146
FT TURN 147 148
FT STRAND 149 151
FT STRAND 159 161
FT STRAND 163 164
FT HELIX 166 181
FT TURN 183 185
FT TURN 187 188
FT STRAND 192 198
FT TURN 199 200
FT STRAND 203 207
FT TURN 208 209
FT HELIX 214 216
FT STRAND 221 222
FT HELIX 223 225
FT STRAND 226 234
SQ SEQUENCE 234 AA; 26306 MW; E95789FF9A1D7AB4 CRC64;
Query Match 8.2%; Score 100; DB 1; Length 234;
Best Local Similarity 24.5%; Pred. No. 0.14;
Matches 48; Conservative 33; Mismatches 61; Indels 54; Gaps 12;
QY 25 NLKQI---YYNSKAITSE-----KSAQQLTNTLLFKGFFGHPWYNDLL-- 68
DB 45 NIKLLDWYSSGSDFTNSEVLDSLSGMRINKTNGSI-SLIIFPS-----PYSPAFK 98
QY 69 ---VDLGSTAAATSEGGSSVDLYGAYGYQCAGGTPNTACMYGGVTLHNNRLTEKKV 125
DB 99 GKRVLD-NTKRTKKSQHTS---EGTVIHFQISGVT-----NTEKLPTPIEL 140
QY 126 PNLMTDGGKQTVPIDKVKTSKEVTQQLDLQARHYLHGKFLY-NSPSFGG--KVQSG 182
DB 141 PLKVKVHGKDSPIKYGP-KFDKKQLAISTLDPEIRHQLTQIHGLYRSSDKTGGYKWT-- 197
QY 183 LIVFHSSEGSTVSVDL 198
DB 198 -----MNDGSTVQSDL 208
RESULT 15
R19E THEVO STANDARD; PRT; 150 AA.
AC Q97CU4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S19E.
GN RPS19E OR TV0007 OR TVG0008143.
OS Thermoplasma volcanium.
OC Archaea; Euryarchaeota; Thermoplasma;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=50339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GSS1 / DSM 4299 / JCM 9571;
RX MEDLINE=20570466; PubMed=11121031;
RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
RA Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
RA Nunoshima T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
RT "Archaeal adaptation to higher temperatures revealed by genomic
RT sequence of Thermoplasma volcanium.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
CC -!- SIMILARITY: Belongs to the S19E family of ribosomal proteins.
CC
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 CC -----

DR EMBL: AP000991; BAB59149.1; -
 DR InterPro: IPR001286; Ribosomal_S19F.
 DR Pfam: PF01090; Ribosomal_S19e; 1.
 DR ProDom: PD003854; Ribosomal_S19e; 1.
 DR PROSITE: PS00628; RIBOSOMAL_S19F; FALSE NEG.
 KW Ribosomal protein; Complete proteome.
 SQ SEQUENCE 150 AA; 17063 MW; FD5881CF694EB415 CRC64;

Query Match 7.8%; Score 95.5; DB 1; Length 150;
 Best Local Similarity 29.5%; Pred. No. 0.2;
 Matches 23; Conservative 17; Mismatches 37; Indels 1; Gaps 1;

QY 116 NNRLTEKKVPINLWDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFLYN-SDS 174
 DB 17 SGKLEKKIKERNVYKVTGSKKEPQLDDWIVYRAASMLRKLINGYLIGRMSSE 76

QY 175 FGKVGORGLIVFHSSEGS 192
 DB 77 YGKGVDRGSKRYHAASGS 94

RESULT 16
 ID P115_MYCHR STANDARD; PRT; 979 AA.
 AC P41508;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE P115 protein.
 OS Mycoplasma hyorhinis.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2100;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=91138990; PubMed=1825306;
 RA Notarnicola S.M., McIntosh M.A., Wise K.S.;
 RT "A Mycoplasma hyorhinis protein with sequence similarities to
 RT nucleotide-binding enzymes."
 RL Gene 97:77-85(1991).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- DOMAIN: Consists of two putative central coiled-coil regions
 CC flanked by putative globular regions at the N- and C-termini.
 CC -!- SIMILARITY: BELONGS TO THE SMC FAMILY. SIMILAR TO OTHER MYCOPLASMA
 CC P115.

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 CC -----

DR EMBL: M34956; AAA25423.1; -
 DR PIR: JQ0894; JQ0894.
 DR InterPro: IPR003439; ABC transporter.
 DR InterPro: IPR005289; GTP-binding_dom.
 DR InterPro: IPR003405; SMC C.
 DR InterPro: IPR003395; SMC N.
 DR Pfam: PF02483; SMC C; 1.
 DR Pfam: PF02463; SMC N; 1.
 DR TIGRfam: TIGR00650; MG442; 2.
 KW ATP-binding; Coiled coil.
 DT NP_BIND 32 39 ATP (POTENTIAL).
 FT DOMAIN 169 224 COILED COIL (POTENTIAL).
 FT DOMAIN 231 400 COILED COIL (POTENTIAL).
 FT

FT DOMAIN 569 821 COILED COIL (POTENTIAL).
 FT DOMAIN 884 912 ALA/ASP-RICH (DA-BOX).
 SQ SEQUENCE 979 AA; 110566 MW; 30D51C56B56280F4 CRC64;
 Query Match 7.8%; Score 93; DB 1; Length 979;
 Best Local Similarity 23.3%; Pred. No. 3.3;
 Matches 55; Conservative 41; Mismatches 92; Indels 48; Gaps 9;

QY 17 ELQGTALGNLQKQIVYNSKAITSSKSADQ-----FLTNLLFKGFFTGH 61
 DB 56 QLRGL---NMDDVIFAGSKVTKPKQKAMVKLTFNDAIEETKQITISRLLRGGGTNE 112
 QY 62 PWYNDLLV---DLGSTAATSEYEGSSVDLYGAYYGYQCAGGTNKTACMY---GGVTLLHD 115
 DB 113 YFYNDQPVRYKDIKNLAVESGISKSLAITSQGTISEIAEATPEQKAVIEAAGTSKYK 172
 QY 116 NNRLTEKKVPINLWDGKQTTVPIDKVTSKKEV--TVQELDLQ---ARHYLHGKFLY 170
 DB 173 LDKEEAQKKL-----RTNDAIDKIQAIKELERQVNSLDKQAKKIYLEKSKALE 224
 QY 171 NSDSFGSKVQORGLIV---FHSSEGSTVSVDLFDQAQQVPTLLRIYRNTTISST 222
 DB 225 S-----VEVGLIVNDLAFNEKLNNTLSLLEVBQQRNDLELNLTQTVSSISQT 273

RESULT 17
 ID DPOL_METJIA STANDARD; PRT; 1634 AA.
 AC Q58295;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE DNA polymerase (EC 2.7.7.7) [Contains: Mja pol-1 intein; Mja pol-2
 DE intein].
 DN POL OR Mj0885.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcaceae; Methanocaldococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RT jannaschii."
 RL Science 273:1058-1073(1996).
 CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
 CC + [DNA](N).
 CC -!- PFM: This protein undergoes a protein self splicing that involves
 CC a post-translational excision of the intervening region (intein)
 CC followed by peptide ligation (Potential).
 CC -!- SIMILARITY: Belongs to the DNA polymerase type-B family.
 CC -----
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 CC -----
 DR EMBL: U67532; AAB98889.1; -
 DR HSSP: P56689; ITGO.
 DR TIGR: MJ0885; -
 DR InterPro: IPR006172; DNA_pol_B.
 DR


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DR InterPro: IPR006134; DNA_pol_B_dom.
DR InterPro: IPR006133; DNA_pol_B_exo.
DR InterPro: IPR003587; Hedgehog_hint_N.
DR InterPro: IPR003586; Hedgehog_hintC.
DR InterPro: IPR006142; INTEIN.
DR InterPro: IPR004042; Intron_endonuc.
DR InterPro: IPR006141; Intron_S.
DR InterPro: IPR004578; Pol2.
DR Pfam: PF00136; DNA_pol_B_3.
DR PRINTS: PR00379; INTEIN.
DR SMART: SMO0305; HintC; 2.
DR SMART: SMO0306; HintN; 2.
DR SMART: SMO0486; POLBc; 1.
DR TIGRFAMs: TIGR01443; intron_Cterm; 2.
DR TIGRFAMs: TIGR01445; intron_Nterm; 2.
DR TIGRFAMs: TIGR00592; pol2; 1.
DR PROSITE: PS00116; DNA_POLYMERASE_B; 1.
DR PROSITE: PS50818; INTEIN_C_TER; 2.
DR PROSITE: PS50819; INTEIN_ENDONUCLEASE; 2.
DR PROSITE: PS50817; INTEIN_N_TER; 2.
KW Transferase; DNA-directed DNA polymerase; DNA replication;
KW DNA-binding; Autocatalytic cleavage; Protein splicing;
KW Complete proteome.
FT CHAIN 1 425 POL, 1ST PART (POTENTIAL).
FT CHAIN 426 794 MJA_POL-1 INTEIN (POTENTIAL).
FT CHAIN 795 882 POL, 2ND PART (POTENTIAL).
FT CHAIN 883 1358 MJA_POL-2 INTEIN (POTENTIAL).
FT CHAIN 1359 1634 POL, 3RD PART (POTENTIAL).
SQ SEQUENCE 1634 AA; 191708 MW; 841FAFAB1F97DDD CRC64;

Query Match 7.5%; Score 91; DB 1; Length 1634;
Best Local Similarity 21.6%; Pred. No. 9.4;
Matches 50; Conservative 36; Mismatches 79; Indels 66; Gaps 10;

QY 12 LRKSELOGTALGNLKIYYNNSKATTSSEKSAQFLTNLLFKGFTGHPWYNDLVL 71
DB 614 VRKKGTGKAITLGCAGKDIYLIKIEIL---KNKEKYLPAAIL-RGFEGDGYVNTVR 669
QY 72 GSTAATSEYE-----GSSVDLYGAYGYQCAGGTPNKTACMYGVTLDHNNRLTEKKVP 126
DB 670 VNQGTNNYDKIKTASLLDLGKYSF-----YTVSYBERGKKLRVY 713
QY 127 INLMDGKQTTPIDKVKTS-----KKEVTVOELDLQARHYLHGKFLGYNLSD----- 173
DB 714 IEIFSKG-----DLIKFSLISFISRRKNNLLNEIRQTKLYKIGDYGFDLDDVCVS 766
QY 174 --SFGKV-----ORGLVPHSSSEGS-TVSYDLFDAGQGYPTDL 209
DB 767 LESYKGEVYDLTLEGRPYFANGILTHNSLYPSIIISYNI-----SPDTL 811

RESULT 18
LEC_PARPC STANDARD; PRT; 447 AA.
AC P83304;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mannose/glucose-specific lectin.
OS Parkia platycephala
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids I; Fabales; Fabaceae; Mimosoideae; Parkieae; Parkia.
OX NCBI_TaxID=185447;
RN [1]
RP SEQUENCE, SUBUNIT, MASS SPECTROMETRY, AND VARIANTS VAL-70; ARG-227 AND
RP ASN-295;
RC TISSUE=Seed;
RX MEDLINE=21393945; PubMed=11502201;
RA Mann K., Farias C.M.S.A., Del Sol F.G., Santos C.F., Grangeiro T.B.,
RA Nagano C.S., Cavada B.S., Calvete J.J.;
RT "The amino-acid sequence of the glucose/mannose-specific lectin
```

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RT isolated from Parkia platycephala seeds reveals three tandemly
RT arranged jacalin-related domains.";
RL Eur. J. Biochem. 268:4414-4422(2001).
RN [2]
RP FUNCTION.
RA Ramos M.V., Cavada B.S., Bomfim L.R., Debray H., Mazard A.-M.,
RA Calvete J.J., Grangeiro T.B., Rouge P.;
RT "Interaction of the seed lectin from Parkia platycephala (Mimosoideae)
RT with carbohydrates and complex glycans.";
RL Protein Pept. Lett. 6:215-222(1999).
CC -!- FUNCTION: Mannose/glucose specific lectin. Shows agglutinating
CC activity against rabbit erythrocytes.
CC -!- SUBUNIT: Homodimer.
CC -!- MASS SPECTROMETRY: MW=47946; MW ERR=6; METHOD=Electrospray.
CC -!- MASS SPECTROMETRY: MW=47951; MW ERR=9; METHOD=VALDI.
CC -!- SIMILARITY: Belongs to the jacalin lectin family.
DR GO: GO:0005536; F:glucose binding; IDA.
DR GO: GO:0005537; F:mannose binding; IDA.
DR GO: GO:0000771; P:agglutination; IDA.
DR InterPro: IPR001229; Jacalin_lectin.
DR Pfam: PF01419; Jacalin; 3.
KW Lectin; Mannose-binding; Repeat.
FT MOD_RES 1 1 BLOCKED.
FT DOMAIN 1 447 3 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 1 149 1.
FT REPEAT 150 295 2.
FT REPEAT 296 447 3.
FT VARIANT 70 70 I -> V.
FT VARIANT 227 227 K -> R.
FT VARIANT 296 296 D -> N.
SQ SEQUENCE 447 AA; 47521 MW; 8F14ED460874BBB2 CRC64;

Query Match 7.4%; Score 90; DB 1; Length 447;
Best Local Similarity 23.1%; Pred. No. 2.3;
Matches 60; Conservative 31; Mismatches 93; Indels 76; Gaps 14;

QY 5 BEINEKDLKKSELOGTALGNLKI-----YYNNSKATTSSEKSAQFLTNL----- 52
DB 206 QDPNDIGVEKVEIDGN-LEHLKSIISGTYGNYKGEVVTSL-----SFTTNVTKHGFPI 259
QY 53 -----LFGKFTGHPWYNDLVLGSAATSEYEGS-SVDLYGAYGYQCAG 98
DB 260 ASOTSFISPIEGSLVTGFHGKSGYILD---SIGIVKPRDVEGSIIGVWG-----SG 310
QY 99 GTP-NKTA-----CMYGG-----VTLHNNRLTEKKVPINLMDGKQTTPID----- 141
DB 311 GDPWSYANEGINQIIYAGSNIKSVAFKDTSLDLSATFGVNPXKDTGKNTVSNWPSE 370
QY 142 -----KVKTSKEVTVOELDLQARHYLHGKFLGYNLSDSFGKGVORGLIV-PHSSE 190
DB 371 YLTISGTYGQYKFDVFTTSLTFTTNLATYGPFGKASATSFSPHNNMVVGFHGRA 430
QY 191 GSTVSYDLFDAGQGY--PDT 208
DB 431 G-----DYLDALGIFVKPDT 445

RESULT 19
R19E_THEAC
ID R19E_THEAC STANDARD; PRT; 150 AA.
AC Q9HM21;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 30S ribosomal protein S19E.
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmatia; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=2303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1728;
```

RX MEDLINE=20479972; PubMed=11029001;
RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
RT acidophilum.";
RL Nature 407:508-513(2000).
CC -!- SIMILARITY: Belongs to the S19E family of ribosomal proteins.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AL445063; CAC11198.1; -
DR InterPro: IPR001266; Ribosomal_S19E.
DR Pfam; PF01090; Ribosomal_S19e; 1.
DR ProDom; PD003854; Ribosomal_S19e; 1.
DR PROSITE; PS00628; RIBOSOMAL_S19E; FALSE_NEG.
KW Ribosomal protein; Complete proteome.
SQ SEQUENCE 150 AA; 17109 MW; F3215035CE0DC22C CRC64;

Query Match 7.3%; Score 88.5; DB 1; Length 150;
Best Local Similarity 26.9%; Pred. No. 0.81;
Matches 21; Conservative 20; Mismatches 36; Indels 1; Gaps 1;

QY 116 NNPLTEKKVPINLWDGQTVTPIDKVTSEKVTQVQLDQARHYLHKGGLYN-SDS 174
DB 17 SEKLSEKIAEPDWSKYVKTGISREKSPVNRDWIYVRAAAMLRKLYINGILGRMSSE 76

QY 175 FGKVGQGLIVFHSRSGS 192
DB 77 YGKVDGSKRYHAAQS 94

RESULT 20
ID TYPH MYCPI STANDARD; PRT; 419 AA.
AC P47717;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Thymidine phosphorylase (EC 2.4.2.4) (TdrPase).
GN DECO.
OS Mycoplasma pium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2122;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BER;
RX MEDLINE=93352438; PubMed=8349569;
RA Tham T.N., Ferris S., Kovacic R., Montagnier L., Blanchard A.;
RT "Identification of Mycoplasma pium genes involved in the salvage
RT pathways for nucleosides.";
RL J. Bacteriol. 175:5281-5285(1993).
CC -!- FUNCTION: THE ENZYMES WHICH CATALYZE THE REVERSIBLE PHOSPHORYLOSIS
CC OF PYRIMIDINE NUCLEOSIDES ARE INVOLVED IN THE DEGRADATION OF THESE
CC COMPOUNDS AND IN THEIR UTILIZATION AS CARBON AND ENERGY SOURCES,
CC OR IN THE RESCUE OF PYRIMIDINE BASES FOR NUCLEOTIDE SYNTHESIS.
CC -!- CATALYTIC ACTIVITY: Thymidine + phosphate = thymine + 2-deoxy-D-
CC ribose 1-phosphate.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: Belongs to the thymidine/pyrimidine-nucleoside
CC phosphorylase family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; L13289; AAA25432.1; -
DR PIR; C53112; C53312.
DR HSSP; P77836; 1BRW.
DR InterPro: IPR000312; Glyco trans 3.
DR Pfam; PF02885; Glycos transf 3N; 1.
DR Pfam; PF00591; Glycos transf 3; 1.
DR PIRSF; PIRSF000478; Thymid phosphis; 1.
DR ProDom; PD001864; Glyco trans 3; 1.
DR ProDom; PD005916; Thymid phosphis; 1.
DR PROSITE; PS00647; THYMID_PHOSPHORYLASE; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 419 AA; 47278 MW; C1620F2EF33929E3 CRC64;

Query Match 7.2%; Score 88; DB 1; Length 419;
Best Local Similarity 27.0%; Pred. No. 3.2;
Matches 38; Conservative 22; Mismatches 57; Indels 24; Gaps 7;

QY 47 FLTNLLFKG-FTGHPWYNDLLVGLGTAATSE-----YEGSSVDLYGYG 93
DB 57 FLTKAMIDSGKIYKHFPEYKKILIDKHSTGGIGKVSIALRPLVDFLGVAKLSRGLG 116

QY 94 YQACAGTPTNKATACMYGVTLLDNNRLTEERKV--PINLWDGK-QTTVPIDKVKTSKEY 150
DB 117 F--TGGTIDKLE---SINVNTDILKSKILNIAMNFVGTNDIVPADKLYALRDV 170

QY 151 --TVQELDLQARHYLHKGGL 169
DB 171 TGTVDLSPLIAASILSKKFFAL 191

RESULT 21
ID_HRP3_SCHPO STANDARD; PRT; 1388 AA.
AC I4139;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Chromodomain helicase hrp3.
GN HRP3 OR SPAC3G6.01.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Howarth T., Howarth S., Huckle E.J., Hunt S., Jagsis K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McJann J.,
RA Money P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkhardt G., Aert R., Robben J., Grymonprez B.,
RA Weigtens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehtz H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux C., Lelaure V., Mottier S.,
RA Galibert P., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,

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CC
CC EMBL; L13289; AAA25432.1; -
DR PIR; C53112; C53312.
DR HSSP; P77836; 1BRW.
DR InterPro: IPR000312; Glyco trans 3.
DR Pfam; PF02885; Glycos transf 3N; 1.
DR Pfam; PF00591; Glycos transf 3; 1.
DR PIRSF; PIRSF000478; Thymid phosphis; 1.
DR ProDom; PD001864; Glyco trans 3; 1.
DR ProDom; PD005916; Thymid phosphis; 1.
DR PROSITE; PS00647; THYMID_PHOSPHORYLASE; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 419 AA; 47278 MW; C1620F2EF33929E3 CRC64;

Query Match 7.2%; Score 88; DB 1; Length 419;
Best Local Similarity 27.0%; Pred. No. 3.2;
Matches 38; Conservative 22; Mismatches 57; Indels 24; Gaps 7;

QY 47 FLTNLLFKG-FTGHPWYNDLLVGLGTAATSE-----YEGSSVDLYGYG 93
DB 57 FLTKAMIDSGKIYKHFPEYKKILIDKHSTGGIGKVSIALRPLVDFLGVAKLSRGLG 116

QY 94 YQACAGTPTNKATACMYGVTLLDNNRLTEERKV--PINLWDGK-QTTVPIDKVKTSKEY 150
DB 117 F--TGGTIDKLE---SINVNTDILKSKILNIAMNFVGTNDIVPADKLYALRDV 170

QY 151 --TVQELDLQARHYLHKGGL 169
DB 171 TGTVDLSPLIAASILSKKFFAL 191

RESULT 21
ID_HRP3_SCHPO STANDARD; PRT; 1388 AA.
AC I4139;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Chromodomain helicase hrp3.
GN HRP3 OR SPAC3G6.01.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
OC Schizosaccharomycetales; Schizosaccharomycetaceae;
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A.,
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
RA Holroyd S., Howarth T., Howarth S., Huckle E.J., Hunt S., Jagsis K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McJann J.,
RA Money P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinowitsch E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volkhardt G., Aert R., Robben J., Grymonprez B.,
RA Weigtens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritze C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehtz H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux C., Lelaure V., Mottier S.,
RA Galibert P., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forburg S.L.,

RA Cezutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,
RA Shpakovskii G.V., Ussery D., Barrell B.G., Nurse P.;
RT "The genome sequence of Schizosaccharomyces pombe.";
RL Nature 415:871-880(2002).
RN [2].
RP GENE NAME, FUNCTION, AND SUBCELLULAR LOCATION.
RX MEDLINE=22122317; PubMed=12127990;
RA Yoo E.J., Jang Y.K., Lee M.A., Ejerling P., Kim J.B., Ekwall K.,
RA Seong R.H., Park S.D.;
RT "Hrp3, a chromodomain helicase/ATPase DNA binding protein, is required
RT for heterochromatin silencing in fission yeast.";
RL Biochem. Biophys. Res. Commun. 295:970-974(2002).
CC -!- FUNCTION: Involved in heterochromatin silencing. Required for
CC transcriptional repression at the silence loci of mat3, where it
CC has a direct role as a chromatin remodeling factor.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: Belongs to the SNF2/RAD54 helicase family.
CC -!- SIMILARITY: Contains 2 chromo domains.
CC -----
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CC -----
CC EMBL; Z99167; CAB16277.1; -.
CC PIR; T38720; T38720.
CC GeneDB SPombe; SPAC3G6.01; -.
DR InterPro; IPR000953; Chromo.
DR InterPro; IPR001410; DEAD.
DR InterPro; IPR001650; Helicase_C.
DR InterPro; IPR000330; SNF2_N.
DR Pfam; PF00385; chromo; 2.
DR Pfam; PF00271; helicase_C; 1.
DR Pfam; PF00176; SNF2_N; 1.
DR SMART; SM00298; CHROMO; 2.
DR SMART; SM00487; DEXDC; 1.
DR SMART; SM00490; HELICC; 1.
DR PROSITE; PS00598; CHROMO 1; 1.
DR PROSITE; PS00013; CHROMO 2; 2.
DR PROSITE; PS00690; DEAD ATP HELICASE; FALSE NEG.
KW Transcription regulation; Hydrolase; Helicase; Repressor;
KW Nuclear protein; ATP-binding; DNA-binding; Repeat.
FT DOMAIN 169 175 POLY-GLU.
FT DOMAIN 191 260 CHROMO 1.
FT DOMAIN 288 349 CHROMO 2.
FT NP_BIND 400 407 ATP (POTENTIAL).
FT SITE 508 511 DEAD BOX.
FT DOMAIN 947 950 POLY-GLU.
SQ SEQUENCE 1388 AA; 159377 MW; F7B431084BD29F8D CRC64;

Query Match 7.1%; Score 86; DB 1; Length 1388;
Best Local Similarity 25.1%; Pred. No. 21;
Matches 45; Conservative 27; Mismatches 69; Indels 38; Gaps 10;

QY 35 KAITSSERSAQFLNLT-----LFLKGF-----FTGHPWYNDLLVGLGTAATSEYE 81
DB 1047 KAVSAEKDLNDQNNKSSKALLITFKGVNNAETLVQRINDLDI-LYDAMPTSGYS 1105
QY 82 GSSVDLY-GAYYGOCAGGTPNKTCMYGGVTLH-----DNNRLTEKKVPINLWI 131
DB 1106 NFQIPMVRVSHVGSQWG-PREDSMLLSGICKGFGAWLEIRDDPELKMCKIFLE--- 1161
QY 132 DGKQT--TVPIDKYTSKKEVTQVQLDQARHYL-----HGKGLYNSD--SFGGKVQ 180
DB 1162 DTQDTSNVPKDKENKCKVPSAVHLVRGEGYLLSALREHFQNFGRKSPAINSTKIQ 1220

RESULT 22
PORD_PSEAE STANDARD; PRT; 443 AA.
ID FORD_PSEAE

AC P32722;
AD 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Porin D precursor (EC 3.4.21.-) (Outer membrane protein D2)
DE (Imipenem)/basic amino acid-specific outer membrane pore).
DE OFRD OR PA0598.
GN Pseudomonas aeruginosa.
OS Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]_TaxID=287;
RP SEQUENCE FROM N.A.
RX MEDLINE=93037310; PubMed=1339257;
RA Yoneyama H., Yoshihara E., Nakae T.;
RT "Nucleotide sequence of the protein D2 gene of Pseudomonas
RT aeruginosa.";
RL Antimicrob. Agents Chemother. 36:1791-1793(1992).
RN [2]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 24-40.
RC STRAIN=ATCC 15692 / PAO1 / H103;
RX MEDLINE=93051258; PubMed=1427017;
RA Huang H., Siehnell R.J., Bellido F., Rawling E., Hancock R.E.W.;
RT "Analysis of two gene regions involved in the expression of the
RT imipenem-specific, outer membrane porin protein OprD of Pseudomonas
RT aeruginosa.";
RL FEMS Microbiol. Lett. 76:267-273(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltry L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
RN [4]
RP SEQUENCE OF 24-48.
RX MEDLINE=94282208; PubMed=8012497;
RA Michea-Hamzehpour M., Sanchez J.-C., Epp S.F., Paquet N., Hughes G.J.,
RA Hochstrasser D.F., Pechere J.-C.;
RT "Two-dimensional polyacrylamide gel electrophoresis isolation and
RT microsequencing of Pseudomonas aeruginosa proteins.";
RL Enzyme Protein 47:11-8(1993).
RN [5]
RP CHARACTERIZATION.
RX MEDLINE=90368779; PubMed=2118530;
RA Trias J., Nikaido H.;
RT "Protein D2 channel of the Pseudomonas aeruginosa outer membrane has
RT a binding site for basic amino acids and peptides.";
RL J. Biol. Chem. 265:15680-15684(1990).
RN [6]
RP SERINE PROTEASE ACTIVITY.
RX MEDLINE=97000016; PubMed=8843159;
RA Yoshihara E., Gotoh N., Nishino T., Nakae T.;
RT "Protein D2 porin of the Pseudomonas aeruginosa outer membrane bears
RT the protease activity.";
RL FEBS Lett. 394:1179-1182(1996).
RN [7]
RP MUTAGENESIS OF HIS-179; ASP-231; SER-319 AND HIS-390, AND ACTIVE
RP SITES.
RX MEDLINE=98300298; PubMed=9636659;
RA Yoshihara E., Yoneyama H., Ono T., Nakae T.;
RT "Identification of the catalytic triad of the protein D2 protease in
RT Pseudomonas aeruginosa.";
RL Biochem. Biophys. Res. Commun. 247:142-145(1998).
CC -!- FUNCTION: Porin with a specificity for basic amino acids. Also
CC possesses serine protease activity.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane.

CC -|- SIMILARITY: Belongs to peptidase family S43.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; X63152; CAA44855.1; --
 CC EMBL; Z14065; CAA78448.1; --
 CC EMBL; AE004529; AAG04347.1; --
 CC PIR; S23771; S23771.
 CC MEROPS; S43.001; --
 CC GO; GO:0045203; C: integral to external outer membrane (sensu . . . ; IDA.
 CC GO; GO:0015288; F: porin activity; IDA.
 CC GO; GO:0008236; F: serine-type peptidase activity; IDA.
 CC GO; GO:0015802; P: basic amino acid transport; IDA.
 CC InterPro; IPR005318; Peptidase_S43.
 CC Pfam; PF03573; OprD; 1.
 CC Hydrolase; Serine protease; Transport; Outer membrane; Transmembrane;
 KW Porin; Signal; Complete proteome.
 FT SIGNAL 1 23
 FT CHAIN 24 443 PORIN D.
 FT ACT_SITE 179 179
 FT ACT_SITE 231 231
 FT ACT_SITE 319 319
 FT MUTAGEN 179 179
 FT MUTAGEN 231 231
 FT MUTAGEN 319 319
 FT MUTAGEN 390 390
 FT MUTAGEN 443 AA; 48360 MW; E083FFE07ADCBE64 CRC64;
 FT CONFLICT 44 44 L -> Y (IN REF. 2).
 FT SEQUENCE 443 AA; 48360 MW; E083FFE07ADCBE64 CRC64;
 SQ
 Query Match 6.9%; Score 84.5; DB 1; Length 443;
 Best Local Similarity 23.2%; Pred. No. 6.9;
 Matches 60; Conservative 30; Mismatches 98; Indels 71; Gaps 14;
 QY 15 KSLQGTALGNLQKQIYYVNSKAITSEKSDAQFLTNLLFKGFFTGHPWYNDLLVGLGST 74
 Db 34 KGFIEDSSLDLLRNYYFRDCKSGGDRVD-----WTQGLFTY-----ESGFT 78
 QY 75 AATSEYEGSSVDLYGAYGYQCAGGTFNKTA-----CMYGGVTLHDNNRLTBEKKVPIN- 128
 Db 79 QGT---VGFQVDAFG-YLGLK-LDGTSDKTGTLNPLVNDGKPRDDYSRAGGAVKVRISK 133
 QY 129 ---LWIDGKQTTPIDKVTSK-----KEVTVOELDLQARHYLHGK----- 166
 Db 134 TMLKWE-NQPTAPVFAAGSRLFPQTATGFLQSSPEGLDEAGHTEGKEPTTVKSR 192
 QY 167 ---FGLY-----NSDSFGKQVQRLIVFHSSEGSTVSVDLFDACQGPDTLLRIYRNT 217
 Db 193 GELYAYIYAGETAKSADFIQGR---YAITDNLASLYGALEDIYQY-----YLSNSY 242
 QY 218 TI---SSTSLISLYLYTT 233
 Db 243 TIPLASDQSLGDFDNIYRT 261
 RESULT 23
 ITAS_XENLA STANDARD; PRT; 1050 AA.
 AC Q06274;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Integrin alpha-5 precursor (Fibronectin receptor alpha subunit)
 DE (Integrin alpha-F) (VLA-5).
 OS Xenopus laevis (African clawed frog).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 CC Xenopodinae; Xenopus.
 CC NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95344994; PubMed=7619730;
 RA Jocs T.O., Whittaker C.A., Meng F., Desimone D.W., Grau V.,
 RA Hausen P.;
 RT "Integrin alpha 5 during early development of Xenopus laevis.";
 RL Mech. Dev. 50:187-199(1995).
 RN [2]
 RP SEQUENCE OF 318-393 FROM N.A.
 RX MEDLINE=94008528; PubMed=8404528;
 RA Whittaker C.A., Desimone D.W.;
 RT "Integrin alpha subunit mRNAs are differentially expressed in early
 RT Xenopus embryos.";
 RL Development 117:1239-1249(1993).
 CC -|- FUNCTION: INTEGRIN ALPHA-5/BETA-1 IS A RECEPTOR FOR FIBRONECTIN.
 CC IT RECOGNIZES THE SEQUENCE R-G-D IN ITS LIGANDS.
 CC -|- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. THE ALPHA
 CC SUBUNIT IS COMPOSED OF AN HEAVY AND A LIGHT CHAIN LINKED BY A
 CC DISULFIDE BOND. ALPHA-5 ASSOCIATES WITH BETA-1.
 CC -|- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -|- SIMILARITY: Belongs to the integrin alpha chain family.
 CC -|- SIMILARITY: Contains 7 FG-GAP repeats.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; U12683; AAA99668.1; --
 CC EMBL; L10191; AAA18249.1; --
 CC PIR; I51527; I51527.
 CC HSP; P06756; JUV2.
 CC InterPro; IPR000413; Integrin_alpha.
 CC Pfam; PF01839; FG-GAP; 4.
 CC Pfam; PF00357; Integrin_A; 1.
 CC SMART; SM00191; Integrin_alpha; 5.
 CC PROSITE; PS00242; INTEGRIN_ALPHA; 1.
 KW Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
 KW Signal; Repeat.
 FT SIGNAL 1 32 POTENTIAL.
 FT CHAIN 33 1050 INTEGRIN ALPHA-5.
 FT CHAIN 33 932 INTEGRIN ALPHA-5 HEAVY CHAIN (POTENTIAL).
 FT CHAIN 933 1050 INTEGRIN ALPHA-5 LIGHT CHAIN (POTENTIAL).
 FT DOMAIN 33 996 EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 997 1022 POTENTIAL.
 FT REPEAT 48 110 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 120 188 FG-GAP 1.
 FT REPEAT 189 246 FG-GAP 2.
 FT REPEAT 259 312 FG-GAP 3.
 FT REPEAT 313 373 FG-GAP 4.
 FT REPEAT 379 438 FG-GAP 5.
 FT REPEAT 442 494 FG-GAP 6.
 FT CA_BIND 324 332 POTENTIAL.
 FT CA_BIND 390 398 POTENTIAL.
 FT CA_BIND 454 462 POTENTIAL.
 FT SITE 1025 1029 GPFKR MOTIF.
 FT DISULFID 145 166 BY SIMILARITY.
 FT DISULFID 182 195 BY SIMILARITY.
 FT DISULFID 502 513 BY SIMILARITY.
 FT DISULFID 519 575 BY SIMILARITY.
 FT DISULFID 636 642 BY SIMILARITY.
 FT DISULFID 708 721 BY SIMILARITY.
 FT DISULFID 862 910 INTERCHAIN (BY SIMILARITY).
 FT DISULFID 917 922 BY SIMILARITY.

FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 95 95 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 172 172 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 287 287 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 297 297 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 306 306 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 507 507 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 515 515 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 521 521 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 600 600 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 649 649 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 714 714 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 763 763 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 861 861 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1050 AA; 115961 MW; 10ED961535B8D918 CRC64;

Query Match 6.9%; Score 84; DB 1; Length 1050;
 Best Local Similarity 21.9%; Pred. No. 22;
 Matches 60; Conservative 38; Mismatches 94; Indels 82; Gaps 14;

QY 12 LRKSEIQ-GTALGNLKOIYYNKAITS-SEKADQFLNTLLFKGFTGHFWNDLIV 69
 DB 242 LEYKQQTQAOASYSDDSYFGYVAVGFSEDATEDFV-----GVPKGNITYGYVTI 295

QY 70 DLGSTAATSEYEGSSVDLYGAYVQACAGTPNKTA---CMYGGVTLHD---NNRLTEEK 123
 DB 296 -LNGTDLRLSNFNGEQM-ASYFGYSVATDLNSDGLDLLIGAPLPMDRTHGRVQEVG 353

QY 124 KVPINLMDIGKQTTVPIDKVKTSKEVTYVQELDLQARHYLHGKFG-----LYNSDS---- 174
 DB 354 RVVYVVLQGDHMESTPHL--ILTMGEE-----YGRFGSSIASLGLDLDQDGFN 397

QY 175 -----FGKGVQGLI-VFHSSSGSTVSYDLFDAQG-----SSTLSIS 227
 DB 398 DIATGAPGGAQAGVAFIFNGPGGVDSKPSQVLOGQWSSQPSFFGLSTRGCHLDG 457

QY 205 --YPTDLRIYRDNNTTI-----SSTLSIS 227
 DB 458 NGYPDLIYVAGVDTLTVYRGRPIIHASASLSIS 491

RESULT 24

PRTA ASPNG STANDARD; PRT; 282 AA.
 ID DNAK STRMU STANDARD; PRT; 612 AA.
 AC P24665;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Aspergillopepsin II precursor (EC 3.4.23.19) (Acid protease A)
 DE (Protease A)
 OS Aspergillus niger.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=5061;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Var. Macrosporus;
 RA MEDLINE=92011747; PubMed=1918060;
 RX Inoue H., Kimura T., Makabe O., Takahashi K.;
 RT "The gene and deduced protein sequences of the zymogen of Aspergillus
 RT niger acid proteinase A.";
 RL J. Biol. Chem. 266:19484-19489 (1991).
 RN [2]
 RP SEQUENCE OF 60-98 AND 110-282.
 RC STRAIN=Var. Macrosporus;
 RA MEDLINE=92011746; PubMed=1918059;
 RX Takahashi K., Inoue H., Sakai K., Kohama T., Kitahara S.,
 RA Takishima K., Tanji M., Athauda S.B.P., Takahashi T., Akanuma H.,
 RA Mamiya G., Yamasaki M.;
 RT "The primary structure of Aspergillus niger acid proteinase A.";
 RL J. Biol. Chem. 266:19480-19483 (1991).
 RN [1]
 RP SEQUENCE FROM N.A.

CC 3-Asn-Gln-4, 13-Gly-Ala-14, and 26-Tyr-Thr-27.
 CC -!- SUBUNIT: Heterodimer of two noncovalently bound light and heavy
 CC chains.
 CC -!- SIMILARITY: Belongs to peptidase family A4.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; V68871; AAA32687.1; -.
 CC PIR; A41025; A41025.
 CC MEROPS; A04.002; -.
 CC InterPro; IPR000250; Peptidase_A4.
 CC Pfam; PF01828; Peptidase_A4; 1.
 CC PRINTS; PR00977; SCYLDPTASE.
 CC ProDom; PD018627; AspartaseA4; 1.
 CC Hydrolase; Aspartyl protease; Zymogen; Signal;
 CC Pyroliadone carboxylic acid. POTENTIAL.
 FT SIGNAL 1 18
 FT PROPEP 19 59 ASPERGILLOPEPSIN II LIGHT CHAIN.
 FT CHAIN 60 98
 FT PROPEP 99 109 ASPERGILLOPEPSIN II HEAVY CHAIN.
 FT CHAIN 110 282
 FT MOD.RES 110 110 PYRROLIDONE CARBOXYLIC ACID.
 FT DISULFID 115 139
 FT DISULFID 127 210
 SQ SEQUENCE 282 AA; 29887 MW; 4EA727F9AE33F72A CRC64;

Query Match 6.9%; Score 83.5; DB 1; Length 282;
 Best Local Similarity 19.2%; Pred. No. 4.8;
 Matches 52; Conservative 34; Mismatches 102; Indels 83; Gaps 10;

QY 13 RKSEIQGTALGNLKOIYYNKAITSSEKADQFLNTLLFKGFTGHFWNDLIVDLG 72
 DB 28 RKEARAAGKRHSNPPYIPGSDKEILKNGTNEEYSSN-----WAGAVLIGD 75

QY 73 STAATSEYEGSSVDL-----YGAVYGY-----QCAG-----GTPNKTCMCGG 110
 DB 76 YTKVTGFTVPSVSAGSSSGSGYGGYGNKRNROSEYCASAWGIDGDTCTAILQTG 135

QY 111 VTLHDNNRLTEKKVPEINLW-----DGKQTTVPIDKVKTSKEVTVOE 154
 DB 136 VDF-----CVEDQTSYDAWYEPDYAYDFSDITISEGDSIKVTVEATSKSGSATVEN 190

QY 155 LDL--CARHYLHGKF-----GLYNSDSFGGKVGKGLIVHSSB-----GSTV 194
 DB 191 LTGQSVTHTFSGNVEGDLCEETNAEWIVDFSGDLSLAFADFSGVTFTNAEATSGGIV 250

QY 195 SYDLFDAQGQYPTDLRIYRDNNTTISSTLS 225
 DB 251 -----GPSDATVMDIEQDGSVLTETSVS 273

RESULT 25

DNAK STRMU STANDARD; PRT; 612 AA.
 ID DNAK STRMU STANDARD; PRT; 612 AA.
 AC O06942;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa
 DE protein) (HSP70).
 GN DNAK OR SMU.82.
 OS Streptococcus mutans.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1309;
 RN [1]
 RP SEQUENCE FROM N.A.


```

RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA Mc Kenney K., Shirley G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Sutton R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.P., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RA "whole-genome random sequencing and assembly of Haemophilus influenzae
RA Rd.";
RA Science 269:496-512(1995).
RA -!- SIMILARITY: TO THE C-TERMINAL OF PARA-AMINOBENZOATE SYNTHASE
RA COMPONENT I.
RA -----
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RA -----
RA EMBL; U32797; AAC22834.1; -
RA PIR; F64187; F64187.
RA TIGR; H11170; -.
RA InterPro; IPR005801; Anth synth chor.
RA Pfam; PF00425; chorismate_bind_1.
RA PRINTS; PR00095; ANTSYNTHASE1.
RA ProDom; PD000779; Anth synth chor; 1.
RA Hypothetical protein; Anth Complete proteome.
RA SQ SEQUENCE 328 AA; 37734 MW; 1C02BCD0088957B0 CRC64;
RA -----
RA Query Match 6.8%; Score 82.5; DB 1; Length 328;
RA Best Local Similarity 27.3%; Pred. No. 7; 1;
RA Matches 24; Conservative 16; Mismatches 35; Indels 13; Gaps 3;
QY 136 TTPIDKVKTSKEVT---VQELDQARHYLHGKFLGYNLSDFGGKVQRGLI-----V 185
DB 237 TLLPAGSISGAPKEKTKTQIOAQEKQKRGYYTGIFGIDFKTKLQSAVAIRFISQVDEKFY 296
QY 186 FHSSEGSTVSVDLPDAQOGYPTLLRIY 213
DB 297 FHSGGGIIH---SNAQDYEELLEKVV 321
RESULT 29
YVAD BACSU STANDARD; PRT; 455 AA.
ID YVAD BACSU STANDARD; PRT; 455 AA.
AC P25152;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical peptidase yvad precursor (EC 3.4.11.-).
GN YVAD OR IPA-8R OR BSU38470.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RS SEQUENCE FROM N.A.
RC STRAIN=168;
RC MEDLINE=95020537; PubMed=7934828;
RA Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzales W.,
RA Hullo M.F., Ionescu M., Dubochinsky B., Marcelino L., Mosser I.,
RA Prescan E., Santana M., Schneider E., Schweizer J., Vertes A.,
RA Rapoport G., Panchin A.;
RA "Bacillus subtilis genome project: cloning and sequencing of the 97
RA kb region from 325 degrees to 333 degrees.";
RA Mol. Microbiol. 10:371-384 (1993).
RN [2]
RS SEQUENCE FROM N.A.
RC STRAIN=168;
RC MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Mosser I., Albertini A.M., Alloni G.,

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CC and skin. Expressed in many tissues in embryonic day 11.
CC -!- DOMAIN: The alpha-helical domains I and II are thought to interact
CC with other laminin chains to form a coiled coil structure.
CC -!- DOMAIN: Domains VI, IV and G are globular.
CC -!- SIMILARITY: Contains 1 laminin N-terminal domains.
CC -!- SIMILARITY: Contains 22 laminin EGF-like domains.
CC -!- SIMILARITY: Contains 2 laminin IV domains.
CC -!- SIMILARITY: Contains 5 laminin G-like domains.
CC -----
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CC -----
CC EMBL; AJ293593; CAB99255.1; -
CC EMBL; U37501; AAC53430.1; -
CC PIR; T10053; T10053.
CC HSSP; P02468; 1TLE.
CC MGD; MGI:105382; Lama5.
CC GO; GO:0005604; C:basement membrane; IDA.
CC GO; GO:0005178; F:integrin binding; IDA.
CC GO; GO:0030324; P:lung development; IMP.
CC InterPro; IPR008985; ConA like lec_gl.
CC InterPro; IPR006209; EGF like.
CC InterPro; IPR008212; Lam_N2.
CC InterPro; IPR000034; Laminin_B.
CC InterPro; IPR002049; Laminin_EGF.
CC InterPro; IPR001791; Laminin_G.
CC InterPro; IPR008211; LamNT.
CC Pfam; PF00052; laminin_B; 1.
CC Pfam; PF00053; laminin_EGF; 17.
CC Pfam; PF00054; laminin_G; 2.
CC Pfam; PF00055; laminin_Nterm; 1.
CC PRINTS; PR00011; EGF_LAMININ.
CC ProDom; PD002082; Lam_N2; 1.
CC ProDom; PD003031; Laminin_B; 1.
CC SMART; SM00180; EGF_Lam; 20.
CC SMART; SM00281; Lam5; 1.
CC SMART; SM00282; LamG; 5.
CC SMART; SM00136; LamNT; 1.
CC PROSITE; PS00022; EGF_1; 19.
CC PROSITE; PS01186; EGF_2; 3.
CC PROSITE; PS01248; LAMININ TYPE EGF; 19.
CC PROSITE; PS50025; Lam_G DOMAIN; 5.
CC Glycoprotein; Basement membrane; Extracellular matrix; Coiled coil;
KW Laminin EGF-like domain; Cell adhesion; Repeat; Signal.
FT SIGNAL 1 40
FT CHAIN 41 3718 LAMININ ALPHA-5 CHAIN.
FT DOMAIN 41 304 LAMININ N-TERMINAL (DOMAIN VI).
FT DOMAIN 305 363 LAMININ EGF-LIKE 1.
FT DOMAIN 364 433 LAMININ EGF-LIKE 2.
FT DOMAIN 434 479 LAMININ EGF-LIKE 3.
FT DOMAIN 500 546 LAMININ EGF-LIKE 4.
FT DOMAIN 547 592 LAMININ EGF-LIKE 5.
FT DOMAIN 593 637 LAMININ EGF-LIKE 6.
FT DOMAIN 638 682 LAMININ EGF-LIKE 7.
FT DOMAIN 683 728 LAMININ EGF-LIKE 8.
FT DOMAIN 729 781 LAMININ EGF-LIKE 9.
FT DOMAIN 782 833 LAMININ EGF-LIKE 10.
FT DOMAIN 834 855 LAMININ EGF-LIKE 11 (INCOMPLETE).
FT DOMAIN 856 1442 LAMININ DOMAIN IV 1 (DOMAIN IV B).
FT DOMAIN 1443 1488 LAMININ EGF-LIKE 12.
FT DOMAIN 1489 1532 LAMININ EGF-LIKE 13.
FT DOMAIN 1533 1581 LAMININ EGF-LIKE 14.
FT DOMAIN 1582 1632 LAMININ EGF-LIKE 15.
FT DOMAIN 1633 1642 LAMININ EGF-LIKE 16 (N-TERMINAL).
FT DOMAIN 1643 1831 LAMININ DOMAIN IV 2 (DOMAIN IV A).
FT DOMAIN 1832 1864 LAMININ EGF-LIKE 16 (C-TERMINAL).
FT DOMAIN 1865 1914 LAMININ EGF-LIKE 17.
FT DOMAIN 1915 1970 LAMININ EGF-LIKE 18.

FT DOMAIN 1971 2024 LAMININ EGF-LIKE 19.
FT DOMAIN 2025 2071 LAMININ EGF-LIKE 20.
FT DOMAIN 2072 2188 LAMININ EGF-LIKE 21.
FT DOMAIN 2119 2168 LAMININ EGF-LIKE 22.
FT DOMAIN 2169 2735 DOMAIN II AND I.
FT DOMAIN 2736 2933 LAMININ G-LIKE 1.
FT DOMAIN 2947 3119 LAMININ G-LIKE 2.
FT DOMAIN 3128 3296 LAMININ G-LIKE 3.
FT DOMAIN 3337 3511 LAMININ G-LIKE 4.
FT DOMAIN 3518 3659 LAMININ G-LIKE 5.
FT DOMAIN 2205 2257 COILED COIL (POTENTIAL).
FT DOMAIN 2330 2464 COILED COIL (POTENTIAL).
FT DOMAIN 2604 2621 COILED COIL (POTENTIAL).
FT DOMAIN 2639 2705 COILED COIL (POTENTIAL).
FT SITE 1723 1725 CELL ATTACHMENT SITE (POTENTIAL).
FT SITE 1839 1841 CELL ATTACHMENT SITE (POTENTIAL).
FT DISULFID 305 314 BY SIMILARITY.
FT DISULFID 307 327 BY SIMILARITY.
FT DISULFID 329 338 BY SIMILARITY.
FT DISULFID 341 361 BY SIMILARITY.
FT DISULFID 364 373 BY SIMILARITY.
FT DISULFID 366 398 BY SIMILARITY.
FT DISULFID 401 410 BY SIMILARITY.
FT DISULFID 413 431 BY SIMILARITY.
FT DISULFID 434 445 BY SIMILARITY.
FT DISULFID 436 452 BY SIMILARITY.
FT DISULFID 454 463 BY SIMILARITY.
FT DISULFID 466 476 BY SIMILARITY.
FT DISULFID 500 512 BY SIMILARITY.
FT DISULFID 502 521 BY SIMILARITY.
FT DISULFID 523 532 BY SIMILARITY.
FT DISULFID 535 544 BY SIMILARITY.
FT DISULFID 547 559 BY SIMILARITY.
FT DISULFID 549 566 BY SIMILARITY.
FT DISULFID 568 577 BY SIMILARITY.
FT DISULFID 580 590 BY SIMILARITY.
FT DISULFID 593 605 BY SIMILARITY.
FT DISULFID 595 611 BY SIMILARITY.
FT DISULFID 613 622 BY SIMILARITY.
FT DISULFID 625 635 BY SIMILARITY.
FT DISULFID 638 650 BY SIMILARITY.
FT DISULFID 640 656 BY SIMILARITY.
FT DISULFID 658 667 BY SIMILARITY.
FT DISULFID 670 680 BY SIMILARITY.
FT DISULFID 683 695 BY SIMILARITY.
FT DISULFID 685 702 BY SIMILARITY.
FT DISULFID 704 713 BY SIMILARITY.
FT DISULFID 716 726 BY SIMILARITY.
FT DISULFID 1443 1455 BY SIMILARITY.
FT DISULFID 1445 1482 BY SIMILARITY.
FT DISULFID 1464 1473 BY SIMILARITY.
FT DISULFID 1476 1486 BY SIMILARITY.
FT DISULFID 1533 1548 BY SIMILARITY.
FT DISULFID 1535 1555 BY SIMILARITY.
FT DISULFID 1557 1566 BY SIMILARITY.
FT DISULFID 1569 1579 BY SIMILARITY.
FT DISULFID 1582 1594 BY SIMILARITY.
FT DISULFID 1584 1601 BY SIMILARITY.
FT DISULFID 1603 1612 BY SIMILARITY.
FT DISULFID 1615 1630 BY SIMILARITY.
FT DISULFID 1865 1874 BY SIMILARITY.
FT DISULFID 1867 1881 BY SIMILARITY.
FT DISULFID 1884 1893 BY SIMILARITY.
FT DISULFID 1896 1912 BY SIMILARITY.
FT DISULFID 1915 1930 BY SIMILARITY.
FT DISULFID 1917 1939 BY SIMILARITY.
FT DISULFID 1941 1950 BY SIMILARITY.
FT DISULFID 1953 1968 BY SIMILARITY.
FT DISULFID 1971 1986 BY SIMILARITY.
FT DISULFID 1973 1993 BY SIMILARITY.
FT DISULFID 1996 2005 BY SIMILARITY.
FT DISULFID 2008 2022 BY SIMILARITY.
FT DISULFID 2072 2083 BY SIMILARITY.

FT DISULFID 2074 2090 BY SIMILARITY.
 FT DISULFID 2092 2101 BY SIMILARITY.
 FT DISULFID 2104 2116 BY SIMILARITY.
 FT DISULFID 2119 2126 BY SIMILARITY.
 FT DISULFID 2121 2133 BY SIMILARITY.
 FT DISULFID 2135 2144 BY SIMILARITY.
 FT DISULFID 2147 2166 BY SIMILARITY.
 FT DISULFID 2169 2169 INTERCHAIN (PROBABLE).
 Query Match 6.7%; Score 82; DB 1; Length 3718;
 Best Local Similarity 28.5%; Pred. No. 1.6e+02;
 Matches 55; Conservative 22; Mismatches 76; Indels 40; Gaps 12;
 QY 58 FTGHPYNDLL-----VDLGSTATSEYSGSDVLYGAYGVCAGTGNKT-ACMY 108
 DB 48 FSLHPYFNLAEAGRTASATCGEEAPTRSVRPTEDLYCKLVGGFVAGGDPNQTIQGY 107
 QY 109 GGVTLHDNNRLTEKKVPINLWIDGKQ---TTVPIDK-VKTSKKEVTQELDL-QARE-- 161
 DB 108 CDICTAANS-----NKHPVSNALDGTETWQSPPLSRGLEYNVNT---LDLGQVHVA 160
 QY 162 YLHGKFG-----LYNSDSFGKQKGLVIFHSSEGSTSVSYDLFDAQGYPTLLRI 212
 DB 161 YVLKFPANSPRDLWLERSTDFGHTYQWQF-FASSK-----RDCLERFG--PRTLRI 212
 QY 213 YRDNTTISSTLS 225
 DB 213 TQDDVICTEYS 225

RESULT 34
 DNAK_STRP3
 ID_DNAK_STRP3 STANDARD; PRT; 607 AA.
 AC QSK624;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Chapterone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70).
 DE DNAK OR SPVX3 1531 OR SPS0335.
 OS Streptococcus pyogenes (serotype M3).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=198466;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=MGAS315 / Serotype M3;
 RX MEDLINE=22133808; PubMed=12122206;
 RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
 RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
 RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
 RA Schlievert P.M., Musser J.M.;
 RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
 RT phage-encoded toxins, the high-virulence phenotype, and clone
 RT emergence.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=SSI-1 / Serotype M3;
 RX MEDLINE=22683278; PubMed=12799345;
 RA Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
 RA Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
 RA Hayaishi H., Hattori M., Hamada S.;
 RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
 RT large-scale genomic rearrangement in invasive strains and new insights
 RT into phage evolution.";
 RL Genome Res. 13:1042-1055(2003).
 CC -!- FUNCTION: Acts as a chaperone (By similarity).
 CC -!- INDUCTION: By stress conditions e.g. heat shock (By similarity).
 CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AE014165; AAM60138.1; -;
 DR HAVAP; MF 00332; -; 1.
 DR InterPro; IPR001023; Hsp70.
 DR Pfam; PF00012; HSP70; 1.
 DR PRINTS; PR00301; HEATSHOCK70.
 DR ProDom; PD000089; Hsp70; 1.
 DR PROSITE; PS00297; HSP70_1; 1.
 DR PROSITE; PS00329; HSP70_2; 1.
 DR PROSITE; PS01036; HSP70_3; 1.
 KW Chapterone; ATP-binding; Heat shock; Phosphorylation;
 KW Complete proteome.
 FT INIT MET 0 BY SIMILARITY.
 FT MOD_RES 172 172 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
 SQ SEQUENCE 607 AA; 64804 MW; D73BD48DD837C4CE CRC64;

Query Match 6.7%; Score 81; DB 1; Length 607;
 Best Local Similarity 27.0%; Pred. No. 21;
 Matches 37; Conservative 19; Mismatches 63; Indels 18; Gaps 5;
 QY 69 VDLGST-AATSEYSGSDVLYGAYGVCAGTGNKTACVGGVTLHDNNRLTEKKVPI 127
 DB 6 IDLGTTNSAVAVLEGTESKIANPEGNRT---TPSVVSPKNGEIIVGDAKRAQAVTNPT 62
 QY 128 NLWIDGKQTTVPIDKVKTSKKEVTQELDLQARHLYHGKFLGYNPSFGKVGQGLIVFH 187
 DB 63 VISIKSKWGT--SEKVSANGKEVTQELISAMIIQLKLG----YAEDYLGEKVEKAVI--- 113
 QY 188 SSEGSTVSVDLFDAGQ 204
 DB 114 -----TVPAYFNDAQRQ 125

RESULT 35
 DNAK_STRP3
 ID_DNAK_STRP3 STANDARD; PRT; 609 AA.
 AC P95693;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Chapterone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70).
 DE DNAK OR GBS0096 OR SAG0097.
 OS Streptococcus agalactiae (serotype III),
 OS Streptococcus agalactiae (serotype V), and
 OS Streptococcus agalactiae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=216495, 216466, 1311;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=NEM316 / Serotype III;
 RX MEDLINE=2242508; PubMed=12354221;
 RA Glaser P., Rusniok C., Buchrieser C., Chevalier F., Frangeul L.,
 RA Mesdek T., Zouine M., Couve E., Lalioui L., Poyart C., Trieu-Cuot P.,
 RA Kunst F.;
 RT "Genome sequence of Streptococcus agalactiae, a pathogen causing
 RT invasive neonatal disease.";
 RL Mol. Microbiol. 45:1499-1513(2002).
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=2603 V/R / Serotype V;
 RX MEDLINE=2222988; PubMed=1200547;
 RA Tettelin H., Masiagnani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
 RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
 RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
 RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,

RA Radune D., Fedorova N.B., Scanlan D., Khouiri H., Mulligan S.,
RA Carty H.A., Cline R.A., Van Aken S.B., Gill J., Scarselli M., Mora M.,
RA Jacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Malone D.,
RA Rinaldo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
RA Fraser C.M.,
RT "Complete genome sequence and comparative genomic analysis of an
RT emerging human pathogen, serotype V Streptococcus agalactiae";
RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
RN [3]
RP SEQUENCE FROM N.A.
RA Rioux C.R., Martin D., Hamel J., Brodeur B.R.;
RT "Heat shock protein HSP70 and amino terminus of DnaJ of Streptococcus
RT agalactiae";
RP Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Acts as a chaperone (By similarity).
CC -!- INDUCTION: By stress conditions e.g. heat shock (By similarity).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
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CC
CC EMBL; AL766943; CAD45741.1; -.
DR EMBL; AE014196; AAM95005.1; -.
DR EMBL; U72719; AAB39219.1; -.
DR HSSP; P04475; 1DC4.
DR SagalList; gbs00096; -.
DR TIGR; SAG0097; -.
DR HAVAP; MF_00332; -; 1.
DR InterPro; IPR001023; Hsp70.
DR Pfam; PF00012; HSP70; 1.
DR PRINTS; PR00301; HEATSHOCK70.
DR ProDom; PD000089; Hsp70; 1.
DR PROSITE; PS00297; HSP70_1; 1.
DR PROSITE; PS00329; HSP70_2; 1.
DR PROSITE; PS01036; HSP70_3; 1.
DR Chaperone; ATP-binding; Heat shock; Phosphorylation;
KW Complete proteome.
KW MOD_RES 173 173 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT MOD_RES 173 173
SQ SEQUENCE 609 AA; 64980 MW; 298D8ADCC9D31E0C CRC64;

Query Match 6.7%; Score 81; DB 1; Length 609;
Best Local Similarity 27.0%; Pred. No. 21;
Matches 37; Conservative 19; Mismatches 63; Indels 18; Gaps 5;

Qy 69 VDLGST-AATSEYEGSSVDLYCAYGYQCAGGTENKTCMYGGVTLHDNNRLTEKKVPI 127
Db 7 IDLGTNSAVALEGTESKIITANPEGNRT---TPSVVSFKNGELIIVGDAKRAQVTPNPT 63

Qy 128 NLWIDGKQTTVPIDKVTSKTEVTVOELDLQARHYLHGKFLGNSDSFGKVGQGLIVFH 187
Db 64 VISIKSKMGT--SEKVSANGKEYTPQEISAMILQYLKG---YAEDYLGEKVEKAVI--- 114

Qy 188 SSEGSTVSVDLYDQGGQ 204
Db 115 -----TVPAYFNDAQRQ 126

RESULT 36
WDRI CAEEL STANDARD; PRT; 611 AA.
AC Q11176;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Actin interacting protein 1 (AIP1) (Uncoordinated protein 78).
GN UNC-78 OR C04F6.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;

OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=21157410; PubMed=11257131;
RA Ono S.;
RT "The Caenorhabditis elegans unc-78 gene encodes a homologue of
RT actin-interacting protein 1 required for organized assembly of muscle
RT actin filaments";
RL J. Cell Biol. 152:1313-1320(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Nhan M.;
RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Induces disassembly of actin filaments in conjunction
CC with ADP/cofilin family proteins. Regulator of actin organization
CC in myofibrils.
CC -!- SIMILARITY: Belongs to the WD-repeat AIP1 family.
CC -!- SIMILARITY: Contains 9 WD repeats.
CC
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CC
CC EMBL; AF324437; AAK11613.1; -.
DR EMBL; U42835; AAG83588.1; -.
DR PIR; T15410; T15410.
DR WormPep; C04F6.4; CE03924.
DR InterPro; IPR001680; WD40.
DR Pfam; PF04000; WD40; 9.
DR PRINTS; PR00320; GPROTEINBREP.
DR ProDom; PD000018; WD40; 1.
DR SMART; SM00320; WD40; 10.
DR PROSITE; PS00678; WD_REPEATS_1; 3.
DR PROSITE; PS00682; WD_REPEATS_2; 6.
DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
KW Actin-binding; Cytoskeleton; Repeat; WD repeat.
FT REPEAT 57 96
FT REPEAT 145 185 WD 1.
FT REPEAT 188 227 WD 3.
FT REPEAT 237 276 WD 4.
FT REPEAT 322 361 WD 5.
FT REPEAT 446 485 WD 6.
FT REPEAT 489 528 WD 7.
FT REPEAT 534 573 WD 8.
FT REPEAT 579 610 WD 9.
SQ SEQUENCE 611 AA; 65323 MW; 821452C661B5D27A CRC64;

Query Match 6.7%; Score 81; DB 1; Length 611;
Best Local Similarity 18.7%; Pred. No. 21;
Matches 53; Conservative 46; Mismatches 78; Indels 106; Gaps 12;

Qy 23 LGNLKQIYYNKAITSSEKSAQQLTNTLLFKGPFTHG--PW-----YNDLLVLDLST 74
Db 313 LGSIDQVRYCHNKAITALSAD-----GKTLFSADAECHNSWDSTGISNRVFPDVHAT 368

Qy 75 AATSEYEGSSVDLYGAYY-----GYQCAGGTENK-----TA 105
Db 369 MITGIKTTSGDLFTVSWDDHLKVPAGSGVDSKAVANKLSQPLGLAVSADGDIYA 428

Qy 106 CMYGGVTLHDNNRLTEKKVPI-----LWIDGKQTTVPIDKV---KTSKK 148
Db 429 ACYKHAIYSHGKLT-----VPISYNSCVVALSNDKQFVAVGGQDSKHVYKLUSGASVSEV 485

Qy 149 EVTVQELDL-----QAR-----HYLHGKFLGNSDSFGKVGQGLIVFHS 188
Db 486 KTIIVHAEITSVAFSNNGAFLVATDQSRKVIPIVSYVANNEFELAHNSW-----TFHT 536

DR PROSITE; PS00513; ADENYLOSUCIN_SYN_2; FALSE NEG.
KW Purine biosynthesis; Ligase; GTP-binding; Metal-binding; Magnesium;
Complete proteome.
FT NP_BIND 18 24 GTP (POTENTIAL).
FT ACT_SITE 144 144 BY SIMILARITY.
FT METAL 19 19 MAGNESIUM (BY SIMILARITY).
FT METAL 48 48 MAGNESIUM (VIA CARBONYL OXYGEN) (BY
SIMILARITY).
SQ SEQUENCE 345 AA; 37820 MW; 9974BEC30DIDEE72 CRC64;

Query Match 6.6%; Score 80; DB 1; Length 345;
Best Local Similarity 22.6%; Pred. No. 13;
Matches 44; Conservative 33; Mismatches 60; Indels 58; Gaps 11;

QY 4 SEENIEK-DLRKSELOGTALCNLKQIYYNSKAITSEKSAOFLNT-----51
DB 166 SEENYALDRGENYLIIEGTQ-GTLISLYGYTPYVTSKDTASSFAADVIGITKVDVI 224
QY 52 LLFKGFFT---GHPWYNDLLVDLGSTAATSEYEGSSVDLYG-----AYGYQCAGG 99
DB 225 VVFKTFTRVCGAGFPFEMSL-----EAESLGIVEYGTGRRRRRVGYDFELA-- 274
QY 100 TPNKTACMYGGVT-----LHNNRLTEKKVPINLWIDGKQTTVPIDKV 143
DB 275 ---RKACRLNGATQALTGLDKYDCEGVTEYNKLSKAKEFINK-IE-EVTGVPVTII 329
QY 144 KTSKKEVTQVQLDLQ 158
DB 330 STGPE--WHQTIDLR 342

RESULT 39
PGK_METH
ID_PGK_METH STANDARD; PRT; 411 AA.
AC 027121;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphoglycerate kinase (EC 2.7.2.3).
GN PGK OR WH1042.
OS Methanobacterium thermoautotrophicum.
OC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
OC Methanobacteriaceae; Methanothermobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Deloughery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzaden R., Blakely D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pothier B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiواني N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrovski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
deltaH: functional analysis and comparative genomics.";
RL J. Bacteriol. 179:7135-7155 (1997).
CC -!- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-
CC phospho-D-glyceroyl phosphate.
CC -!- PATHWAY: Second phase of glycolysis; second step.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the phosphoglycerate kinase family.
CC
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DR EMBL; AB000876; AAB85538.1; --.
DR FIR; B69006; B69006.
DR HSSP; P36204; 1VPE.
DR HAMAP; MF_00145; -; 1.
DR InterPro; IPR001576; PGK.
DR Pfam; PF00162; PGK; 1.
DR PRINTS; PR00477; PHGLYCKINASE.
DR PROSITE; PS00111; PGLYCERATE_KINASE; 1.
KW Transferase; Kinase; Glycolysis; Complete proteome.
SQ SEQUENCE 411 AA; 44997 MW; E82D9737C6F74F76 CRC64;

Query Match 6.6%; Score 80; DB 1; Length 411;
Best Local Similarity 22.5%; Pred. No. 16;
Matches 47; Conservative 35; Mismatches 75; Indels 52; Gaps 11;

QY 7 INEKDLRKSELOGTALGNLKO--IYYNSKAITSS-----EKSADQLTNTLLPK 55
DB 184 VMERELR---TLQG-ALENVERPCVVLGGVKVDSIMVMKNVLENGSADLVLTGLVAN 239
QY 56 GFETGHPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHD 115
DB 240 IFLAG-----CGVKGKV-----NMDIKS-RGY-----CDFIKVAKKL 272
QY 116 NNRLTEKKVPINLMI--DGKQTTVPIDKVTSK-KEVTQVQLDLQARH-----YLHG 165
DB 273 KKRFFERIVVPDVAVCRDGRKRVDPVKIPNHPIDQIGMETIKLYARRIREARTLFANG 332
QY 166 KFGLYNSDSFGCKVQGLVHFHSSEGSTV 194
DB 333 PAGVFENPDFSTGTEDILNAISSEGFISI 361

RESULT 40
ITAL_HUMAN
ID_ITAL_HUMAN STANDARD; PRT; 1151 AA.
AC P56199;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Integrin alpha-1 (Laminin and collagen receptor) (VLA-1) (CD49a).
GN ITGA1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93155124; PubMed=8428973;
RA Briesewitz R., Epstein M.R., Marcantonio E.E.;
RT "Expression of native and truncated forms of the human integrin alpha
1 subunit.";
RL J. Biol. Chem. 268:2989-2996 (1993).
CC -!- FUNCTION: INTEGRIN ALPHA-1/BETA-1 IS A RECEPTOR FOR LAMININ AND
CC COLLAGEN. IT RECOGNIZES THE PROLINE-HYDROXYLATED SEQUENCE G-P-P-G-
CC E-R IN COLLAGEN.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-1
CC ASSOCIATES WITH BETA-1.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS
CC WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
CC -!- SIMILARITY: Contains 1 VWFA domain.
CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD49a entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd49a.htm".
CC
DR FIR; A45226; A45226.
DR PDB; 1OC5; 17-MAY-00.
DR Genew; HGNC:6134; ITGA1.
DR MIM; 192968; -.
DR GO; GO:0008305; C:integrin complex; TAS.
DR GO; GO:0004895; F:cell adhesion receptor activity; NAS.
DR GO; GO:0005518; F:collagen binding; TAS.
DR GO; GO:0007160; P:cell-matrix adhesion; NAS.

DR InterPro: IPR000413; Integrin_alpha.
 DR InterPro: IPR002035; VWF_A.
 DR Pfam: PF01839; FG-GAP 3.
 DR Pfam: PF00357; Integrin_A; 1.
 DR Pfam: PF00092; vwa; 1.
 DR SMART: SM00191; Int_alpha; 5.
 DR SMART: SM00327; VWA; 1.
 DR SMART: SM00242; INTEGRIN_ALPHA; 1.
 DR PROSITE: PS00234; VWF_A; 1.
 DR PROSITE: PS00242; INTEGRIN_ALPHA; 1.
 KW Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
 KW Repeat; Calcium; Magnesium; 3D-structure.
 FT DOMAIN 1 1113 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 1114 1136 POTENTIAL.
 FT DOMAIN 1137 1151 CYTOPLASMIC (POTENTIAL).
 FT REPEAT 16 75 FG-GAP 1.
 FT REPEAT 16 75 FG-GAP 2.
 FT REPEAT 147 360 VWF_A.
 FT REPEAT 349 404 FG-GAP 3.
 FT REPEAT 405 457 FG-GAP 4.
 FT REPEAT 459 520 FG-GAP 5.
 FT REPEAT 540 599 FG-GAP 6.
 FT REPEAT 602 654 FG-GAP 7.
 FT CA_BIND 470 478 POTENTIAL.
 FT CA_BIND 552 560 POTENTIAL.
 FT CA_BIND 614 622 POTENTIAL.
 FT SITE 1139 1142 GFPR MOTIF.
 FT DISULFID 54 64 BY SIMILARITY.
 FT DISULFID 660 669 BY SIMILARITY.
 FT DISULFID 675 728 BY SIMILARITY.
 FT DISULFID 780 786 BY SIMILARITY.
 FT DISULFID 850 858 BY SIMILARITY.
 FT DISULFID 1002 1034 BY SIMILARITY.
 FT DISULFID 1037 1044 BY SIMILARITY.
 FT CARBOHYD 46 46 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 72 72 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 77 77 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 84 84 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 189 189 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 313 313 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 374 374 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 432 432 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 504 504 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 671 671 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 720 720 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 752 752 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 812 812 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 855 855 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 880 880 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 887 887 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 911 911 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 938 938 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 946 946 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 980 980 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1045 1045 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1055 1055 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1074 1074 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 1085 1085 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 1151 AA; 127837 MW; 6B3F3C1AABF52808 CRC64;

Query Match 6.6%; Score 80; DB 1; Length 1151;
 Best Local Similarity 27.3%; Pred. No. 56;
 Matches 53; Conservative 25; Mismatches 66; Indels 50; Gaps 12;
 QY 72 GSTAATSEYEGSSV-----DLYGAYGYQCAGGTPNKTACMYGGVTL----- 113
 DB 596 GGDGKTLKFFQSGIHGEMDLNG-----DGLTDVTIGLGLGAALFNSRDVAVVKVTWN 647
 QY 114 HDNRLTESEKYPINLWIDGKOT-----TVPIDKVKTSKKEVTVOELDLQARHYLHGKFG 168
 DB 648 FEFNKVNIQK---NCHMEGKETVCINATVCFE-VLKLSKEDTIYEADLQYRVTLDSLRQ 703

QY 169 LYNDSDFEGG---KVQRLIVFHSSSGSTVSVDLFDQAQGYPTDLARIYRD-----NT 217
 DB 704 ISRS-FFSGTQERKVRQNTIV-RKSECTKHSFYMLD-KHDFQDS-VAILDLFNLTPENG 759
 QY 218 TISSTSLISLYLY 231
 DB 760 PVLDDSLPNSVHEY 773
 RESULT 41
 YE64_PASMU
 ID YE64_PASMU STANDARD; PRT; 324 AA.
 AC Q9CKY6;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical paba-like protein PM1464.
 OS Pasteurella multocida.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
 OC Pasteurellaceae; Pasteurella.
 OX NCBI_TaxID=747;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Pm70;
 RX MEDLINE=21145866; PubMed=11248100;
 RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
 RL "Complete genomic sequence of Pasteurella multocida Pm70.";
 CC Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).
 CC -!- SIMILARITY: TO THE C-TERMINAL OF PARA-AMINOBENZOATE SYNTHASE COMPONENT I.
 CC
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 CC
 CC EMBL: AE006183; AAK03548.1; .
 DR InterPro: IPR005801; Anth synth chor.
 DR Pfam: PF00425; chorismate_bind; 1.
 DR PRINTS: PR00095; ANTSINHA5E1.
 DR PRODOM: PD000779; Anth synth chor; 1.
 DR Hypothetical protein; Complete proteome.
 SQ SEQUENCE 324 AA; 37309 MW; E9336FF3890A32AE CRC64;

Query Match 6.5%; Score 79.5; DB 1; Length 324;
 Best Local Similarity 27.3%; Pred. No. 13; Mismatches 17; Indels 13; Gaps 3;
 Matches 24; Conservative 17;
 QY 136 TTVPIDKVKTSKKEVTVOEL---DLQARHYLHGKFGLYNSDFGGKVGQRLI-----V 185
 DB 236 TLLPAGSISGAPKEKTVIIHAAEQRPGRYTGIFGLFDGESLQSAVAIRFIQVDEKLI 295
 QY 186 FHSSEGSTVSVDLFDQAQGYPTDLRIY 213
 DB 296 FRSGGGITLSELED---EYQELIQKY 320

RESULT 42
 VE1_HPV35
 ID VE1_HPV35 STANDARD; PRT; 637 AA.
 AC P27220;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Replication protein E1.
 GN E1.
 OS Human papillomavirus type 35.
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
 OC Papillomavirus.

NCBI_TaxID=10587;
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=92124753; PubMed=1310198;
 RX Marich J.E., Pontsler A.V., Rice S.M., McGraw K.A., Dubensky T.W.;
 RA "Primer-directed sequencing of human papillomavirus types.";
 RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
 [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE=92124753; PubMed=1310198;
 RX Marich J.E., Pontsler A.V., Rice S.M., McGraw K.A., Dubensky T.W.;
 RA "The phylogenetic relationship and complete nucleotide sequence of
 human papillomavirus type 35.";
 RL Virology 186:770-776(1992).
 CC -!- FUNCTION: ATP-DEPENDENT DNA HELICASE REQUIRED FOR INITIATION OF
 CC VIRAL DNA REPLICATION. IT FORMS A COMPLEX WITH THE VIRAL E2
 CC PROTEIN. THE E1-E2 COMPLEX BINDS TO THE REPLICATION ORIGIN WHICH
 CC CONTAINS BINDING SITES FOR BOTH PROTEINS.
 CC -!- SUBCELLULAR LOCATION: Nuclear.
 CC
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 CC
 CC EMBL; X74477; CRA52563.1; -;
 DR EMBL; M74117; AAA46968.1; -;
 DR PIR; A40824; WML35.
 DR PIR; S36523; S36523.
 DR InterPro; IPR001177; Papillom_E1.
 DR Pfam; PF00519; E1; 1.
 DR Pfam; PF00524; E1; 1.
 DR Early protein; DNA replication; Helicase; ATP-binding; DNA-binding;
 KW Nuclear protein.
 FT NP_BIND 463 470 ATP (POTENTIAL).
 FT CONFLICT 31 34 DPVS -> SSV (IN REF. 2).
 FT CONFLICT 142 143 QQ -> HE (IN REF. 2).
 FT CONFLICT 235 258 ESKTLKPYCLYHIQCLCSWG ->
 FT CONFLICT 269 281 NFKHITYVYVYVRVHGA (IN REF. 2).
 FT CONFLICT 269 281 CAKNTTIEKLS -> VEKREQLKTLDA (IN REF. 2).
 FT CONFLICT 417 418 EK -> AQ (IN REF. 2).
 FT CONFLICT 515 552 WAYIDQYRNALDGNPISLDVVKHAKLVOLKCPPLITS ->
 FT CONFLICT 515 552 GIYRPFKCKTRWKSYSFRCKALSIVHIMPTFTYI (IN REF. 2).
 FT CONFLICT 587 587 V -> E (IN REF. 2).
 FT CONFLICT 613 613 D -> V (IN REF. 2).
 FT SEQUENCE 637 AA; 72122 MW; 3C694D4451791003 CRC64;
 Query Match 6.5%; Score 79.5; DB 1; Length 637;
 Best Local Similarity 20.3%; Pred. No. 30;
 Matches 50; Conservative 39; Mismatches 88; Indels 69; Gaps 11;
 QY 21 TALGNLKOIYYNSKAITSSSEKSDQFLTNLLKGRFTGHPWYNDLLVLDLSTAAATSEY 80
 DB 310 TAMSINSEV-----DGETPWIORQIVLQHSF-----NDALFDL-SEWQWAY 351
 QY 81 EGSVDLYGAYGYQACGTPNKTACMY-----GGVTLDDNNRLTEKKVPINL 129
 DB 352 DNDFDDSDIAYKQAQLAET-NSNACFLKNSQAKIVKDCATMCRHYKRAEKREMTMSQ 410
 QY 130 WIDGQKTTVPID-KYKTSKEVTQVQLDQA-----RHYLACK-----FGLYNSDSF 175
 DB 411 WTKRCEKVDGDDWRDIDVFLRYQOQDFVAFLSALKNFLGVPKNCILLYGAPNT--- 467
 QY 176 GGVKQKGLIVFHSSSGSTVSV-----DLFDAQ-----GOYPTLLRIYR 214
 DB 468 -CKSLFGLMSLHFLQALISYNSKSHFWLQLYDAKIAMLDATSPCKWAYIDQYLRNAL 526
 QY 215 DNTTIS 220

DB 527 DGNPIS 532
 RESULT 43
 Y650 METUA STANDARD; PRT; 692 AA.
 AC Q57852;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MJ0650 precursor.
 GN MJ0650.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcales; Methanocaldococcus.
 OX NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=868087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kervlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.R., Fuhrmann J.L., Nguyen D.,
 RA Uitterback L.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Borodovsky M.,
 RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
 RT jannaschii";
 RL Science 273:1058-1073(1996).
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 CC
 CC EMBL; U67512; AAB98647.1; -;
 DR PIR; B64381; B64381.
 DR TIGR; MJ0650; -;
 KW Hypothetical protein; Signal; Complete proteome.
 FT SIGNAL 1 24 HYPOTHETICAL PROTEIN MJ0650.
 FT CHAIN 25 692
 SQ SEQUENCE 692 AA; 80607 MW; 25D0A91A08177188 CRC64;
 Query Match 6.5%; Score 79.5; DB 1; Length 692;
 Best Local Similarity 19.1%; Pred. No. 33;
 Matches 59; Conservative 39; Mismatches 98; Indels 109; Gaps 12;
 QY 7 INEKDLRKSELOGTAL-----GNLKOIYYNSKAITSSSEKSDQFLTNLLIF 54
 DB 363 INNSKIDKKIYKRGKLTSGYNGKYCLGGKGLLYNGKNITDLTKSAN--ISNSDLI 420
 QY 55 KGF-----FTGHPWY-----NDLLVLDLS 73
 DB 421 SSTAYGKDWLGLDEVNLHPSKSLIKEDKKFYDLTNISNITICKILSKNKEYILIGT 480
 QY 74 TAATSEYEGSSVDL-----YGAYGYQACGTPNKTACMYGGVTLDDNNRLTEKKV 125
 DB 481 KNLVLIKNGSFITIIYNTVYKGYGLCYIFEAMDYNPKERYWLVGGVCLY--NHPYSDAI 538
 QY 126 PINLWIDGKTTVPIDKVKTSKEVTQVQLDQARHVLHGKFG-----LYNSDSFG 176
 DB 539 LYKYDNGSYESLFIN-----DNLHKIYDGFGLVSLIKIYKPNKSNFL 582
 QY 177 GRVQGLI-----IVFHSSEGSTV--SYDLFDAQOQYPTLLRIYRDNNTTIS 220
 DB 583 IKVWGLNDHWHLYKNTLTLEFVTQKNPGSIEIDNTLYIF--NYNT-IEIYDNNKLLS 639

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QY 221 STSL 224
DB 640 TVEL 643

RESULT 44
CHIT NPVAC
ID CHIT NPVAC STANDARD; PRT; 551 AA.
AC P41684;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Probable endochitinase precursor (EC 3.2.1.14).
OS Autographa californica nuclear polyhedrosis virus (AcMNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=46015;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C6;
RX MEDLINE=94303173; PubMed=8030224;
RA Ayres M.D., Howard S.C., Kuzio J., Lopez-Ferber M., Possee R.D.;
RT "The complete DNA sequence of Autographa californica nuclear
polyhedrosis virus."
RL Virology 202:586-605(1994).
CC -|- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages of N-
acetyl-D-glucosamine polymers of chitin.
CC -|- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen (Potential).
CC -|- SIMILARITY: Belongs to chitinase class II (family 18 of glycosyl
hydrolases).
CC
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CC
CC EMBL; L22859; AAA66756.1; -.
DR PIR; G72865; G72865.
DR HSSP; P07254; ICTN.
DR InterPro; IPR000896; ER target S.
DR InterPro; IPR001223; Glyco_hydro_18.
DR InterPro; IPR001579; Glyco_hydro_18AS.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR000601; PKD.
DR Pfam; PF00704; Glyco_hydro_18; 1.
DR ProDom; PD000471; Glyco_hydro_18; 1.
DR SMART; SM00636; Glyco_18; 1.
DR SMART; SM00089; PKD; 1.
DR PROSITE; PS00014; ER_TARGET; 1.
DR PROSITE; PS01095; CHITINASE_18; 1.
KW Hydrolase; Glycosidase; Chitin degradation; Signal; Glycoprotein;
KW Endoplasmic reticulum.
FT SIGNAL 1 17
FT CHAIN 18 551
FT ACT_SITE 305 305
FT CARBOHYD 173 173
FT CARBOHYD 444 444
FT SITE 548 551
SQ SEQUENCE 551 AA; 61368 MW; 4DDAAD1873BBA2 CRC64;

Query Match 6.5%; Score 79; DB 1; Length 551;
Best Local Similarity 23.8%; Pred. No. 27;
Matches 44; Conservative 22; Mismatches 71; Indels 48; Gaps 11;

QY 32 YNSKAITS---SEKSAQQLTNTLTKFKFTGHPWYNDLLDGLGTAATSEYEGSSVDLY 88
DB 358 YDKIAVYNAEAQKSLGKIFLMSYDFKG-----AMSN---TDLGYQTTVYAPSNSEELY 409
QY 89 GAYGVYQC---AGGTENKT---ACMYG---CVTLHDN-NRLTEKKYP-INLWIDGQOT 136

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DB 410 TTHYAVDALLKQGVDPNKIIIVGMYGRGWTGVTNTDNYFSGTGNGPGSGTWEDG--- 466
QY 137 TVPIDKYTKSKKEYTVQCELDLQARHYLHGKFLGFLYNSDSFGKQVQRGLIVFHSSEGSTVSY 196
DB 467 -----VVDFRQIQKDLNNY-----VTFDS-----AAQASYVFDKSGDLISF 504
QY 197 DLFDA 201
DB 505 DSVDS 509

RESULT 45
SLA2_BACAA
ID SLA2_BACAA STANDARD; PRT; 862 AA.
AC P94217;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE S-layer protein EAI precursor.
GN EAG OR BA0887.
OS Bacillus anthracis (strain Ames), and
OS Bacillus anthracis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094; 1392;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Ames;
RX MEDLINE=22608414; PubMed=12721629;
RA Read T.D., Peterson S.N., Tourasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzapple E.K., Ostad O.A., Helgason E., Ralston J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madupu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nierman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
RA Thomason B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of Bacillus anthracis Ames and comparison to
RT closely related bacteria."
RL Nature 423:81-86(2003).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sterne / 9131;
RX MEDLINE=9726011; PubMed=9106206;
RA Mesnage S., Tosi-Couture E., Mock M., Gounon P., Fouet A.;
RT "Molecular characterization of the Bacillus anthracis main S-layer
RT component: evidence that it is the major cell-associated antigen.";
RL Mol. Microbiol. 23:1147-1155(1997).
CC -|- FUNCTION: The S-layer is a paracrystalline mono-layered assembly
of proteins which coat the surface of bacteria.
CC -|- SUBCELLULAR LOCATION: Cell wall.
CC -|- SIMILARITY: Contains 3 S-layer homology (SLH) domains.
CC
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CC
CC EMBL; AE017027; AAP24884.1; -.
DR EMBL; X99724; CAA68063.1; -.
DR TIGR; BA0887; -.
DR InterPro; IPR001119; SLH.
DR Pfam; PF00395; SLH; 3.
DR SIGNAL 1 29
DR CHAIN 30 862
FT DOMAIN 34 76
FT DOMAIN 95 136
FT DOMAIN SLH 1.
FT DOMAIN SLH 2.

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PT DOMAIN 157 197 SLH 3.
SQ SEQUENCE 862 AA; 91362 MW; CBI6B202F62CCCA0 CRC64;

Query Match 6.5%; Score 79; DB 1; Length 862;
Best Local Similarity 22.6%; Pred.No. 48;
Matches 55; Conservative 29; Mismatches 97; Indels 62; Gaps 10;

Qy 33 NSKAITSEKADQFLNTLLFKGFFTGHPWYNDLLVLDLSTAASTSEYSSVDLYGAYY 92
Db 432 NSQNLVVGKASLNKLAVIAGE-----DKVVDPGSISIKSNHG-IISVNNYI 480
Qy 93 GYCAGGTPNKATACWYGGVT-----LHDNRLTEEEKVPIPNLWIDGKQTTVPIDKVK 145
Db 481 TAEAGEA--TLTIKVGDTVVDKVKFTTDSRKLVSVKANPKLOV-VQNKTLIPVFVTT 537
Qy 146 SK-----KEV-----TVQELDLQARHYLHGKFGLYNSDSFGKVGQRLIVFHS 188
Db 538 DQYGDPPGANTAAIKVELPKTGVVAEGGLDVTVDTSIGTKTIGVTGNDVGEQTVHFQN 597
Qy 189 SEGSTV-----SYDLFDAQGY-----PTLLRIYRDNTTISTSLISLYL 230
Db 598 NGATLGLSYNVTEGNAVFNFELSVKVGQYGGSPDKLDN-----VSTTVEYQJSK 651
Qy 231 YTT 233
Db 652 YTS 654

RESULT 46
LMA5 HUMAN STANDARD; PRT; 3695 AA.
ID LMA5 HUMAN STANDARD; PRT; 3695 AA.
AC Q15230; Q9WZ47; Q9HUP1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 18-FEB-2003 (Rel. 41, Last sequence update)
DI 15-MAR-2004 (Rel. 43, Last annotation update)
DE Laminin alpha-5 chain precursor.
GN LMA5 OR KIAA0533 OR KIA1907.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21638749; PubMed=11780052;
RA Jones M., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
RA DeLukas P., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beasley O.P., Bird C.P., Blakey S.E., Bridgman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Copley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Grahnam D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
RA Levaeslaio M.H., Leversha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
RA Marsh V.L., Martin S.L., McConachie L.J., McKay K., McMurray A.A.,
RA Mine S.A., Mistry D., Moore M.J.P., Mullikin J.C., Nickerson T.,
RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
RA Phillimore B.U.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Showkeen R., Sims S.,
RA Skuce C.D., Smith M.N., Soderlund C., Steward C.A., Suleston J.E.,
RA Swann R.M., Sycamore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
RA Tracey A., Tromas A.C., Vaudin M., Wall M., Wallis J.M.,
RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
RA Rogers J.;
RT "The DNA sequence and comparative analysis of human chromosome 20."
RL Nature 414:865-871(2001).
RN [2]
RP SEQUENCE OF 197-1934 FROM N.A.

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RC TISSUE=Brain;
RX MEDLINE=21456161; PubMed=11572484;
RA Nagase T., Kikuno R., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XI.
RT The complete sequences of 60 new cDNA clones from brain which code for
RT large proteins."
RL DNA Res. 8:179-187(2001).
RN [3]
RP SEQUENCE OF 2051-3695 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98290545; PubMed=9628581;
RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
RA Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. IX.
RT The complete sequences of 100 new cDNA clones from brain which can
RT code for large proteins in vitro."
RL DNA Res. 5:31-39(1998).
RN [4]
RP SEQUENCE OF 2743-3695 FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=97415425; PubMed=9271224;
RA Durkin M.E., Joehel F., Mattei M.-G., Gilpin B.J., Albrechtsen R.,
RA Wewer U.M.;
RT "Tissue-specific expression of the human laminin alpha5-chain, and
RT mapping of the gene to human chromosome 20q13.2-13.3 and to distal
RT mouse chromosome 2 near the locus for the ragged (Ra) mutation."
RL FEBS Lett. 411:296-300(1997).
RN [5]
RP EXPRESSION IN RETINA.
RX MEDLINE=20422761; PubMed=10964957;
RA Libby R.T., Champlaud M.-F., Claudepierre T., Xu Y., Gibbons E.P.,
RA Koch M., Burgeson R.E., Hunter D.D., Brunken W.J.;
RT "Laminin expression in adult and developing retinae: evidence of two
RT novel CNS laminins."
RL J. Neurosci. 20:6517-6528(2000).
CC -1- FUNCTION: Binding to cells via a high affinity receptor, laminin
CC is thought to mediate the attachment, migration and organization
CC of cells into tissues during embryonic development by interacting
CC with other extracellular matrix components.
CC -1- SUBUNIT: Laminin-15 complex is an heterotrimer composed of three
CC chains (alpha-5/beta-2/gamma-3) which are bound to each other by
CC disulfide bonds into a cross-shaped molecule comprising one long
CC and three short arms with globules at each end.
CC -1- SUBCELLULAR LOCATION: Extracellular; found in the basement
CC membranes (major component).
CC -1- TISSUE SPECIFICITY: Expressed in heart, lung, kidney, skeletal
CC muscle, pancreas, retina and placenta. Little or no expression in
CC brain and liver.
CC -1- DOMAIN: Domain G is globular and is part of the major cell-binding
CC site located in the long arm of the laminin heterotrimer.
CC -1- SIMILARITY: Contains 1 laminin N-terminal domain.
CC -1- SIMILARITY: Contains 22 laminin EGF-like domains.
CC -1- SIMILARITY: Contains 2 laminin IV domains.
CC -1- SIMILARITY: Contains 5 laminin G-like domains.
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CC -----
CC EMBL; AJ354836; CAC22309.1; ALT_SEQ.
CC EMBL; AJ354836; CAC22309.1; -.
CC EMBL; AB067494; BAB67800.1; -.
CC EMBL; AB011105; BAA25459.1; -.
CC EMBL; Z95636; CAB09137.1; -.
CC HSP; P02468; IXL0.
CC Genew; HGNC:6485; LAMA5.
CC MIN; 601033; -.
CC InterPro; IPR008985; ConA_like_lec_gl.
CC InterPro; IPR006209; EGF_like.

```

FT	DISULFID	494	506	BY SIMILARITY.
FT	DISULFID	496	515	BY SIMILARITY.
FT	DISULFID	517	526	BY SIMILARITY.
FT	DISULFID	529	538	BY SIMILARITY.
FT	DISULFID	541	553	BY SIMILARITY.
FT	DISULFID	543	560	BY SIMILARITY.
FT	DISULFID	562	571	BY SIMILARITY.
FT	DISULFID	574	584	BY SIMILARITY.
FT	DISULFID	587	599	BY SIMILARITY.
FT	DISULFID	589	605	BY SIMILARITY.
FT	DISULFID	607	616	BY SIMILARITY.

Query Match 6.5%; Score 79; DB 1; Length 3695;
Best Local Similarity 29.4%; Pred.No. 2.9e+02; Indels 44; Gaps 13;
Matches 58; Conservative 20; Mismatches 75; Indels 44; Gaps 13;

QY	56	GFFTGHWINDLLVLDLGSTAATSEYEGSSV-----	-----DLYGAYGYQCAGGTPEKT-	104
DB	41	GGFSLHPYPFNLAE--GARIAASATCGEAPARGSPRPTDLVCKLVGGPVGAGDPNQTI	98	
QY	105	ACMTGGVTLHDNNLITEKKVPINLIDGQ-----	TTVPIDK-VKTSKEVTVQELDL-OA	159
DB	99	QGQVCDICTAANS-----NKAHPASNAIDGTERWQSPPLSRGLEYNVNVNT---	LDLGGV	151
QY	160	RH--YLHGKFG-----	LYNSDFGGKVQRGLIVFHSSSGSTVSYVDLFDACQGYPT	208
DB	152	FHVAVLIKANSRPPDLWLERSMDFGRYQPWF-FASSK-----	RDCLERFG--PQT	203
QY	209	LLRIYRNTTISLSLS	225	
DB	204	LERITRDAATCTEYS	220	

RESULT 47
YURL_YEAST
ID YURL_YEAST STANDARD; PRT; 396 AA.
AC P46992;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 43.0 kDa protein in CP51-FPPI intergenic region.
GN JDL71C OR J0512.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RL Obermayer B., Piravandi E., Rinke M., Domdey H.;
CC Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
CC -! SIMILARITY: TO YEAST YBR162C.
CC
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CC
CC EMBL; Z49446; CAA89466.1; --
DR F01; S56954; S56954.
DR Germonline; 141783; --
DR SGD; S0003707; YJL171C.
KW Hypothetical protein.
SQ SEQUENCE 396 AA; 43014 MW; 279E858E7512670A CRC64;

Query Match 6.4%; Score 78.5; DB 1; Length 396;
Best Local Similarity 21.6%; Pred.No. 20;
Matches 64; Conservative 29; Mismatches 86; Indels 117; Gaps 16;

QY	26	LKQIYYNSKAIT-----	-----SSEKSDAQF-----	LTNTLFL-K	55
----	----	-------------------	---------------------	-----------	----

RA Read T.D., Peterson S.N., Tournasse N., Baillie L.W., Paulsen I.T.,
RA Nelson K.E., Tettelin H., Fouts D.E., Eisen J.A., Gill S.R.,
RA Holtzaple E.K., Okstad O.A., Helgason E., Rilstone J., Wu M.,
RA Kolonay J.F., Beanan M.J., Dodson R.J., Brinkac L.M., Gwinn M.,
RA DeBoy R.T., Madpu R., Daugherty S.C., Durkin A.S., Haft D.H.,
RA Nelson W.C., Peterson J.D., Pop M., Khouri H.M., Radune D.,
RA Benton J.L., Mahamoud Y., Jiang L., Hance I.R., Weidman J.F.,
RA Berry K.J., Plaut R.D., Wolf A.M., Watkins K.L., Nieman W.C.,
RA Hazen A., Cline R., Redmond C., Thwaite J.E., White O., Salzberg S.L.,
RA Thomson B., Friedlander A.M., Koehler T.M., Hanna P.C., Kolsto A.-B.,
RA Fraser C.M.;
RT "The genome sequence of *Bacillus anthracis* Ames and comparison to
RT closely related bacteria.";
RL Nature 423:81-86(2003).
CC -!- FUNCTION: Catalyzes the reversible phosphatidyl group transfer
CC from one phosphatidylglycerol molecule to another to form
CC cardiolipin (CL) (diphosphatidylglycerol) and glycerol (By
CC similarity).
CC -!- CATALYTIC ACTIVITY: 2 Phosphatidylglycerol =
CC diphosphatidylglycerol + glycerol.
CC -!- SUBCELLULAR LOCATION: Membrane-bound (By similarity).
CC -!- SIMILARITY: Belongs to the phospholipase D family. Cardiolipin
CC synthase subfamily.
CC -!- SIMILARITY: Contains 2 PLD phosphodiesterase domains.
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CC or send an email to license@isb-sib.ch).
CC EMBL: AE017026; AAP24642.1; -
DR TIGR: BA0625; -
DR HAMAP: MF_00190; -; 1.
DR InterPro: IPR001736; PLD.
DR Pfam: PF00614; PLDC; 2.
DR SMART: SM00155; PLDC; 2.
DR PROSITE: PS00035; PLD; 2.
KW Transferase; Phospholipid biosynthesis; Transmembrane; Repeat;
KW Complete proteome.
FT TRANSMEM 5 22 Potential.
FT TRANSMEM 27 49 Potential.
FT TRANSMEM 58 80 Potential.
FT DOMAIN 238 265 PLD phosphodiesterase 1.
FT DOMAIN 422 449 PLD phosphodiesterase 2.
FT ACT_SITE 243 243 POTENTIAL.
FT ACT_SITE 427 427 POTENTIAL.
SQ SEQUENCE 509 AA; 58107 MW; 54AFD680C2A095FA CRC64;
Query Match 6.4%; Score 78.5; DB 1; Length 509;
Best Local Similarity 25.6%; Pred. No. 27;
Matches 30; Conservative 26; Mismatches 30; Indels 31; Gaps 7;
QY 115 DNNRLTEKKVPLNLDGKQTVPIDKV-----KTSKKEVT-----VQE 154
DB 105 EGRRLSLKVLPLS-----ERSVHUTEVQVFGGPAADRTTKLLTNGDGTFSGLQA 158
QY 155 LDLDQARHYLHGKFGLYNSDSFGKVGORGLIVFHSSEGTSTVSYDLFDACQYPTLLR 211
DB 159 IE-QAKSHIHQYIYKSDIGTKV-RDALIKKADGVIVRF-LYDGLGS--NTLRR 210

CC Bacteria; Firmicutes; Clostridia; Thermoanaerobacteriales;
CC Thermoanaerobacteriaceae; Thermoanaerobacter.
OX NCBI_TaxID=2125;
[1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC STRAIN=DSM 2030;
RC MEDLINE=90036724; PubMed=2681162;
RA Peters J., Peters M., Lottspeich F., Baumeister W.;
RT "S-layer protein gene of *Acetogenium kivui*: cloning and expression in
RT *Escherichia coli* and determination of the nucleotide sequence.";
RL J. Bacteriol. 171:6307-6315(1989).
[2]
RP PARTIAL SEQUENCE, AND CARBOHYDRATE-LINKAGE SITES.
RC STRAIN=DSM 2030;
RC MEDLINE=92281680; PubMed=1596358;
RA Peters J., Rudolf S., Oschkinat H., Mengele R., Sumper M.,
RA Kellermann J., Lottspeich F., Baumeister W.;
RT "Evidence for tyrosine-linked glycosaminoglycan in a bacterial
RT surface protein.";
RL Biol. Chem. Hoppe-Seyler 373:171-176(1992).
[3]
RP DOMAINS.
RX MEDLINE=94156823; PubMed=8113161;
RX Lupas A., Engelhardt H., Peters J., Santarius U., Volker S.,
RA Baumeister W.;
RT "Domain structure of the *Acetogenium kivui* surface layer revealed by
RT electron crystallography and sequence analysis.";
RL J. Bacteriol. 176:1224-1233(1994).
CC -!- FUNCTION: The S-layer is a paracrystalline mono-layered assembly
CC of proteins which coat the surface of bacteria.
CC -!- SUBCELLULAR LOCATION: Cell wall. This bacterium is covered by a S-
CC layer with hexagonal symmetry.
CC -!- PTM: THE CARBOHYDRATE CONTENT OF THIS PROTEIN IS ABOUT 8% WHICH
CC CORRESPOND TO ABOUT 40 TO 50 SUGAR MOLECULES PER MONOMER. O-LINKED
CC GLYCANS CONSIST OF GLC, GALNAC AND GLCNAC.
CC -!- SIMILARITY: Contains 3 S-layer homology (SLH) domains.
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CC or send an email to license@isb-sib.ch).
CC EMBL: M31069; AAA21930.1; -
DR PIR: A34355; A34355.
DR InterPro: IPR001119; SLH.
DR Pfam: PF00395; SLH; 2.
DR PROSITE: PS01072; SLH_DOMAIN; 2.
KW Signal; Glycoprotein; Repeat; Cell wall; S-layer.
FT SIGNAL 1 26
FT CHAIN 27 762 CELL SURFACE PROTEIN.
FT DOMAIN 30 94 SLH 1.
FT DOMAIN 95 145 SLH 2.
FT DOMAIN 146 204 SLH 3.
FT DOMAIN 473 479 SER/THR-RICH.
FT DOMAIN 625 630 SER/THR-RICH.
FT CARBOHYD 297 297 O-LINKED (GLC. . .).
FT CARBOHYD 516 516 O-LINKED (GLC. . .).
FT CARBOHYD 520 520 O-LINKED (GLC. . .).
FT CARBOHYD 632 632 O-LINKED (GLC. . .).
SQ SEQUENCE 762 AA; 82785 MW; 34EC9C784DECA67E CRC64;
Query Match 6.4%; Score 78.5; DB 1; Length 762;
Best Local Similarity 24.8%; Pred. No. 45;
Matches 60; Conservative 28; Mismatches 105; Indels 49; Gaps 11;
QY 3 KSEINEKDLRKKSELQGTALGNLKIYY-----NSKAITSSSEKSDQFLNTLLFK 55
DB 90 KSESAFKDVPQNH-----WAVGQINLAYKLGLAQGVNGKFDNSSELRYAQLAFVLRAL 145
QY 56 GFTFGHPWYNDLLVDLGLSTAAATSEYSGSSVDLYGAYYGYQCAGGTNKTACMYGGVTLHD 115

RESULT 50

SLAP_ACEKI

ID SLAP_ACEKI

AC P222E8;

DT 01-AUG-1991 (Rel. 19, Created)

DT 01-AUG-1991 (Rel. 19, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Cell surface protein precursor (S-layer protein).

OS Acetogenium kivui.

```
Db 146 GF-----KLDWPG-----YLAQAQL-GLVHGLNLA-----YGVKRG 180
QY 116 NNRLEEK--KYPINLWIDGKQTTVP--IDKVKTSKKEVTVQELDLQARHYLHGKFGLYN 171
Db 181 DLALILDRALEVPMVKYVDGKEVLGKPLISKVAT-KAEYTVIATNAQSRVSEEGKVAVLD 239
QY 172 SPSPGKVGQGLIVFHSSEGSVSDLDPAQOQYDPTLLIRYDRNTTISST-----SLSIS 227
Db 240 KDGKLTINAGLVDFSEYLGKV-----IVYSRFGDPVIVAEAGNDVVVSFTFEGQDSVGT 295
QY 228 LY 229
Db 296 VY 297

RESULT 51
ADH1_ORYSA
ID ADH1_ORYSA STANDARD; PRT; 376 AA.
AC P20306;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Alcohol dehydrogenase 1 (EC 1.1.1.1).
GN ADH1.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzeae; Oryza.
OX NCBI_TaxID=4530;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=cv. Indica-IR26; TISSUE=Seedling;
RX MEDLINE=93357433; PubMed=2562760;
RA Xie Y., Wu R.;
RT "Rice alcohol dehydrogenase genes: anaerobic induction, organ
specific expression and characterization of cDNA clones.";
RL Plant Mol. Biol. 13:53-68(1989).
CC -!- CATALYTIC ACTIVITY: An alcohol + NAD(+) = an aldehyde or ketone +
NADH.
CC -!- COFACTOR: Binds 2 zinc ions per subunit.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to the zinc-containing alcohol dehydrogenase
family.
CC
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CC
CC EMBL; X16296; CAA34363.1; -
DR PIR; JQ0474; JQ0474.
DR HSSP; F11766; ITEX.
DR Gramene; P20306; -.
DR InterPro; IPR002328; ADH zinc.
DR InterPro; IPR002085; Adh zn family.
DR InterPro; IPR002025; NAD_BS.
DR Pfam; PF01107; ADH zinc_N; 1.
DR PROSITE; PS00059; ADH_ZINC; 1.
KW Oxidoreductase; Zinc; Metal-binding; NAD; Multigene family.
FT METAL 45 45 ZINC 1 (CATALYTIC).
FT METAL 67 67 ZINC 1 (CATALYTIC).
FT METAL 98 98 ZINC 2.
FT METAL 100 100 ZINC 2.
FT METAL 103 103 ZINC 2.
FT METAL 111 111 ZINC 2.
FT METAL 175 175 ZINC 1 (CATALYTIC).
SQ SEQUENCE 376 AA; 40852 MW; B8ED6E025863D64F CRC64;
```

```
Query Match 6.4%; Score 78; DB 1; Length 376;
Best Local Similarity 23.8%; Pred. NO. 21;
Matches 47; Conservative 29; Mismatches 77; Indels 46; Gaps 7;
QY 3 KSEINEKDLRKSELSQGTALGNLKIYYNSKAI-----TSSE-----KS 43
Db 104 KSAESNCDLLRINTDRGVWIGDGKSRFSINGKPIYHFIGTSTFSEVTVMHVGCVAKINP 163
QY 44 ADQFLNTLLFKGFFFGHPWYNLLVDLGSTAATSEYEGSSVDLYG-AYGYQCAGTGN 102
Db 164 AAPLDKVCVLSGCI--STG-----LGATINVARPKGSTVAIFGLGAVGLAAAGARI 213
QY 103 KTACMYGGVTLHDNRLTEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELD----- 156
Db 214 RGSRIIGIDL-NANRFEARKEGCTEFYNPKDHPVQOVLA---EMTNGGVDRSVECT 269
QY 157 -----LQARHYLHGKFG 169
Db 270 GNINAMIAFEVCVHDGWI 288

RESULT 52
DNAK_STRPN
ID DNAK_STRPN STANDARD; PRT; 607 AA.
AC P95829; O66035;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa
protein) (HSP70).
DE DNAK OR SP0517.
GN DNAK OR SP0517.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1313;
RN [1]
SEQUENCE FROM N.A.
RP Rioux C.R., Martin D., Hamel J., Brodeur B.R.;
RA "Heat shock protein HSP70 and amino terminus of DnaJ of Streptococcus
pneumoniae.";
RT Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
SEQUENCE FROM N.A.
RC STRAIN=Rx / CP1200;
RX MEDLINE=98231633; PubMed=9570114;
RA Kim S.-W., Choi I.-H., Kim S.-N., Kim Y.-H., Pyo S.-N., Rhee D.-K.;
RT "Molecular cloning, expression, and characterization of dnaK in
Streptococcus pneumoniae.";
RL FEMS Microbiol. Lett. 161:217-224(1998).
RN [3]
SEQUENCE FROM N.A.
RC STRAIN=ATCC BAA-334 / TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
pneumoniae.";
RN Science 293:498-506(2001).
CC -!- FUNCTION: Acts as a chaperone (By similarity).
CC -!- INDUCTION: By stress conditions e.g. heat shock (By similarity).
CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.
CC
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CC -----

DR ENBL; U72720; AAB39221.1; -.

DR ENBL; U84387; AAC15892.1; -.

DR ENBL; AE007363; AAK74575.1; -.

DR PIR; B95060; B95060.

DR HSP; P04475; IDG4.

DR TIGR; SP0517; -.

DR HAMAP; MF_00332; -; 1.

DR InterPro; IPR001023; Hsp70.

DR Pfam; PF00012; Hsp70; 1.

DR PRINTS; PR00301; HEATSHOCK70.

DR PRODOM; PD000089; Hsp70; 1.

DR PROSITE; PS00297; Hsp70; 1.

DR PROSITE; PS00329; Hsp70; 1.

DR PROSITE; PS01036; Hsp70; 1.

DR PROSITE; PS01036; Hsp70; 1.

DR Chapterone; ATP-binding; Heat shock; Phosphorylation;

KW Complete proteome.

FT MOD RES 173 173 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

FT CONFLICT 493 493 A -> P (IN REF. 2).

FT CONFLICT 495 495 A -> S (IN REF. 1).

FT CONFLICT 530 530 A -> P (IN REF. 2).

FT CONFLICT 556 556 T -> A (IN REF. 1 AND 2).

FT CONFLICT 601 602 DG -> E (IN REF. 2).

FT SEQUENCE 607 AA; 64842 MW; 11D626F1837D0760 CRC64;

Query Match 6.4%; Score 78; DB 1; Length 607;

Best Local Similarity 27.0%; Pred. No. 38;

Matches 37; Conservative 18; Mismatches 64; Indels 18; Gaps 5;

QY 69 VDLGST-AATSEYEGSSVDLYGAYGYQCAGGTPNKACMYGVTLHDNNRLTEKKVPI 127

DB 7 IDLGTNSAVAVLEGTESKIANPEGNRT---TPSVVSFKNGEIIYGDAAKRAQVNPDT 63

QY 128 NLMDGKQTTVPIDKVKTSKKEVTQVQLDQARHYLHGKFGLYNSDFGKVGKVGRLIVFH 187

DB 64 VISIKSRMGT--SEKVSANGKEYTPQEISAMILQYLKG---YAEDYLGEKVTKAVI--- 114

QY 188 SSEGSTVSYDLFDAQGG 204

DB 115 -----TVPAYFNDARQ 126

RESULT 53

DNAX_STR6

ID DNAX_STR6 STANDARD; PRT; 607 AA.

AC QSCWT3;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Chapterone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (Hsp70).

DE DNAX OR SPRO455.

OS Streptococcus pneumoniae (strain ATCC BAA-255 / R6).

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxID=171101;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=1429245; PubMed=11544234;

RA Hoskins J., Alborn W.E. Jr., Arnold J., Blaszcak L.C., Burtett S., Dehoff B.S., Estrem S.T., Fritz L., Fu D.-J., Fuller W., Geringer C., Gilmour R., Glass J.S., Kuoja H., Kraft A.R., Lagace R.E., LeBlanc D.J., Lee L.N., Lefkowitz E.J., Lu J., Matsushima P., McAhren S.M., McHenry M., McLeaster K., Mundy C.W., Niclas T.I., Norris F.H., O'Gara M., Peery R.B., Robertson G.T., Rockey P., Sun P.-M., Winkler M.E., Yang Y., Young-Bellido M., Zhao G., Zook C.A., Baltz R.H., Jaskunas S.R., Rostock P.R. Jr., Skatrud P.L., Glass J.I.;

RT "Genome of the bacterium Streptococcus pneumoniae strain R6";

RL J. Bacteriol. 183:5709-5717(2001).

CC -!- FUNCTION: Acts as a chaperone (By similarity).

CC -!- INDUCTION: By stress conditions e.g. heat shock (By similarity).

CC -!- SIMILARITY: Belongs to the heat shock protein 70 family.

CC -----

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CC -----

CC EMBL; AE008426; AAK99259.1; -.

DR PIR; G97928; G97928.

DR HAMAP; MF_00332; -; 1.

DR InterPro; IPR001023; Hsp70.

DR Pfam; PF00012; Hsp70; 1.

DR PRINTS; PR00301; HEATSHOCK70.

DR PRODOM; PD000089; Hsp70; 1.

DR PROSITE; PS00297; Hsp70; 1.

DR PROSITE; PS00329; Hsp70; 1.

DR PROSITE; PS01036; Hsp70; 1.

DR Chapterone; ATP-binding; Heat shock; Phosphorylation;

KW Complete proteome.

FT MOD RES 173 173 PHOSPHORYLATION (AUTO-) (BY SIMILARITY).

FT SEQUENCE 607 AA; 64812 MW; 11D626EB37D1DD0 CRC64;

Query Match 6.4%; Score 78; DB 1; Length 607;

Best Local Similarity 27.0%; Pred. No. 38;

Matches 37; Conservative 18; Mismatches 64; Indels 18; Gaps 5;

QY 69 VDLGST-AATSEYEGSSVDLYGAYGYQCAGGTPNKACMYGVTLHDNNRLTEKKVPI 127

DB 7 IDLGTNSAVAVLEGTESKIANPEGNRT---TPSVVSFKNGEIIYGDAAKRAQVNPDT 63

QY 128 NLMDGKQTTVPIDKVKTSKKEVTQVQLDQARHYLHGKFGLYNSDFGKVGKVGRLIVFH 187

DB 64 VISIKSRMGT--SEKVSANGKEYTPQEISAMILQYLKG---YAEDYLGEKVTKAVI--- 114

QY 188 SSEGSTVSYDLFDAQGG 204

DB 115 -----TVPAYFNDARQ 126

RESULT 54

BGH3_RABIT

ID BGH3_RABIT STANDARD; PRT; 683 AA.

AC Q95215;

DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Transforming growth factor-beta induced protein IG-H3 precursor (Beta IG-H3) (Kerato-epithelin) (RGD-containing collagen associated protein) (RGD-CAP).

DE (RGD-CAP).

GN TGFB1.

OS Oryctolagus cuniculus (Rabbit).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=New Zealand white; TISSUE=Cornea;

RX MEDLINE=97267655; PubMed=9112985;

RA Rave I.M., Zhan Q., Burrows R., Bennett K., Cintron C., "Beta-1g. Molecular cloning and in situ hybridization in corneal tissues".

RT Invest. Ophthalmol. Vis. Sci. 38:893-900(1997).

CC -!- FUNCTION: BINDS TO TYPE I, II, AND IV COLLAGENS. THIS ADHESION PROTEIN MAY PLAY AN IMPORTANT ROLE IN CELL-COLLAGEN INTERACTIONS. IN CARTILAGE, MAY BE INVOLVED IN ENDOCHONDRAL BONE FORMATION. MAY PLAY AN IMPORTANT ROLE IN THE MORPHOGENESIS OF CORNEAL TISSUES.

CC CC PLAY AN IMPORTANT ROLE IN THE MORPHOGENESIS OF CORNEAL TISSUES.

CC -!- SUBCELLULAR LOCATION: Extracellular. May be associated both with microfibrils and with the cell surface (By similarity).

CC -!- TISSUE SPECIFICITY: LOCATED PRIMARILY IN THE EPITHELIUM OF NORMAL

Db 206 GNTSGMGTGSSVVVKAIVGVAHSDYSLTLTGRTA-NWNGPSYDLTGKIVPGQYNNVDFW 264
 QY 131 ---IDGKQTTVPIDKVKTSKEVTVOELDLQARHY-----LHGKFGLYNSDSFGG 177
 Db 265 VKFVNGNDT---EQIKATVKATSDKONYIQVNDFAVNKNGWTEIKGSFTLIPVAD----- 316
 QY 178 KVQKGLIVFHSSEGSTVSX--DLFDAGQGYPTLLRIYRD 215
 Db 317 --YSGISIVESQNPTELFYIDDFSVGEISNNQIIOND 354

RESULT 56
 GTF2_STRDO
 ID -GTF2_STRDO STANDARD; PRT; 1592 AA.
 AC P27470;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Glucosyltransferase-I precursor (EC 2.4.1.5) (GTF-I) (Dextranucrase)
 DE (Sucrose 6-glucosyltransferase)
 OS Streptococcus downei (Streptococcus sobrinus)
 OS Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1317;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=6715 / Serotype G;
 RX MEDLINE=91123227; PubMed=1704006;
 RA Abo H., Matsumura T., Kodama T., Ohta H., Fukui K., Kato K.,
 RA Kigawa H.;
 RT "Peptide sequences for sucrose splitting and glucan binding within
 RT Streptococcus sobrinus glucosyltransferase (water-insoluble glucan
 RT synthetase).";
 RL J. Bacteriol. 173:989-996(1991).
 CC -!- FUNCTION: PRODUCTION OF EXTRACELLULAR GLUCANS, THAT ARE THOUGHT
 CC TO PLAY A KEY ROLE IN THE DEVELOPMENT OF THE DENTAL PLAQUE BECAUSE
 CC OF THEIR ABILITY TO ADHERE TO SMOOTH SURFACES AND MEDIANE THE
 CC AGGREGATION OF BACTERIAL CELLS AND FOOD DEBRIS.
 CC -!- CATALYTIC ACTIVITY: Sucrose + ((1,6)-alpha-D-glucosyl) (N) = D-
 CC fructose + ((1,6)-alpha-D-glucosyl) (N+1).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MISCELLANEOUS: GTF-I SYNTHESIZES WATER-INSOLUBLE GLUCANS (ALPHA
 CC 1,3-LINKED GLUCOSE AND SOME 1,6 LINKAGES), GTF-S SYNTHESIZES
 CC WATER-SOLUBLE GLUCANS (ALPHA 1,6-GLUCOSE). GTF-SI SYNTHESIZES BOTH
 CC FORMS OF GLUCANS.
 CC -!- SIMILARITY: Belongs to family 70 of glycosyl hydrolases.
 CC -!- SIMILARITY: Contains 16 cell wall binding repeats.
 CC
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 CC
 CC EMBL; D90213; BAA14241.1; --
 CC InterPro; IPR002479; CW binding.
 CC InterPro; IPR003318; Glyco_hydro_70.
 CC Pfam; PF01473; CW binding 1; 13.
 CC Pfam; PF02324; Glyco_hydro_70; 1.
 CC Transferase; Glycosyltransferase; Signal; Repeat; Dental caries.
 KW SIGNAL
 FT CHAIN 1 38 POTENTIAL.
 FT CHAIN 39 1592 GLUCOSYLTRANSFERASE-I.
 FT DOMAIN 39 1044 CATALYTIC (APPROXIMATE).
 FT DOMAIN 1093 1592 GLUCAN-BINDING (APPROXIMATE).
 FT REPEAT 1093 1592 6.5 X TANDEM REPEATS.
 FT REPEAT 1093 1142 1.
 FT REPEAT 1158 1207 1.
 FT REPEAT 1222 1272 3.
 FT REPEAT 1287 1337 4.
 FT REPEAT 1402 1451 5.
 FT REPEAT 1514 1563 6.

FT REPEAT 1577 1592 7 (INCOMPLETE).
 SQ SEQUENCE 1592 AA; 176167 MW; BCOA66D079351ECF CRC64;
 Query Match 6.4%; Score 78; DB 1; Length 1592;
 Best Local Similarity 25.4%; Pred. No. 1.2e+02;
 Matches 48; Conservative 21; Mismatches 84; Indels 36; Gaps 8;
 QY 34 SKAITSSEKSAQDLTNTLLFKGFTGHPWVNDLLVGLSGTAATSEYEGS-SVDLYGAYY 92
 Db 28 ASALGASVASADTDTASDDSNQTVVTGQTTNNQATQTSIAATATSEQASTD--AATD 85
 QY 93 GYQCAGGTTPNKTACMYGGV-----TLHDNNRLTEKKVPINLWIDGKQTVTP 139
 Db 86 QASAAEQITGTTASTDTAAQTNNANEAKWPTENENQGTDEMLAEAKNVATAESDSIP 145
 QY 140 IDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRLIVFHSSEGSTVSVDLF 199
 Db 146 SDLAKMS-----NVKQVD-----GKYYYDDQD---GNVKNFAV---SVGDKIYY--F 185
 QY 200 DAQGYPT 208
 Db 186 DETGAYKDT 194

RESULT 57
 RLF_HUMAN
 ID -RLF_HUMAN STANDARD; PRT; 1914 AA.
 AC Q13129; Q5NU60;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Zinc finger protein RLF (Rearranged L-myc fusion gene protein) (Zn-15
 DE related protein).
 DE RLF.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96132723; PubMed=8545128;
 RA Makela T.P., Hellsten E., Vesa J., Hirvonen H., Palotie A.,
 RA Peltonen L., Altalo K.,
 RA The rearranged L-myc fusion gene (RLF) encodes a Zn-15 related zinc
 RT finger protein.";
 RL Oncogene 11:2699-2704(1995).
 RN [2]
 RP SEQUENCE OF 317-1914 FROM N.A.
 RA Donnelly S.;
 RA Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: May function as a transcription factor.
 CC -!- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -!- TISSUE SPECIFICITY: Widely expressed in fetal and adult tissues.
 CC -!- DISEASE: In some small cell lung carcinoma (SCLC) cell lines,
 CC there is an intrachromosomal rearrangements at ip32 fusing the
 CC first exon of the RLF gene with L-myc.
 CC -!- SIMILARITY: BELONGS TO THE KRUEPPEL FAMILY OF C2H2-TYPE ZINC-
 CC FINGER PROTEINS.
 CC
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 CC
 CC EMBL; U23777; AAC50396.1; --
 CC EMBL; AL050341; CAB81608.1; --
 CC Genew; HGNC:10025; RLF.
 CC MIM; 180610; --
 CC GO; GO:0003700; F:transcription factor activity; TAS.
 CC GO; GO:0008270; F:zinc ion binding; TAS.

InterPro; IPR007087; Znf C2H2.
DR PFAM; PF00096; Znf C2H2; 12.
DR SMART; SM00355; Znf C2H2; 14.
DR PROSITE; PS00028; ZINC_FINGER_C2H2_1; 14.
DR PROSITE; PS00157; ZINC_FINGER_C2H2_2; 11.
KW Transcription regulation; DNA-binding; Zinc-finger; Metal-binding;
Nuclear protein; Repeat.
FT ZN_FING 582 604 C2H2-TYPE.
FT ZN_FING 671 696 C2H2-TYPE.
FT ZN_FING 714 736 C2H2-TYPE.
FT ZN_FING 742 766 C2H2-TYPE.
FT ZN_FING 771 795 C2H2-TYPE.
FT ZN_FING 801 825 C2H2-TYPE.
FT ZN_FING 954 979 C2H2-TYPE.
FT ZN_FING 1127 1152 C2H2-TYPE.
FT ZN_FING 1172 1195 C2H2-TYPE.
FT ZN_FING 1310 1335 C2H2-TYPE.
FT ZN_FING 1352 1387 C2H2-TYPE.
FT ZN_FING 1407 1432 C2H2-TYPE.
FT ZN_FING 1444 1469 C2H2-TYPE.
FT ZN_FING 1549 1574 C2H2-TYPE.
FT CONFLICT 1546 1548 LSL -> HTQ (IN REF. 2).
SQ SEQUENCE 1914 AA; 217899 MW; 1E7529139F6528AA CRC64;

Query Match 6.4%; Score 78; DB 1; Length 1914;
Best Local Similarity 23.9%; Pred. No. 1.6e+02;
Matches 51; Conservative 31; Mismatches 55; Indels 76; Gaps 11;

QY 7 INEKLKRSKELQGTALGNLQIYYNS--KATTSSEKSAQF-----LTNTILF 54
DB 1745 VPXENFRKHSQPSFLDKTYKMPGESSFLKFIQSESEKEDFDWEPSEHLTSLNSQS 1804
QY 55 KGFTHGHPWYNDLVGLSTATSEYSGSVLDLYGAYGYOCAGGTPNKTACMYGGVTLH 114
DB 1805 SNDLTGNVANNMND-----SEPE--VDI-----PHSSS-----DSTIH 1837
QY 115 DNNRLTEKKVPINLWIDGKQTTVP-----IDKVKTSKKEVTQVELDQARHYLHGK 166
DB 1838 EN--LT-----ALPPIVAETTVPSLENLRVLDAKLTGELAKQL-----HYL---- 1882
QY 167 FGLYNSDFGGKVQRLIVFHSSEGSTVSYDLF 199
DB 1883 -----RPVVVLERSKFSTPILDLF 1901

RESULT 58
Y653 HAEIN
ID Y653 HAEIN STANDARD; PRT; 254 AA.
AC P44029;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative glycosyl transferase HI0653 (EC 2.-.-.-).
GN HI0653.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]_TaxID=727;
RP SEQUENCE FROM N.A.
RC STRAIN=rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA Kervatage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "whole-genome random sequencing and assembly of Haemophilus influenzae
rd.";

Science 269:496-512(1995).
-1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2. WAAE/KDTX
SUBFAMILY.
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CC -----
DR EMBL; U32748; AAC22312.1; -.
DR PIR; B64011; B64011.
DR TIGR; HI0653; -.
DR InterPro; IPR001173; Glyco trans. 2.
DR Pfam; PF00535; Glycos transf 2; 1.
KW Hypothetical protein; Transferase; Glycosyltransferase;
KW Complete proteome.
SQ SEQUENCE 254 AA; 29137 MW; 1F520A67EC07B149 CRC64;

Query Match 6.4%; Score 77.5; DB 1; Length 254;
Best Local Similarity 24.9%; Pred. No. 14;
Matches 48; Conservative 23; Mismatches 55; Indels 67; Gaps 12;

QY 42 KSADQFLTNTLLFKGFTGHFWNDLLV-DLGSTAATSEYSGSVLDLYGA--YGYQCAG 98
DB 11 KNEAQDLANCL-----DTVKQWVDEIIILDSGSTDNKTALSL--YGAKFYNSDWOG 61
QY 99 -GTPNKTACMYGGVTLWNNRLTEKKVPINLWIDGKQTTVP-----IDKVKTSKKEVT 151
DB 62 FGKQRLAQY-----VTSD-----YVLWLDADERTVPLQQAISAVK-NDRENT 106
QY 152 VQELDQARHYLHGKGLYNSDSFGKVGORGLIVFHSSEGSTVSYDLFQAQGYPTLLR 211
DB 107 VYBIPRV-----SEVFGREIR-----HS-----GWYPDYVVR 133
QY 212 IYRDNITTSSTSL 224
DB 134 LYRTNVAQYNDL 146

RESULT 59
Y786 CORGL
ID Y786 CORGL STANDARD; PRT; 985 AA.
AC Q8NS93;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Hypothetical UPF0182 protein Cgi0786.
GN Cgi0786.
OS Corynebacterium glutamicum (Brevibacterium flavum).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=1718;
RN [1]_TaxID=1718;
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;
RA Nakagawa S.;
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: Belongs to the UPF0182 family.
CC -----
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CC -----
DR EMBL; AP005276; BAB98179.1; -.

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DR HAMAP; MF 01600; -; 1.
DR InterPro; IPR005372; UPF0182.
DR Pfam; PF03699; UPF0182.1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 21 43 POTENTIAL.
FT TRANSMEM 58 80 POTENTIAL.
FT TRANSMEM 115 132 POTENTIAL.
FT TRANSMEM 174 196 POTENTIAL.
FT TRANSMEM 217 234 POTENTIAL.
FT TRANSMEM 263 282 POTENTIAL.
FT TRANSMEM 287 309 POTENTIAL.
SQ SEQUENCE 985 AA; 109120 MW; 022E752333CF3824 CRC64;

Query Match 6.4%; Score 77.5; DB 1; Length 985;
Best Local Similarity 20.4%; Pred. No. 76;
Matches 62; Conservative 37; Mismatches 94; Indels 111; Gaps 15;

QY 17 ELQGTALGNLKO-----IYYNSKAITSSSEXSADQFLNTLLFKGFTGHPWYNDLLV 69
DB 419 ELDPNALQQQQQDWINRHTYTHNGOFIAAQANQVDEVARDVGSTRG---GYPVYT--VS 473
QY 70 DLGASTATSEYE-----GSSVDLYGYG----- 93
DB 474 DLQSNARAASEDAEELGIKVDPRVYGLIASATGDADYAIVGTDGDPVEYDITSS 533
QY 94 --YOCAGTGP-----NKT--ACMYGGVTLHNNRLTEKKV-----PINLWIDG 133
DB 534 YTEGAGGVGIGNMVRNAMPALRYQENMMLLSDRVGSESKILPERDPRSRKVKVAPWLTT 593
QY 134 KQTTVP-ID-----KVKTSKSVTVQEL--DLQARHYLHGKFG-LY 170
DB 594 DSKTYPIVIGRIKWIIVDGVTTLDSPYSTRISLTATQDAVNDPTGQPLIDRVGYTR 653
QY 171 NS-----DSFGGKQV-----RGLIVFHSSEGSTVSVDLFDACQGYDPDLLR 211
DB 654 NSVKAVVDAYDGVTELYEFDTEDPVLKAWRGVFPDVTVDKGSSEIS-DELRAHLRYPEDLFK 712
QY 212 IYRD 215
DB 713 VQRD 716

RESULT 60
MDR_PLAFF STANDARD; PRT; 1419 AA.
AC PF3568;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Multidrug resistance protein (Chloroquine resistance protein).
GN MDR1
OS Plasmodium falciparum (isolate FC27 / Papua New Guinea).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5837;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89288297; PubMed=2701941;
RA Foote S.J., Thompson J.K., Cowman A.F., Kemp D.J.;
RT "Amplification of the multidrug resistance gene in some chloroquine-
RL resistant isolates of P. falciparum.";
RN Cell 57:921-930(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92017800; PubMed=1922044;
RA Triglia T., Foote S.J., Kemp D.J., Cowman A.F.;
RT "Amplification of the multidrug resistance gene pfmdr1 in Plasmodium
RL falciparum has arisen as multiple independent events.";
RN Mol. Cell. Biol. 11:5244-5250(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93149200; PubMed=8426608;
RA Wilson C.M., Volkman S.K., Thaitong S., Martin R.K., Kyle D.E.,
RA Milhous W.K., Wirth D.F.;

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"Amplification of pfmdr1 associated with mefloquine and halofantrine resistance in Plasmodium falciparum from Thailand."; Mol. Biochem. Parasitol. 57:151-160(1993).

-!- FUNCTION: Energy-dependent efflux pump responsible for decreased drug accumulation in multidrug-resistant cells.

-!- SUBCELLULAR LOCATION: Integral membrane protein.

-!- MISCELLANEOUS: P.falciparum resistant to the drug chloroquine have multiple copies of the gene coding for MDR.

-!- SIMILARITY: Belongs to the ABC transporter family. MDR subfamily.

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EMBL; M29154; AAA29646.1; -;
EMBL; X56851; CAA40180.1; -;
EMBL; S53996; AAD13870.1; -;
PIR; S18204; DVZQF.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABC_TM_transpt.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00664; ABC_membrane; 2.
DR Pfam; PF00005; ABC_tran; 2.
DR ProDom; PD000006; ABC_transporter; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00929; ABC_TMIF; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
KW ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat.
FT DOMAIN 1 55 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 56 82 POTENTIAL.
FT TRANSMEM 91 116 POTENTIAL.
FT TRANSMEM 160 188 POTENTIAL.
FT TRANSMEM 194 212 POTENTIAL.
FT TRANSMEM 279 298 POTENTIAL.
FT TRANSMEM 314 338 POTENTIAL.
FT TRANSMEM 339 788 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 789 807 POTENTIAL.
FT TRANSMEM 825 846 POTENTIAL.
FT TRANSMEM 908 928 POTENTIAL.
FT TRANSMEM 1028 1048 POTENTIAL.
FT TRANSMEM 1063 1083 POTENTIAL.
FT DOMAIN 1084 1419 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 643 661 POLY-ASN.
FT NP_BIND 413 420 ATP (POTENTIAL).
FT NP_BIND 1161 1168 ATP (POTENTIAL).
FT REPEAT 1 721
FT REPEAT 722 1419
FT CARBOHYD 228 258
FT CARBOHYD 258 258
FT CARBOHYD 964 964
SQ SEQUENCE 1419 AA; 162251 MW; 0F96C7C1850B33D0 CRC64;

Query Match 6.4%; Score 77.5; DB 1; Length 1419;
Best Local Similarity 21.3%; Pred. No. 1.2e+02;
Matches 47; Conservative 31; Mismatches 100; Indels 43; Gaps 8;

QY 27 KQIYYN-----SKAITSSEKSADQFLNTLLFKGFF---TGHFWYNDLLVLDGST 74
DB 1011 KADYKNGKGRRIIVNAALWGFQSQAQLFNSFAYWFGSLIKRGITLVDDEPKSLFTE 1070
QY 75 AATSEYSGSSVDLYG-----AYGYQCA-----GGTPNKTAQMYGGVTLHD 115
DB 1071 IFTGSYAGKLSLKGDSENAKLSFEKYIPLMIKRSINIDVRDDGGIRINKNLKGVDIKD 1130
QY 116 -NNRLTEKKVPI-----NLWIDGKQTTVPIDKVKTSKK---EVTQELDLQARHYL---- 163
DB 1131 VNFYISPNVPIYKNLSFTCDKSKTTAIVGETSGSGKSTFNNLLLRFYDLKNDHILKND 1190

QY 164 HGKFLYNSDFGGKVGRLVIFHSSEGSTVSYDLFDAQQ 204
 Db 1191 MTNFQYQNNNSLVKXNVNFGNSQSGSAEDYTFVFNNGE 1231

RESULT 61
 MOKC SCHPO STANDARD; PRT; 2352 AA.
 ID AC Q9UTL4; O13605;
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2004 (Rel. 43, Last annotation update)
 DE Cell wall alpha-1,3-glucan synthase mok12 (EC 2.4.1.183).
 GN MOK12 OR SPBC32H8.13C OR P1011.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxID=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=99189260; PubMed=10087262;
 RA Katayama S., Hirata D., Arellano M., Perez P., Toda T.;
 RA "Fission yeast alpha-glucan synthase Mok1 requires the actin
 RT cytoskeleton to localize the sites of growth and plays an essential
 RT role in cell morphogenesis downstream of protein kinase C function.";
 RL J. Cell Biol. 144:1173-1186 (1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=20089027; PubMed=10620777;
 RA Machida M., Yamazaki S., Kunihiro S., Tanaka T., Kuchida N., Jinno K.,
 RA Haikawa Y., Yamazaki J., Yamamoto S., Sekine M., Oguchi A., Nagai Y.,
 RA Sakai M., Aoki K., Ogura K., Kudo H., Zhang M.Q.,
 RA Yanagida M.;
 RA "A 38 kb segment containing the cdc2 gene from the left arm of fission
 RT yeast chromosome II: sequence analysis and characterization of the
 RT genomic DNA and cDNAs encoded on the segment.";
 RL Yeast 16:71-80 (2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RX MEDLINE=21848401; PubMed=11859360;
 RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,
 RA Sgouros J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,
 RA Collins M., Brown D., Brown S., Chillingworth T., Church C.M.,
 RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,
 RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,
 RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
 RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,
 RA Oliver P., O'Neil S., Pearson D., Quail M.A., Rabinowitsch E.,
 RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
 RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,
 RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
 RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,
 RA Welljens I., Vancraels E., Rieger M., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Frizc C., Holzer E., Moestl D., Hilbert H.,
 RA Bozym K., Langer I., Beck A., Leirach H., Reinhardt R., Pohl T.M.,
 RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,
 RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
 RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
 RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,
 RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
 RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Foreburg S.L.,
 RA Cerrutti L., Lowe I., McCombie W.R., Paulsen I., Potashkin J.,
 RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;
 RT "The genome sequence of Schizosaccharomyces pombe.";
 RL Nature 415:871-880 (2002).
 CC -1- CATALYTIC ACTIVITY: UDP-glucose + {alpha-D-glucosyl-(1,3)}(N) =
 CC UDP + {alpha-D-glucosyl-(1,3)}(N+1).
 CC -1- SIMILARITY: Belongs to the glycosyltransferase family 1.

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 or send an email to license@isb-sib.ch).

 EMBL; AB018381; BAA76558.1; -
 EMBL; AB004534; BAA21388.1; ALT_INIT.
 EMBL; AL590971; CAC37503.1; -
 EIR; T43431; T43431.
 GeneDB; Spombe; SPBC32H8.13C; -
 InterPro; IPR006047; Alpha_amy_cat.
 InterPro; IPR001296; Glyco_transf_1.
 Pfam; PF00128; alpha-amyliase; 1.
 Pfam; PF00534; Glycosyltransf_1; 1.
 KW Cell wall; Transferase; Glycosyltransferase.
 SQ SEQUENCE 2352 AA; 266561 MW; 78ADPFC2P7140BBA CRC64;

 Query Match 6.4%; Score 77.5; DB 1; Length 2352;
 Best Local Similarity 20.5%; Pred. No. 2.2e+02;
 Matches 60; Conservative 35; Mismatches 72; Indels 125; Gaps 15;

 4 SEINEKDLKKSELOQTALGNLKQIYYNKAITSS-----EKSADQFL 48
 769 SEEVCKDLFKR-----IG-----FNSRTLNSSPAFKILEDISICGLDQAPQEV 814

 49 TMTLLFKGFTG-----HPWYNDLLVLDGSA----- 75
 815 TNAPVTKWPFNATLDSVPNGMHELLNEVKSTNQTMQSKIALRIPEVGNENPLVYPNN 874

 76 ATSE-----YEGSSVDLYGAYGYQCAGGTPNKACMYGVTLHDNNRLTEEEKVPINLWI 131
 875 ATFSPLLYKASNGDLYVNHGT---AGADKYRSLNYGTT-----YSKW- 915

 132 DGKQTTVPIDKV-KTSKKEVTVOELD-----LQARHYLHG-----KF--- 167
 916 --KTVSTPSEKLRKPTWNGTNLQKWDGDLHLYQVWSSIALSTAHVQHGDTLNSYRQFENL 973

 168 ---GLYNSDSFGKVGKGLIVFHSSEGSTVSYDL-----FDAQGGYPD 207
 974 FVQGAENRFYDGMFPMFKM---SYNLENRTWSYDLISTWPAELVLYNWGMNPD 1023

RESULT 62
 FEN_AERPE STANDARD; PRT; 351 AA.
 ID AC Q9YFY5;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Flap structure-specific endonuclease (EC 3.1.1.1).
 DE FEN OR APE0115.
 OS Aeropyrum pernix.
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
 OC Desulfurococaceae; Aeropyrum.
 OX NCBI_TaxID=56636;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K1;
 RX MEDLINE=99310339; PubMed=10382966;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
 RA Jinno K., Takahashi M., Sekine M., Baba S.-I., Anka A., Kosugi H.,
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudo Y.,
 RA Yamazaki J., Kuchida N., Oguchi A., Aoki K.-I., Kubota K.,
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.;
 RA "Complete genome sequence of an aerobic hyper-thermophilic
 RT crenarchaeon, Aeropyrum pernix K1.";
 RL DNA Res. 6:83-101 (1999).
 CC -1- FUNCTION: Endonuclease that cleave the 5'overhanging flap

structure that is generated by displacement synthesis when DNA polymerase encounters the 5' end of a downstream Okazaki fragment. Has 5' endo-/exonuclease and 5' pseudo-Y-endonuclease activities. Cleaves the junction between single and double-stranded regions of flap DNA (By similarity).
 CC COFACTOR: Binds 2 magnesium ions per subunit (By similarity).
 CC -!- SIMILARITY: Belongs to the XPG/RAD2 endonuclease family. FEN1 subfamily.
 CC
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 CC
 CC EMBL; AP000558; BAA79026.1; ALT_INIT.
 CC HSPSP; Q58839; IA76.
 CC DR HAMAP; MF 00614; -; 1.
 CC DR InterPro; IPR008916; 5_3_exo_C.
 CC DR InterPro; IPR000513; EXO_N_I.
 CC DR InterPro; IPR006086; XPG_I.
 CC DR InterPro; IPR006085; XPG_N.
 CC DR InterPro; IPR006084; XPGC_Rad.
 CC DR Pfam; PF00867; XPG_I; 1.
 CC DR Pfam; PF00752; XPG_N; 1.
 CC DR PRINTS; PR00853; XPGRADSUPER.
 CC DR SMART; SM00279; HhH2; 1.
 CC DR SMART; SM00484; XPGI; 1.
 CC DR SMART; SM00485; XPGN; 1.
 CC DR SMART; SM00485; XPGN; 1.
 CC DR PROSITE; PS00841; XPG_1; FALSE NEG.
 CC DR HydroLase; Nuclease; Endonuclease; Magnesium; Metal-binding; Complete proteome.
 CC KW METAL 158 MAGNESIUM 1 (BY SIMILARITY).
 CC FT SEQUENCE 351 AA; 40153 MW; 28AD3B5598A5DA9 CRC64;
 CC
 CC Query Match 6.3%; Score 77; DB 1; Length 351;
 CC Best Local Similarity 21.4%; Pred. No. 23;
 CC Matches 50; Conservative 35; Mismatches 87; Indels 62; Gaps 11;
 CC
 CC QY 3 KSEINEKDLKKSELO-----GTALGNLKOIYYNSKA--ITSSEKSDQFLTNTLLPK 55
 CC Db 91 KSEVEER-LRKAEEAEARVRAVEAGEVEAEKAYMMARLITSDMVESEKLLDAM--- 146
 CC QY 56 GFTGHPWYNDLLVGLGTAATSEYEGSSVDLYGAYGYQCAGTPNKACMYGVGVLHD 115
 CC Db 147 ---GMPW-----VQPAEGEAGAAVMARKGDAWATGSDYDLSLLFGSPRLVR 190
 CC QY 116 NNRLTEKKVPIINWIDGKQTTVPIDKVKTSKEVTVQSLDQARHYLHGKGL----- 169
 CC Db 191 NLAITGRKKLP-----GRQYVEI-----KPEI-----LUSKLGITREQLI 231
 CC QY 170 -----YNSDSFGKVGQRLVPHFSSEGSTVSVDLFDAGQY-PDTLLRIY 213
 CC Db 232 AVGILLGTDYNGPGVGRVGYGKPTALRLVLSGLDPMKVLASVPRGEYDPDYLKRVY 285
 CC
 CC RESULT 63
 CC MSN2 YEAST STANDARD; PRT; 704 AA.
 CC ID MSN2 YEAST
 CC AC P33748;
 CC DT 01-FEB-1994 (Rel. 28, Created)
 CC DT 01-FEB-1994 (Rel. 28, Last sequence update)
 CC DT 10-OCT-2003 (Rel. 42, Last annotation update)
 CC DE Zinc finger protein MSN2 (Multicopy suppressor of SNF1 protein 2).
 CC GN MSN2 OR YMR037C OR YM9532.02C.
 CC OS Saccharomyces cerevisiae (Baker's yeast).
 CC OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 CC OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 CC NCBI_TaxID=4932;
 CC RN [1]
 CC SEQUENCE FROM N.A.

RC STRAIN=S288c;
 RX MEDLINE=93309420; PubMed=8321194;
 RT Estruch F., Carlson M.;
 RT "Two homologous zinc finger genes identified by multicopy suppression in a SNF1 protein kinase mutant of *Saccharomyces cerevisiae*.";
 RT Mol. Cell. Biol. 13:3872-3881(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RX MEDLINE=97313268; PubMed=9169872;
 RA Bowman S., Churche C.M., Badcock K., Brown D., Chillingworth T., Connor R., Dedman K., Devlin K., Gentles S., Hamlin N., Hunt S., Jagals K., Lye G., Moule S., Odell C., Pearson D., Rajandream M.A., Rice P., Skelton J., Walsh S., Whitehead S., Bartell B.G.;
 RA "The nucleotide sequence of *Saccharomyces cerevisiae* chromosome XIII.";
 RT Nature 387:90-93(1997).
 RL [3]
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=96208509; PubMed=8641288;
 RA Martinez-Pastor M.T., Marchler G., Schueller C., Marchler-Bauer A., Ruiz H., Estruch F.;
 RA "The *Saccharomyces cerevisiae* zinc finger proteins Men2p and Msn4p are required for transcriptional induction through the stress response element (STRE).";
 RT EMBO J. 15:2227-2235(1996).
 RN [4]
 RP NUCLEOCYTOPLASMIC SHUTTLING.
 RX MEDLINE=22628141; PubMed=12732613;
 RA Jaquet M., Renault G., Lallet S., De Mey J., Goldbeter A.;
 RA "Oscillatory nucleocytoplasmic shuttling of the general stress response transcriptional activators Msn2 and Msn4 in *Saccharomyces cerevisiae*.";
 RT J. Cell Biol. 161:497-505(2003).
 RL [5]
 CC -!- FUNCTION: POSITIVE TRANSCRIPTIONAL FACTOR THAT ACTS AS A COMPONENT OF THE STRESS RESPONSIVE SYSTEM. RECOGNIZES AND BINDS TO THE STRESS RESPONSE ELEMENT (STRE) WHICH IS INVOLVED IN THE RESPONSE TO VARIOUS FORMS OF STRESS (HEAT, OXIDATIVE, OSMOTIC, ETC.). INVOLVED IN THE REGULATION OF THE CTT1, DDR2, HSP12 GENES.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic and nuclear.
 CC -!- SIMILARITY: Contains 2 C2H2-type zinc fingers.
 CC
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 CC
 CC EMBL; L08838; AAA34806.1; -;
 CC EMBL; Z48502; CAA88403.1; -;
 CC PIR; S39004; S39004.
 CC HSPSP; P08047; 1SP1.
 CC GeneOnline; 142706; -;
 CC TRANSFAC; T01257; -;
 CC SGD; S0004640; MSN2.
 CC GO; GO:0005829; Cytoplasm; IDA.
 CC GO; GO:0005634; Nucleus; IDA.
 CC GO; GO:0006950; P:response to stress; IMP.
 CC InterPro; IPR007087; Znf_C2H2.
 CC Pfam; PF00096; zf-C2H2; 2.
 CC ProDom; PD000003; Znf_C2H2; 1.
 CC SMART; SM00355; Znf_C2H2; 2.
 CC PROSITE; PS00028; ZINC_FINGER_C2H2_1; 2.
 CC PROSITE; PS01517; ZINC_FINGER_C2H2_2; 2.
 CC DNA-binding; Nuclear protein; Zinc-finger; Metal-binding; Activator; Transcription regulation; Repeat.
 CC DOMAIN 1 109 ASP-RICH (ACIDIC).
 CC FT DOMAIN 260 279 ASP-RICH (ACIDIC).
 CC FT ZN_FING 647 665 C2H2-TYPE 1.
 CC FT ZN_FING 676 698 C2H2-TYPE 2.
 CC SEQUENCE 704 AA; 77860 MW; EDF6F07446819DF1 CRC64;

[illegible]

CC -----
DR EMBL; X68366; CAA48426.1; -.

```

DR PIR; S30302; S26437.
KW Hypothetical protein; Plasmid.
SQ SEQUENCE 284 AA; 33212 MW; 0E48AC80241417FE CRC64;

Query Match
Best Local Similarity 24.8%; Pred. No. 20; Length 284;
Matches 35; Conservative 22; Mismatches 43; Indels 41; Gaps 8;

Qy 25 NLKQIYYI-NSKAITSEKSAQDELNTLLFKGFF---TGHWPYNLLVDLSTATSEY 80
Db 114 NLQRMVYHLSNVISKWPSSGDMC-----FPDPKTGS-----VDWGELASFLDL 157

Qy 81 EGSSVDLYGAYGYQCAGGTGPNK-----TACMYGGVTLHDNNRLTEKKVPINLWID-- 132
Db 158 GGSQVDL-NEFNIRINSNEVDKDNVLVQVADFAGLSVFSKEL-----GLYVDWK 208

Qy 133 ---GKQTTVPIDKVKTSKKE 149
Db 209 FEKGGQQLVPEVKIDLSKXD 229

RESULT 66
YQPI CAEEL STANDARD; PRT; 428 AA.
AC Q09302;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 48.3 kDa protein F07F6.1 in chromosome III.
GN F07F6.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2.
RA Chisoe S.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
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CC
CC EMBL; U23486; AAC46775.1; -.
DR PIR; T15966; T15966.
DR Wormpep; F07F6.1; CE01894.
KW Hypothetical protein.
FT DOMAIN 9 13 POLY-SER.
FT DOMAIN 121 124 POLY-VAL.
FT DOMAIN 283 286 POLY-SER.
SQ SEQUENCE 428 AA; 48267 MW; 69A6A2AF86D5E2C CRC64;

Query Match
Best Local Similarity 26.7%; Pred. No. 33; Length 428;
Matches 43; Conservative 16; Mismatches 63; Indels 39; Gaps 7;

Qy 93 GYCAGTGNKTCMYGGVTLHDNNRLTE-----EKK-----VPINLWID 133
Db 148 GYSYRGHILAVRFC-YPDGTYGDESALTQLVQCTNSAKGRILEKDDIVQDTFAVECW--- 203

Qy 134 KQTTPIDKVKTSKKEVQVQELDLQARHYLHGKFGLYN-SDSGGKVGQGLIVFHSSEGS 192
Db 204 --TKTFEDSLKVEKELTNL--LKAHAYLPYHTVLQSMRNLFCTCKVQSEL----- 249

Qy 193 TVSVLDPAQGVDPDTLLRIYRNTTISSTLSISLYTT 233
Db 250 -SSMFIISDALAQWPTGLIRIFNRNVKVSNTMCLSSSSYYT 289

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RESULT 67
NUCD SALTY STANDARD; PRT; 600 AA.
ID NUCD SALTY STANDARD; PRT; 600 AA.
AC P33902;
DT 01-FEB-1994 (Rel. 28, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE NADH-quinone oxidoreductase chain C/D (EC 1.6.99.5) (NADH
DE dehydrogenase I, chain C/D) (NDH-1, chain C/D).
DE NUOC OR NUOCD OR NUOD OR STM2326 OR STY2556 OR T0538.
OS Salmonella typhimurium, and
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=602, 601;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
RC MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E.; Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA Waterston R., Wilson R.K.;
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT LT2."
RL Nature 413:852-856(2001).
RN [2]
RP SEQUENCE OF 520-600 FROM N.A.
RC SPECIES=S.typhimurium;
RC MEDLINE=94052195; PubMed=8234329;
RA Archer C.D., Wang X., Elliott T.;
RT "Mutants defective in the energy-conserving NADH dehydrogenase of
RT Salmonella typhimurium identified by a decrease in energy-dependent
RT proteolysis after carbon starvation."
RL Proc. Natl. Acad. Sci. U.S.A. 90:9877-9881(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=CT18;
RC MEDLINE=21534947; PubMed=11677608;
RA Parkhill J., Dougan G., James K.B., Thomson N.R., Pickard D., Wain J.,
RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin P., Haque A., Hien T.T., Holtroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrall B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
RC MEDLINE=22531367; PubMed=12644504;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18."
RL J. Bacteriol. 185:2330-2337(2003).
CC -!- FUNCTION: Ndh-1 shuttles electrons from NADH, via FMN and iron-
CC sulfur (Fe-S) centers, to quinones in the respiratory chain. The
CC immediate electron acceptor for the enzyme in this species is
CC believed to be ubiquinone. Couples the redox reaction to proton
CC translocation (for every two electrons transferred, four hydrogen
CC ions are translocated across the cytoplasmic membrane), and thus
CC conserves the redox energy in a proton gradient (By similarity).
CC -!- CATALYTIC ACTIVITY: NADH + quinone = NAD(+) + quinol.
CC -!- SUBUNIT: Composed of 13 different subunits. Subunits nuoCD, E, F,
CC and G constitute the peripheral sector of the complex.
CC -!- SIMILARITY: In the N-terminal section; belongs to the complex I 30
CC kDa subunit family.

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CC -!- SIMILARITY: In the C-terminal section; belongs to the complex I 49
 CC kDa subunit family.
 CC -----
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 CC -----
 CC EMBL; AB015885; BAA88798.1; -
 CC InterPro; IPR001410; DEAD.
 CC InterPro; IPR002464; DEAH box.
 CC InterPro; IPR001650; Helicase C.
 CC Pfam; PF00271; Helicase C; 1.
 CC SMART; SM00487; DEXDC; 1.
 CC PROSITE; PS00690; DEAD_ATP_HELICASE; 1.
 CC KX Helicase; Transcription regulation; Activator; ATP-binding.
 CC NP BIND 45 52 ATP (POTENTIAL).
 CC SITE 135 138 DEXH BOX.
 CC SQ SEQUENCE 635 AA; 73289 MW; BFD459B5A1D1854 CRC64;
 CC
 CC Query Match 6.3%; Score 76.5; DB 1; Length 635;
 CC Best Local Similarity 21.5%; Pred. No. 54;
 CC Matches 55; Conservative 39; Mismatches 101; Indels 61; Gaps 11;
 CC
 CC 6 EINEKD---LRK-----KSELQGTALGNLKOIYYNSKAITSSSEKSDQF---LTNT 51
 CC 252 KLQEKDYNNVVKLCNNEMFEKNNVSLAVLGQLNFINNLDILFQEQDKELYPNLKISNG 311
 CC
 CC 52 LLFKGFTGHPWNLVLDLSTAAATSEYEGSSVDLYG---AYGQCAGGTENKACMY 108
 CC 312 IL-----YGEDELTTLNISKFKYFIKTSITGKQFIYFSNSTYGLIIRKIMLS 361
 CC
 CC 109 GGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDKVTSEKVTVOELDLQARHYLHGKFG 168
 CC 362 NGIYSENGSQTPK-----LINGKPTFAI---VTSKMKSSLEDL-----LN 401
 CC
 CC 169 LYNDSFGGKVGRLIVFHSSEGSTVSVDLF-----DAQGYPTLLRIYDNT 217
 CC 402 VYNSQL--NKDGSQIMFLPSSNIMSESYTLKEVNIWFMPTIPDTFSQYNIQLGERSIR-KF 458
 CC
 CC 218 TISSTSLISLYLYTT 233
 CC 459 SYFDISKPVNLYLAT 474
 CC
 CC RESULT 69
 CC RPAL SCHPO STANDARD; PRT; 1689 AA.
 CC ID RPAL SCHPO STANDARD; PRT; 1689 AA.
 CC AC P15398;
 CC DT 01-APR-1990 (Rel. 14, Created)
 CC DT 15-JUL-1998 (Rel. 36, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE DNA-directed RNA polymerase I 190 kDa polypeptide (EC 2.7.7.6).
 CC GN RPAL OR NUC1 OR SPBC4C3.05C.
 CC OS Schizosaccharomyces pombe (Fission yeast).
 CC OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 CC OC Schizosaccharomycetes.
 CC OX NCBI_TaxID=4896;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RA MEDLINE=89139548; PubMed=2537310;
 CC RA Hirano T., Konoha G., Toda T., Yanagida M.;
 CC RT "Essential roles of the RNA polymerase I largest subunit and DNA
 CC RT topoisomerases in the formation of fission yeast nucleolus";
 CC RL J. Cell Biol. 108:243-253 (1989).
 CC RN [2]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=972 / HMI23;
 CC RX MEDLINE=89232741; PubMed=2854522;
 CC RA Yanagishi M., Nomura M.;
 CC RT "Cloning and sequence determination of the gene encoding the largest

CC -!- SIMILARITY: In the C-terminal section; belongs to the complex I 49
 CC kDa subunit family.
 CC -----
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 CC -----
 CC EMBL; AB015885; BAA88798.1; -
 CC InterPro; IPR001410; DEAD.
 CC InterPro; IPR002464; DEAH box.
 CC InterPro; IPR001650; Helicase C.
 CC Pfam; PF00271; Helicase C; 1.
 CC SMART; SM00487; DEXDC; 1.
 CC PROSITE; PS00690; DEAD_ATP_HELICASE; 1.
 CC KX Helicase; Transcription regulation; Activator; ATP-binding.
 CC NP BIND 45 52 ATP (POTENTIAL).
 CC SITE 135 138 DEXH BOX.
 CC SQ SEQUENCE 635 AA; 73289 MW; BFD459B5A1D1854 CRC64;
 CC
 CC Query Match 6.3%; Score 76.5; DB 1; Length 635;
 CC Best Local Similarity 21.5%; Pred. No. 54;
 CC Matches 55; Conservative 39; Mismatches 101; Indels 61; Gaps 11;
 CC
 CC 6 EINEKD---LRK-----KSELQGTALGNLKOIYYNSKAITSSSEKSDQF---LTNT 51
 CC 252 KLQEKDYNNVVKLCNNEMFEKNNVSLAVLGQLNFINNLDILFQEQDKELYPNLKISNG 311
 CC
 CC 52 LLFKGFTGHPWNLVLDLSTAAATSEYEGSSVDLYG---AYGQCAGGTENKACMY 108
 CC 312 IL-----YGEDELTTLNISKFKYFIKTSITGKQFIYFSNSTYGLIIRKIMLS 361
 CC
 CC 109 GGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDKVTSEKVTVOELDLQARHYLHGKFG 168
 CC 362 NGIYSENGSQTPK-----LINGKPTFAI---VTSKMKSSLEDL-----LN 401
 CC
 CC 169 LYNDSFGGKVGRLIVFHSSEGSTVSVDLF-----DAQGYPTLLRIYDNT 217
 CC 402 VYNSQL--NKDGSQIMFLPSSNIMSESYTLKEVNIWFMPTIPDTFSQYNIQLGERSIR-KF 458
 CC
 CC 218 TISSTSLISLYLYTT 233
 CC 459 SYFDISKPVNLYLAT 474
 CC
 CC RESULT 69
 CC RPAL SCHPO STANDARD; PRT; 1689 AA.
 CC ID RPAL SCHPO STANDARD; PRT; 1689 AA.
 CC AC P15398;
 CC DT 01-APR-1990 (Rel. 14, Created)
 CC DT 15-JUL-1998 (Rel. 36, Last sequence update)
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
 CC DE DNA-directed RNA polymerase I 190 kDa polypeptide (EC 2.7.7.6).
 CC GN RPAL OR NUC1 OR SPBC4C3.05C.
 CC OS Schizosaccharomyces pombe (Fission yeast).
 CC OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 CC OC Schizosaccharomycetes.
 CC OX NCBI_TaxID=4896;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RA MEDLINE=89139548; PubMed=2537310;
 CC RA Hirano T., Konoha G., Toda T., Yanagida M.;
 CC RT "Essential roles of the RNA polymerase I largest subunit and DNA
 CC RT topoisomerases in the formation of fission yeast nucleolus";
 CC RL J. Cell Biol. 108:243-253 (1989).
 CC RN [2]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=972 / HMI23;
 CC RX MEDLINE=89232741; PubMed=2854522;
 CC RA Yanagishi M., Nomura M.;
 CC RT "Cloning and sequence determination of the gene encoding the largest

DR PROSITE; PS00174; P. GLUCOSE ISOMERASE 2; 1.
 KW Isomerase; Gluconeogenesis; Glycolysis.
 FT ACT SITE 312 BY SIMILARITY.
 FT ACT SITE 426 BY SIMILARITY.
 SQ SEQUENCE 449 AA; 49814 MW; 996D637623C6C72F CRC64;

Query Match 6.2%; Score 76; DB 1; Length 449;
 Best Local Similarity 23.3%; Pred. No. 39;
 Matches 50; Conservative 31; Mismatches 74; Indels 60; Gaps 12;

QY 32 YNSKAITSSSEKSDAQFLNTLLFKGFTGHPWYNDLLVDLGLGTAATSEYEGSSVDLYGAY 91
 DB 241 YSSSKISENEAYQAAARNILYRGY-----TTEILANYEPLS--QYFAE 283
 QY 92 YGYQCAGTGNK-----TACMYGGVTLHNNRLTBEKKVPINLWDGKQTTPIDKVK 144
 DB 284 WVKQLAGESEKDGQGIYPTISANF--STDLHSLGQFIOEG--TRNLF-----ETVVRVDK-- 334
 QY 145 TSKEVTQVEL--DLQARHYLHGKFLYNSDSFGKQVQGLIVFHSSEGSTVSVDLFDQAQ 202
 DB 335 -PRKNVPIPEAEDELGLGLOK-----DVFVNKATDGLLAHT-----D 376
 QY 203 GQYPTDILLRI-YRDNMTIS-----STLSISLYL 230
 DB 377 GDVENMFTIPEQDAFTGLVYIYFFELAIASGLYL 411

RESULT 73
 YF08 MYCPN STANDARD; PRT; 509 AA.
 AC P75278;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MPN508 (P02_orf509).
 GN MPN508 OR MP334.
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29342 / M129;
 RX MEDLINE=97105885; PubMed=9948633;
 RA Himmelreich R., Hilbert H., Plagens H., Pirkel E., Li B.-C.,
 RA Herrmann R.
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae".
 RT Nucleic Acids. Res. 24:4420-4449 (1996).
 CC -!- SIMILARITY: BELONGS TO THE MG032 / MG096 / MG288 FAMILY.
 CC
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 CC
 CC EMBL; AE000031; AAB95982.1; -.
 DR PIR; S73660; S73660.
 DR InterPro; IPR004306; MG032/096/288.1.
 DR InterPro; IPR004319; MG032/096/288-2.
 DR Pfam; PF03072; DUF237; 1.
 DR Pfam; PF03086; DUF240; 1.
 DR ProDom; PD004834; MG032/096/288.2; 1.
 DR Hypothetical protein; Complete proteome.
 SQ SEQUENCE 509 AA; 57625 MW; 8CDC95BB94A6987 CRC64;

Query Match 6.2%; Score 76; DB 1; Length 509;
 Best Local Similarity 22.7%; Pred. No. 45;
 Matches 54; Conservative 35; Mismatches 97; Indels 52; Gaps 13;

QY 3 KSEINEKDLRKSELQGTALGNLKKQIYYNSKAITSSEK-----SADQFLNTLL 52

DB 234 KAEYVKLEAREAFNKSLSLTAASEFKQYWSKKKNDVTDKKQALAKLSLEADNRRTSF 293
 QY 53 LFKGFTGHPWY-----NDLLVD-LGSTAATSEYEGSSVDLYGAYGYQCAGTGNKT 104
 DB 294 LIAGFRTAIDWYNACKENNDKAKFGSQGIQPKDG-----LNGIYMPDWLRLGSLTSKS 349
 QY 105 ACMYGGVTLHNNRLTBEKV-----PINLWDGKQTTPIDKVKSKKEVTQVELDLQ 158
 DB 350 -----NINLIKELKVKQNKIESPTINWDG--VGIKODKANPNFYAFEV-DIKYT 396
 QY 159 ARHYLHGKF---GLVNS--DSFGKQVQGLIVFHSSEGSTVSVDLFDQAQGYPTDILLR 211
 DB 397 GGYQLYGYFAAALFTKFPSSWSGEMNLKFIV---DGSIPVYTV--AKKDYPSLFLQ 448

RESULT 74
 PBP STAAU STANDARD; PRT; 670 AA.
 AC P07344;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 01-NOV-1990 (Rel. 16, Last annotation update)
 DE Beta-lactam-inducible penicillin-binding protein.
 GN PBP.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87304805; PubMed=3305073;
 RA Song M.D., Wachi M., Doi M., Ishino F., Matsushashi M.;
 RT "Evolution of an inducible penicillin-target protein in methicillin-resistant Staphylococcus aureus by gene fusion."
 RL FEBS Lett. 221:167-171 (1987).
 CC -!- INDUCTION: IN THE PRESENCE OF BETA-LACTAM ANTIBIOTICS, MRSA CELLS PRODUCE THIS UNIQUE PBP IN EXCESSIVELY LARGE AMOUNTS AND CAN STILL PROLIFERATE, WHILE ALL THE NORMAL PBPS ARE INACTIVATED (REVERSIBLE SWITCHING ABILITY OF PBP FORMATION).
 CC -!- MISCELLANEOUS: PBP HAS EXTREMELY LOW AFFINITY TO PENICILLIN AND MOST OTHER BETA-LACTAM ANTIBIOTICS
 CC -!- SIMILARITY: TWO DIFFERENT SETS OF CONSERVED SEQUENCES CONTAINING S-X-X-K FOR PENICILLIN-BINDING WERE FOUND IN MRSA PBP, THE FIRST BEING LOCATED AROUND SER-25 (HOMOLOGY WITH THE PENICILLIN-BINDING DOMAIN OF THE PENICILLINASE) AND THE SECOND AROUND SER-405 (HIGH HOMOLOGY WITH BOTH THE PUTATIVE TRANSGLYCOSYLASE (N-TERMINAL) AND TRANSPEPTIDASE (C-TERMINAL) PENICILLIN-BINDING DOMAIN OF E. COLI PBPS 2 AND 3). THE AUTHORS SUGGEST THE SER-405 RESIDUE TO BE THE PENICILLIN-BINDING SITE AND THE SEQUENCE AROUND SER-25 TO BE A RELIC OF THE EVOLUTION OF THIS DOMAIN FROM A PENICILLINASE GENE.
 CC
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 CC
 CC EMBL; Y00688; CAA68684.1; -.
 DR MEROPS; S12 UNW; -.
 DR InterPro; IPR007887; Meca.N.
 DR InterPro; IPR005311; PBP_dimer.
 DR InterPro; IPR001460; Transpeptidase.
 DR Pfam; PF05223; Meca.N; 1.
 DR Pfam; PF03717; PBP_dimer; 1.
 DR Pfam; PF00905; Transpeptidase; 1.
 DR Peptidoglycan synthesis; Cell division; Antibiotic resistance; Cell wall.
 KW BINDING 25 25 PENICILLIN (PROBABLE).
 FT BINDING 405 405 PENICILLIN (PROBABLE).
 FT SEQUENCE 670 AA; 76463 MW; 2DAA414D35DA993A CRC64;

Query Match 6.2%; Score 76; DB 1; Length 670;
 Best Local Similarity 26.4%; Pred. No. 64;
 Matches 33; Conservative 19; Mismatches 41; Indels 32; Caps 6;
 QY 64 YNDLLVLDGTAATSEYEGS-----SVDLYGAYGYOCAGTGNKTYACMYGGVTLHD 115
 Db 339 YNNKNDYGGGTGTAHPGTGELLALVSTPSYDVTFMY-----GMSNEE 381
 QY 116 NNRLTEKKVP-INLWIDGKQTTVP--IDKVKTSKKEVTQELDLQARHYLHGKFGLYNS 172
 Db 382 YNKLTEDKKEPLNKF---QITTSFGSTQKILTAMIGLNNKTLDDKTSYKIDGK-GWQXD 437
 QY 173 DSFGG 177
 Db 438 KSWG 442

RESULT 75
 NEUL_HUMAN STANDARD; PRT; 704 AA.
 ID NEUL_HUMAN Q95YU8; Q9ULJ4;
 AC 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE Neurolysin, mitochondrial precursor (EC 3.4.24.16) (Neurotensin
 endopeptidase) (Mitochondrial oligopeptidase M) (Microsomal
 endopeptidase) (NEP).
 GN NLN OR KIAA1226.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chen J.M., Rawlings N.D., Barrett A.J.;
 RT "Cloning and sequencing of human neurolysin, an oligopeptidase of
 family M3";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=20033619; PubMed=10574462;
 RA Nagase T., Ishikawa K.-I., Kikuno R., Hirose M., Nomura N.,
 RA Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. XV.
 for large proteins in vitro";
 RL DNA Res. 6:337-345(1999).
 CC -!- FUNCTION: Hydrolyzes oligopeptides such as neurotensin,
 bradykinin, dynorphin A, etc. (By similarity).
 CC -!- CATALYTIC ACTIVITY: Preferential cleavage in neurotensin: 10-
 Pro-|-Tyr-11.
 CC -!- COPACITOR: Binds 1 zinc ion per subunit (By similarity).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial intermembrane space and
 also cytoplasmic (By similarity).
 CC -!- SIMILARITY: Belongs to peptidase family M3.
 CC
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 or send an email to license@ebi.ac.uk).
 CC
 CC EMBL; AJ300837; CAC27329.1; --
 CC EMBL; AB033052; BAA86540.2; --
 CC Genbank; HGNC:16058; NLN.
 CC InterPro; IPR006025; Peptidase M3.
 CC InterPro; IPR001567; Peptidase M3.
 CC Pfam; PF01432; Peptidase M3; 1.
 CC PROSITE; PS00142; ZINC PROTEASE; 1.
 CC Metalloprotease; Hydrolase; Zinc; Mitochondrion; Transit peptide.

FT TRANSIT 1 37 MITOCHONDRION (BY SIMILARITY).
 FT CHAIN 38 704 NEUTROLYSIN.
 FT METAL 497 498 ZINC (CATALYTIC) (BY SIMILARITY).
 FT ACT SITE 498 499 BY SIMILARITY.
 FT METAL 501 501 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 504 504 ZINC (CATALYTIC) (BY SIMILARITY).
 SQ SEQUENCE 704 AA; 80651 NW; 80136688D79BBEDF CRC64;
 Query Match 6.2%; Score 76; DB 1; Length 704;
 Best Local Similarity 22.0%; Pred. No. 68;
 Matches 61; Conservative 32; Mismatches 92; Indels 92; Gaps 16;
 QY 1 SEKSEINEKD-----LRKKS-----ELQGTALGNLKOIYYVNSKAITSEK---SAD 45
 Db 323 SQKLPGLGEAREFNLNKKCKDRGFYDGKI--NAWDLYYY---MTQTEELKYSID 376
 QY 46 Q-----FLTNT-----LLPKGFFTHPWYNDLLVDLSTAAATSEYEGS-S 84
 Db 377 QEFLEKYEPIEVVTRGLLNTYQELLGLSFEQMTDAHVWVNSVTLYTVKDKATGEVLGQFY 436
 QY 85 VDIY---GAYGYQCAGTGNKTCMYGGVTLHNNRLTEKKVPEINLW--IDGKQTTVP 139
 Db 437 LDLYPREGKYNHACFGLOP-----GCLLPDGSRWMAVALVNFSPQVAGRPSSLR 488
 QY 140 IDKVKTSKKEVTQVELDLQARHYLHGKFGLYNSDSFGGKQVQ--GLIVFHSSEGSTVSVD 197
 Db 489 HDEVT-----YFH-----EFGHVMHQICAQTDFAFPSTGNTVETD 523
 QY 198 LFDAGQY-----PDILLRI---YRNTTISSTSL 224
 Db 524 FVEVPSQMLENWMVWDVDSLRLSKHYKDGSPIDADLL 560
 Search completed: August 12, 2004, 13:30:31
 Job time : 10.1186 secs



GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 12, 2004, 13:23:20 ; Search time 20.2698 Seconds
(without alignments)
3626.866 Million cell updates/sec

Title: US-09-900-766-2

Perfect score: 1218

Sequence: 1 SEKSEENKDLKKSELOG.....RDNTTISSTLSLSLYLYTT 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

SPTREMBL 25:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_plage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_ivirus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	948	77.8	260	16 Q931M4	Q931M4 staphylococ
2	918	75.4	260	16 Q99SU3	Q99SU3 staphylococ
3	754	61.9	268	2 O85217	O85217 staphylococ
4	438.5	36.0	229	16 Q8NM97	Q8NM97 staphylococ
5	420.5	34.5	258	16 Q9EZM4	Q9EZM4 staphylococ
6	372.5	30.6	260	16 Q99T46	Q99T46 staphylococ
7	372.5	30.6	261	2 Q9EZM8	Q9EZM8 staphylococ
8	355	29.1	179	2 Q52075	Q52075 staphylococ
9	311	25.5	240	16 Q9F0L7	Q9F0L7 staphylococ
10	310	25.5	240	16 Q8NXJ5	Q8NXJ5 staphylococ
11	308	25.3	217	2 Q8RR76	Q8RR76 staphylococ
12	308	25.3	241	16 Q53585	Q53585 staphylococ
13	296.5	24.3	242	16 Q85383	Q85383 staphylococ
14	294.5	24.2	225	2 Q8VVM1	Q8VVM1 streptococ
15	293.5	24.1	225	2 Q91921	Q91921 streptococ
16	288.5	23.7	218	2 Q8RR75	Q8RR75 staphylococ

17	288.5	23.7	239	2	O05157	O05157 staphylococ
18	287.5	23.6	225	16	Q99Z21	Q99Z21 streptococ
19	287.5	23.6	239	2	O06535	O06535 staphylococ
20	284.5	23.4	239	2	O06531	O06531 staphylococ
21	284	23.3	239	2	Q9EZM7	Q9EZM7 staphylococ
22	282	23.2	239	16	Q99T47	Q99T47 staphylococ
23	278.5	22.9	242	16	Q8NMV3	Q8NMV3 staphylococ
24	278.5	22.9	256	2	Q8VLM7	Q8VLM7 staphylococ
25	278.5	22.9	266	16	Q8NXJ6	Q8NXJ6 staphylococ
26	277.5	22.8	239	2	O06533	O06533 staphylococ
27	277.5	22.8	239	2	O06533	O06533 staphylococ
28	276.5	22.7	234	2	Q9RSX4	Q9RSX4 staphylococ
29	276.5	22.7	242	2	Q93CC6	Q93CC6 staphylococ
30	275.5	22.6	207	2	Q7X0E8	Q7X0E8 staphylococ
31	271.5	22.3	218	2	Q7X0E7	Q7X0E7 staphylococ
32	270.5	22.2	218	2	Q7X0E9	Q7X0E9 staphylococ
33	268.5	22.0	251	16	Q8K6K5	Q8K6K5 streptococ
34	265.5	21.8	271	2	Q9F0L6	Q9F0L6 staphylococ
35	264.5	21.7	239	2	Q7X0E6	Q7X0E6 staphylococ
36	264.5	21.7	239	2	Q53678	Q53678 staphylococ
37	264	21.7	242	16	Q8NMV2	Q8NMV2 staphylococ
38	263	21.6	242	2	Q93CC5	Q93CC5 staphylococ
39	263	21.6	242	2	O54476	O54476 staphylococ
40	258.5	21.2	239	2	O06534	O06534 staphylococ
41	254.5	20.9	236	2	P97163	P97163 streptococ
42	253.5	20.8	236	2	Q54779	Q54779 streptococ
43	252.5	20.7	222	2	Q9R931	Q9R931 streptococ
44	251.5	20.6	236	2	Q54696	Q54696 streptococ
45	251	20.6	260	2	Q54738	Q54738 streptococ
46	251	20.6	260	2	Q54971	Q54971 streptococ
47	251	20.6	260	16	Q54739	Q54739 streptococ
48	250	20.5	222	2	Q9S5Z4	Q9S5Z4 streptococ
49	250	20.5	222	2	Q938P4	Q938P4 streptococ
50	249	20.4	258	2	Q92NF2	Q92NF2 staphylococ
51	248.5	20.4	236	2	Q57453	Q57453 streptococ
52	241	19.8	233	2	Q8RR77	Q8RR77 staphylococ
53	241	19.8	258	2	Q9EZM3	Q9EZM3 staphylococ
54	238.5	19.6	259	2	Q936G4	Q936G4 staphylococ
55	222	18.2	209	2	Q9RQJ5	Q9RQJ5 streptococ
56	219	18.0	209	2	Q9LAE0	Q9LAE0 streptococ
57	219	18.0	209	2	Q9LAD8	Q9LAD8 streptococ
58	217	17.8	209	2	Q9LAC6	Q9LAC6 streptococ
59	217	17.8	209	2	Q9LAD1	Q9LAD1 streptococ
60	215	17.7	209	2	Q9LAE1	Q9LAE1 streptococ
61	215	17.7	209	2	Q9LAC4	Q9LAC4 streptococ
62	213	17.5	209	2	Q9LAC5	Q9LAC5 streptococ
63	211	17.3	209	2	Q9LAD9	Q9LAD9 streptococ
64	210	17.2	209	2	Q9LAD2	Q9LAD2 streptococ
65	210	17.2	209	2	Q9LAD6	Q9LAD6 streptococ
66	209.5	17.2	233	16	Q8NZ89	Q8NZ89 streptococ
67	209	17.2	207	2	Q7WY99	Q7WY99 streptococ
68	207	17.0	209	2	Q9LAC9	Q9LAC9 streptococ
69	206	16.9	209	2	Q9LAC7	Q9LAC7 streptococ
70	206	16.9	209	2	Q9LAD4	Q9LAD4 streptococ
71	205	16.8	209	2	Q9LAC8	Q9LAC8 streptococ
72	205	16.8	209	2	Q9LAC3	Q9LAC3 streptococ
73	204.5	16.8	256	2	Q9SIH8	Q9SIH8 streptococ
74	203	16.7	209	2	Q9LAD5	Q9LAD5 streptococ
75	201	16.5	209	2	Q9LAD3	Q9LAD3 streptococ
76	200	16.4	209	2	Q9LAD7	Q9LAD7 streptococ
77	198.5	16.3	233	16	Q99XW1	Q99XW1 streptococ
78	198	16.3	209	2	Q9LAD0	Q9LAD0 streptococ
79	190	15.6	136	16	Q99T49	Q99T49 staphylococ
80	187	15.4	236	2	Q9L920	Q9L920 streptococ
81	186.5	15.3	234	16	Q8K8Q7	Q8K8Q7 streptococ
82	184	15.1	240	16	Q8P2R5	Q8P2R5 streptococ
83	182.5	15.0	210	2	Q9K2G9	Q9K2G9 streptococ
84	178	14.6	157	16	Q99TP7	Q99TP7 staphylococ
85	160	13.1	232	16	Q99QN1	Q99QN1 streptococ
86	156	12.8	234	2	Q53RR9	Q53RR9 streptococ
87	156	12.8	234	2	Q8G9K7	Q8G9K7 streptococ
88	153.5	12.6	108	2	Q9EZM5	Q9EZM5 staphylococ
89	153.5	12.6	235	16	Q8NKK2	Q8NKK2 streptococ

90 153.5 12.6 256 2 Q9XR8 streptococc
 91 153.5 12.6 256 2 Q9SR8 streptococc
 92 143 11.7 206 2 Q54512 streptococc
 93 138.5 11.4 167 2 Q7X0E4 staphylococc
 94 130.5 10.7 167 2 Q7X0E5 staphylococc
 95 125.5 10.3 167 2 Q7WS59 staphylococc
 96 119.5 9.8 227 2 Q843U3 streptococc
 97 118.5 9.7 262 16 Q8P0S0 streptococc
 98 117.5 9.6 259 16 Q938J1 streptococc
 99 115 9.2 162 16 Q99TP8 staphylococc
 100 113.5 9.3 209 16 Q879B0 streptococc

ALIGNMENTS

RESULT 1

Q931M4 PRELIMINARY; PRT; 260 AA.
 AC Q931M4
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Enterotoxin P.
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
 RA Mizukami-Ui Y., Takahashi N.K., Sawano T., Inoue R.I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 DR EMBL: AP003364; BAB58110.1; --
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0015070; F:toxin activity; IEA.
 DR GO: GO:0009405; P:pathogenesis; IEA.
 DR InterPro: IPR008992; Bact_endotox.
 DR InterPro: IPR006177; Bctrl_tox.
 DR InterPro: IPR006123; Staph/Strep_toxin.
 DR InterPro: IPR006126; Staph/Strep_tox.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR Pfam: PF01123; Staph_strep_toxin; 1.
 DR Pfam: PF02876; Staph_strep_tox_C; 1.
 DR PRINTS: PR00279; BACTRLTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 260 AA; 30016 MW; 15C2D36270FA8241 CRC64;

Query Match 77.8%; Score 948; DB 16; Length 260;
 Best Local Similarity 76.4%; Pred. No. 6.7e-69;
 Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOGTALGNLKIYYNKAITSSEKSAQDPLNTLLFKGFTG 60
 DB 28 SEKSEINEKDLRKSELOGTALGNLKIYYNKAITSSEKSAQDPLNTLLFKGFTG 87
 QY 61 HPWYNDLLVDLSTAAITSSEYEGSSVDLYGAYGYOCAGGTPNKTCMGVTLHDNNRLT 120
 DB 88 HSWYNDLLVDFDSKDIDVKYKKVDLYGAYGYOCAGGTPNKTCMGVTLHDNNRLT 147
 QY 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKQV 180
 DB 148 EEKVPINLWIDGKQNTVPLETVKTKNKNVTQVELDLQARRYLQEKYLNLYNSDVFQKQV 207

QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTDLRIYRDNTTISTSLSLYLTT 233
 DB 208 RGLIVFHTSTPSVNYDLFGAQGYSTLLRIYRDNTKINSNNHIDIYLYTS 260

RESULT 2

Q99SU3 PRELIMINARY; PRT; 260 AA.
 ID Q99SU3
 AC Q99SU3
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Enterotoxin P.
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158879;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,
 RA Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
 RA Takahashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
 RA Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanehisa M.,
 RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
 RA Ogasawara N., Hayashi H., Hiramatsu K.,
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus.";
 RL Lancet 357:1225-1240(2001).
 DR EMBL: AP003135; BAB43036.1; --
 DR PIR: C89984; C89984.
 DR HSP: P13163; 1SXT.
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0015070; F:toxin activity; IEA.
 DR GO: GO:0009405; P:pathogenesis; IEA.
 DR InterPro: IPR008992; Bact_endotox.
 DR InterPro: IPR006177; Bctrl_tox.
 DR InterPro: IPR006123; Staph/Strep_toxin.
 DR InterPro: IPR006126; Staph/Strep_tox.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR Pfam: PF01123; Staph_strep_toxin; 1.
 DR Pfam: PF02876; Staph_strep_tox_C; 1.
 DR PRINTS: PR00279; BACTRLTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 260 AA; 29708 MW; 087C5B4EC028CFDB CRC64;

Query Match 75.4%; Score 918; DB 16; Length 260;
 Best Local Similarity 73.0%; Pred. No. 1.8e-66;
 Matches 170; Conservative 21; Mismatches 42; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOGTALGNLKIYYNKAITSSEKSAQDPLNTLLFKGFTG 60
 DB 28 SEKSEINEKDLRKSELOGTALGNLKIYYNKAITSSEKSAQDPLNTLLFKGFTG 87
 QY 61 HPWYNDLLVDLSTAAITSSEYEGSSVDLYGAYGYOCAGGTPNKTCMGVTLHDNNRLT 120
 DB 88 HSWYNDLLVDFDSKDIDVKYKKVDLYGAYGYOCAGGTPNKTCMGVTLHDNNRLT 147
 QY 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKQV 180
 DB 148 EEKVPINLWIDGKQNTVPLETVKTKNKNVTQVELDLQARRYLQEKYLNLYNSDVFQKQV 207

QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTDLRIYRDNTTISTSLSLYLTT 233
 DB 208 RGLIEFHPSSGDSVGYDLFQAQGYPTDLRIYRDNTKIKSNHIDIYLYTT 260

RESULT 3
 C85217

RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Ogasawara N., Hayashi H., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Yamasita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RT "Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*."
RL Lancet 357:1225-1240 (2001).
DR EMBL; AF285760; AAC36956.1; -
DR EMBL; AP003363; BAB57987.1; -
DR EMBL; AP003335; BAB42911.1; -
DR PIR; H89968; H89968.
DR HSP; P13163; IESF.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph Strep toxin; 1.
DR Pfam; PF02876; Staph Strep tox C; 1.
DR PRINTS; PR00279; BACTRTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 258 AA; 29676 MW; 8A6C074F3E1F82D2 CRC64;

Query Match 34.5%; Score 420.5; DB 16; Length 258;
Best Local Similarity 38.0%; Pred. No. 3.7e-26;
Matches 87; Conservative 50; Mismatches 85; Indels 7; Gaps 4;

QY 6 EINEKDLRKSELOGTALGNLKIYYNSKAITSEK-SADQFLTNLLFKGFFTGHWPY 64
DB 32 EVDKDLKKKSLDSSKFLNLTSTYDITWQDESNIKSTQDQNNLTILKIDISVLKT 91
QY 65 NDLVLVLGTAATSEYEGSSVDLYGAYGQAGGTPNKTACMYGGVTHDNNRITTEKK 124
DB 92 SSLKVFNSDLANQFKGNIDITYGFGNCKVGLTEERTSLCYGGVTHDGNQDLDEKV 151
QY 125 VPINLWDGKQTVPIDKVTSKEVTVOELDLQASHYLGKFGLYNSDFGKVGQGLI 184
DB 152 IGVNFKDGVQGGFV--IKTKAKTVQELDTKVFLENLYKYNKDT--GNIQKGI 207
QY 185 VFHS--SEGTVSYDLFDAGQGVPTDLLRIYRDNNTTSSISLSLYLT 231
DB 208 FFHSHNQDQSFYDLYNVKSGVGAFFQFQSDNRTVSSSNHYHDVFLY 256

RESULT 6
Q99T46 PRELIMINARY; PRT; 260 AA.
AC Q99T46;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Enterotoxin Sec.
GN SEQ OR SAV1830 OR SA1648.
OS *Staphylococcus aureus* (strain Mu50 / ATCC 700699), and
OS *Staphylococcus aureus* (strain N315).
OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
OX NCBI_TaxID=158878, 158879;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES-S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; PubMed1418446;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

RA Kanehisa M., Yamasita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*."
RL Lancet 357:1225-1240 (2001).
DR EMBL; AP003363; BAB57992.1; -
DR EMBL; AP003335; BAB42916.1; -
DR PIR; E89969; E89969.
DR HSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph Strep toxin; 1.
DR Pfam; PF02876; Staph Strep tox C; 1.
DR PRINTS; PR00279; BACTRTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 260 AA; 29836 MW; AC927DDCC3B3B8EF CRC64;

Query Match 30.6%; Score 372.5; DB 16; Length 260;
Best Local Similarity 38.8%; Pred. No. 2.9e-22;
Matches 93; Conservative 32; Mismatches 92; Indels 23; Gaps 7;

QY 8 NEKD-----LRKSELOGTALGNLKIYYNS-KAITSEKSDQFLTNLLFKGFFTGH 61
DB 29 NEEDPKIESLCKSSVDPALHNDYINNRFTTVKSVSTTEKFLDFLLFKSI----- 84
QY 62 PW-----YNDLVLGTAATSEYEGSSVDLYGAYGQAGGTPNKTACMYGGVTLH 114
DB 85 NWLDGISAEPKDLKAVEPSSAISKEFLGKTVDIVGVYKACHGEHQVDTACTYGGVTPH 144
QY 115 DNNPLTEKKVPINLWDGKQTVPIDKVTSKEVTVOELDLQASHYLGKFGLYNSDS 174
DB 145 ENKLSLSPKINAVAYKDNVNVNFTI--VTDDKKVTAQELDIKVRTKLNAYKLY--DR 200
QY 175 FGGVQVQGLIVFHSSEGSTVS--YDLFDAQGVPTDLLRIYRDNNTTSSISLSLYLT 232
DB 201 MTSVDQGVYIKFHSSEHSHSFYDLFIKGNLPDQVLIYNDNKIDSSDYHDVYLF 260

RESULT 7
Q9EZM8 PRELIMINARY; PRT; 261 AA.
AC Q9EZM8;
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE SEQ.
GN SEQ.
OS *Staphylococcus aureus*.
OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A900322;
RX MEDLINE=20571956; PubMed1123352;
RA Jarraud S., Peyrat M.A., Lim A., Tristant A., Bes M., Mougel C.,
RA Etienne J., Vandenesch F., Bonneville M., Lina G.,
RT "esc, A highly prevalent operon of enterotoxin gene, forms a putative
RT nursery of superantigens in *Staphylococcus aureus*."
RL J. Immunol. 166:669-677 (2001).
DR EMBL; AF285760; AAC36951.1; -
DR HSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.

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DR InterPro: IPR006177; Bctr1 tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph tox OB.
DR Pfam: PF01123; Staph/Strep toxin; 1.
DR Pfam: PF02876; Staph/Strep tox C; 1.
DR PRINTS: PS00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 261 AA; 29949 MW; 24DA4DD766288EC CRC64;

Query Match 30.6%; Score 372.5; DB 2; Length 261;
Best Local Similarity 38.8%; Pred. No. 2.9e-22;
Matches 93; Conservative 32; Mismatches 92; Indels 23; Gaps 7;

QY 8 NEKD-----LRKSELOQTALGNLQIYYNS-KAITSSEKSAQOFLNTLLFGFTGH 61
DB 30 NEEDPKIESLCKSSVDPIALHNDDYINNRFTTVKSIIVTTEKFLDFDLFSI---- 85
QY 62 PW-----YNDLLVDLGSTAATSEYEGSSVDLYGAYGYOCAGTTPNKTACMYGGVTLH 114
DB 86 NWLDGISAEFKDLKVEFSSAISKEPLGKTVDIYGVYKACHGEHQVDTHACTYGGVTPH 145
QY 115 DNNRLTEKKVPIINLWIDKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDS 174
DB 146 ENKLSSEPKNIGVAVYKNNVNTFII--VTTDKKVTQAQELDKVTKLNNAYKLY--DR 201
QY 175 FGGKVORGLIVPHSSEGSTVS--YDLFDAQGYPTLLRIYRDNTTISSTLSLSLYLYT 232
DB 202 MTSVDYKGYIKPHSHSEKESFYDLYFKGNLPQYLIQIYNDNKTIIDSSYDHIDVILFT 261

RESULT 8
Q52075 PRELIMINARY; PRT; 179 AA.
AC Q52075;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Enterotoxin D.
GN VIRC2.
OS Staphylococcus aureus.
OG Plasmid pB485.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89359112; PubMed=2549000;
RA Bayles K.W., Iandolo J.D.;
RT "Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin D.";
RL J. Bacteriol. 171:4799-4806 (1989).
DR EMBL: W94872; AAA98133.1; -.
DR HSSP: P13163; 1SXT.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0046821; C:extrachromosomal DNA; IEA.
DR GO: GO:0015070; F:toxin activity; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph/Strep tox OB.
DR Pfam: PF01123; Staph/Strep toxin; 1.
DR Pfam: PF02876; Staph/Strep tox C; 1.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Plasmid.
SQ SEQUENCE 179 AA; 20563 MW; 579FFEB11BC08747 CRC64;

Query Match 29.1%; Score 355; DB 2; Length 179;
Best Local Similarity 45.3%; Pred. No. 4.7e-21;
Matches 68; Conservative 26; Mismatches 56; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLKKSELOQTALGNLQIYYNSKAITSSEKSAQOFLNTLLFGFTGH 60

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DB 26 NENIDSVKEKELHKKSELSTALNNKHSYADKNPIIGENKSTGDFLENTLLYKKFFTD 85
QY 61 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYOCAGTTPNKTACMYGGVTLHDNRLT 120
DB 86 LINFEDLLINFNSKEMAQHFKSKQVDPYPIRYSINCYGGEIDRTACTYGGVTPHEGNK 145
QY 121 EEKVPINLWIDKQTTVPIDKVKTSKEV 150
DB 146 ERKKIPINLWINGVQKEVSLDKVQTDKKNL 175

RESULT 9
Q52075 PRELIMINARY; PRT; 240 AA.
AC Q52075;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Sel (Extracellular enterotoxin L).
GN SEL OR SAV2008 OR SA1816.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
OS Staphylococcus aureus (strain N315), and
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878, 158879, 1280;
RN [1]
RP SEQUENCE FROM N.A.
RX SPECIES=S.aureus; PubMed=11114901;
RX MEDLINE=20586688; PubMed=11418146;
RA Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
RA Meaney W.J., Smyth C.J.;
RT "Characterization of a putative pathogenicity island from bovine Staphylococcus aureus encoding multiple superantigens.";
RL J. Bacteriol. 183:63-70 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX SPECIES=S.aureus;
RX MEDLINE=20586688; PubMed=11114901;
RA Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
RA Meaney W.J., Smyth C.J.;
RT "Characterization of a putative pathogenicity island from bovine Staphylococcus aureus encoding multiple superantigens.";
RL J. Bacteriol. 183:63-70 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RX SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kaito C.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus aureus";
RL Lancet 357:1225-1240 (2001).
DR EMBL: AF217235; AAC29598.1; -.
DR EMBL: AP003364; BAB58170.1; -.
DR EMBL: AP003135; BAB43096.1; -.
DR PIR: G89991; G89991.
DR HSSP: P13163; 1ESF.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0015070; F:toxin activity; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bctr1 tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph/Strep tox OB.
DR Pfam: PF01123; Staph/Strep toxin; 1.
DR Pfam: PF02876; Staph/Strep tox C; 1.
DR PRINTS: PS00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 240 AA; 27496 MW; F40D62DA73197881 CRC64;

Query Match 25.5%; Score 311; DB 16; Length 240;
Best Local Similarity 33.3%; Pred. No. 2.5e-17;
Matches 74; Conservative 36; Mismatches 78; Indels 34; Gaps 6;

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QY 24 GNLRQIY----YNSKAITSEKSADQFLNTLLFKGFTTGHFWYND-LLVDLGSTAATS 78
DB 31 GNLRNFYTKYEVNLRKNVKNKSPESHRL------YSKNDTLTYAEFDNEYITS 79
QY 79 EYEGSSVDLYGAYGYQCAGTGNKACMGVYTLHDNNRLTEKKVPINLMDGKQTV 138
DB 80 DLKGNVDVFGISYK-----GNSRT--YGVGTAKENKLDSPRIIPINLINGKHQTV 133
QY 139 PIDKVKTSKEVTVOELDLQARHLYHGKFGLY-----NSDSFGGKVQRLIYF 186
DB 134 TTKSVSTDKQWTAQEI-DVKLRKYLODEFNIYGHNDTGKGEYGTSSKFGYSGFDKGSVVF 193
QY 187 HSSEGSTVSYDLFDAQOQYPTLLRIYRDNNTTSSLSISL 228
DB 194 HMDGNSFSDLYFTGYGLPESFLKIYKDNKNTVDSTQFHLDV 235

RESULT 10
QSNXJ5 PRELIMINARY; PRT; 240 AA.
AC QSNXJ5, 20040717; PubMed=12044378;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Extracellular enterotoxin L.
GN SEL2 OR MW0760.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Ngai Y., Iwama N., Amano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
DR EMBL: AP004824; BAB94625.1; -.
DR GO: GO:000576; C:extracellular; IEA.
DR GO: GO:0015070; F:toxin activity; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006173; Bact_tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph tox OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 240 AA; 27478 MW; 85CD62DA731C3D95 CRC64;

Query Match 25.3%; Score 310; DB 16; Length 240;
Best Local Similarity 33.3%; Pred. No. 3e-17;
Matches 74; Conservative 36; Mismatches 78; Indels 34; Gaps 6;

QY 24 GNLRQIY----YNSKAITSEKSADQFLNTLLFKGFTTGHFWYND-LLVDLGSTAATS 78
DB 31 GNLRNFYTKYEVNLRKNVKNKSPESHRL------YSKNDTLTYAEFDNEYITS 79
QY 79 EYEGSSVDLYGAYGYQCAGTGNKACMGVYTLHDNNRLTEKKVPINLMDGKQTV 138
DB 80 DLKGNVDVFGISYK-----GNSRT--YGVGTAKENKLDSPRIIPINLINGKHQTV 133
QY 139 PIDKVKTSKEVTVOELDLQARHLYHGKFGLY-----NSDSFGGKVQRLIYF 186
DB 134 TTKSVSTDKQWTAQEI-DVKLRKYLODEFNIYGHNDTGKGEYGTSSKFGYSGFDKGSVVF 193
QY 187 HSSEGSTVSYDLFDAQOQYPTLLRIYRDNNTTSSLSISL 228
DB 194 HMDGNSFSDLYFTGYGLPESFLKIYKDNKNTVDSTQFHLDV 235

RESULT 11
QSNR76 PRELIMINARY; PRT; 217 AA.
AC QSNR76, 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin H (Fragment).
GN SEH.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21871379; PubMed=11880405;
RA Omeo K., Ishikawa M., Shimoda Y., Hu D.L., Ueda S., Shinagawa K.;
RT "Detection of seg, seh, and sei genes in Staphylococcus aureus
RT isolates and Determination of the Enterotoxin Productivities of S.
RT aureus Isolates Harboring seg, seh, or sei Genes.";
RL J. Clin. Microbiol. 40:857-862(2002).
DR EMBL: AB060536; BAB85990.1; -.
DR GO: GO:000576; C:extracellular; IEA.
DR GO: GO:0015070; F:toxin activity; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bactl_tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006173; Staph tox OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 217 AA; 25143 MW; A8A44E23F31DE80D CRC64;

Query Match 25.3%; Score 308; DB 2; Length 217;
Best Local Similarity 33.9%; Pred. No. 3.9e-17;
Matches 76; Conservative 46; Mismatches 90; Indels 12; Gaps 7;

QY 10 KDLRKKSELQALGNLKIYYNSKAITSEKSADQFLNTLLFKGFTTGHFWYNDLLV 69
DB 1 EDLHDKSELDTLALAN--AYQYNHPPIKENIKSDEISGEKDLIFRN--QGDGSG-NDLRV 55
QY 70 DLGSTAATSEYEGSSVDLYGAYGYQCAGTGNKACMGVYTLHDNNRLTEKKVPINL 129
DB 56 KFATADLAQRFKNKNVDIYGASFYKCEKISENISECLYGGTTL-NSEKLAQSRVIGANV 114
QY 130 WIDGKQITVPIDKVKTSKEVTVOELDLQARHLYHGKFGLYNSDSFGGKVQRLIYFSS 189
DB 115 WVDGIQKETEL--IRTNKNVTLQELDKIRKILSDKVKIYKDS---EISKGLIEFDMK 169
QY 190 EGSTVSYDLFDAQOQYPTLLRIYRDNNTTSSLSISL-ISLYLT 232
DB 170 TPRDYSFDIYDLKGENDYEIDKIYEDNKNLTKSDSDISHIDVNLAT 213

RESULT 12
Q33585 PRELIMINARY; PRT; 241 AA.
AC Q33585, 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin H.
GN SEH OR MW0051.
OS Staphylococcus aureus, and
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280, 196620;

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RP SEQUENCE FROM N.A.
RC STRAIN=D4508;
RX MEDLINE=95053699; PubMed=7964453;
RA Ren K., Bannan J.D., Pancholi V., Cheung A.L., Robbins J.C.,
RA Fischetti V.A., Zabriskie J.B.;
RT "Characterization and biological properties of a new staphylococcal
RT exotoxin";
RL J. Exp. Med. 180:1675-1683(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MW2;
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yanamoto K., Hirakatsu K.;
RT "Genomic and virulence determinants of high virulence community-
RT acquired MRSA";
RL Lancet 359:1819-1827(2002).
DR EMBL; U11702; AA19777.1; -.
DR EMBL; AF004822; BAB3916.1; -.
DR PDB; 1ENF; 10-JAN-01.
DR PDB; 1EMC; 10-JAN-01.
DR PDB; 1F77; 10-JAN-01.
DR PDB; 1JXY; 27-JUN-01.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Stap/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Stap_strep_toxin; 1.
DR Pfam; PF02876; Stap_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal; Complete proteome.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 241 ENTEROTOXIN H.
SQ SEQUENCE 241 AA; 27858 MW; 70F7798587616CE CRC64;

Query Match 33.3%; Score 308; DB 16; Length 241;
Best Local Similarity 25.9%; Pred. No. 4.4e-17;
Matches 76; Conservative 46; Mismatches 90; Indels 12; Gaps 7;

QY 10 KDLRKSLOGTALGNLQIYYNSKAITSEKADQFLTWLTKGFFTHPNYLLV 69
DB 25 EDLHDKSELTLALAN--AYQYNHPFIKENIKSDEISGEKDLIFRN--QGDG-NDLRV 79
QY 70 DLGSTAATSEYEGSVLDYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINL 129
DB 80 KFTADLAQKPKNKVDIYGASFYKCEKISENISECLYGGTTL-NSEKLAQERVIGANV 138
QY 130 WIDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFLGYNDSFGKVQVGLIVPHSS 189
DB 139 WVDGIQKETEL--ITNKKVNTLQELDKIRKILSDKYKIYKDS--EISKGLIEFDMK 193
QY 190 EGSTVYDLFAQQQYPTLARIYDNTTISSTLS--LSLYLT 232
DB 194 TPRDYSDIYDLKGNDYEIDKIDVNTLKSDDISHIDVNLTY 237

RESULT 13
O85383 PRELIMINARY; PRT; 242 AA.
AC O85383;
DT 01-NOV-1998 (TREMBLrel. 08, Created)
DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Extracellular enterotoxin type I precursor (SEI).
GN SEI OR SAV1828 OR SAV1646.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
OS Staphylococcus aureus (strain N315), and

Staphylococcus aureus.
Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=158878, 158879, 1280;
[1]
RN SEQUENCE FROM N.A.
RC SPECIES=S.aureus; STRAIN=FR1445;
RX MEDLINE=9898056; PubMed=9632603;
RA Munson S.H., Tremaine M.T., Betley M.J., Welch R.A.;
RT "Identification and characterization of staphylococcal enterotoxin
RT types G and I from Staphylococcus aureus";
RL Infect. Immun. 66:3337-3348(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus; STRAIN=A900322;
RX MEDLINE=20571956; PubMed=11123352;
RA Jarraud S., Peyrat M.A., Lim A., Tristan A., Bes M., Mougel C.,
RA Etienne J., Vandenesch F., Bonneville M., Lina G.;
RT "egc, A highly prevalent operon of enterotoxin gene, forms a putative
RT nursery of superantigens in Staphylococcus aureus";
RL J. Immunol. 166:669-677(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hizamatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus";
RL Lancet 357:1225-1240(2001).
DR EMBL; AF064774; AAC26661.1; -.
DR EMBL; AF285760; AAG36953.1; -.
DR EMBL; AP003363; BAB57990.1; -.
DR EMBL; AP003135; BAB42914.1; -.
DR PIR; C89969; C89969.
DR HSP; P3163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Stap/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Stap_strep_toxin; 1.
DR Pfam; PF02876; Stap_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal; Complete proteome.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 242 ENTEROTOXIN TYPE I.
SQ SEQUENCE 242 AA; 27863 MW; C5C8B4ACEB5414A8 CRC64;

Query Match 24.3%; Score 296.5; DB 16; Length 242;
Best Local Similarity 32.4%; Pred. No. 3.8e-16;
Matches 77; Conservative 39; Mismatches 85; Indels 37; Gaps 10;

QY 8 NENDLRKSELQGTALGNLQIY-----YNSKAITSEKADQFLTWLTKGFFTHP 62
DB 17 NIKDL---TVAQDGIQVGNLRFYTKHYIDLKGVTDKNLP----IANQLEFS---TG-- 64
QY 63 WYNDLLVDLGSTAATSEYEGSVLDYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLTEE 122
DB 65 -TNDLISESNWDEISKFKGKLDIFGIDYNGPC-----KSKYMGATL-SGOYLNSA 116
QY 123 KKPYPINLWIDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFLGYNDSFG-CK--- 178
DB 117 RKIPINLWNGKHKTTSTDKIATNKKLVTAQEDVKRLRYLQBEVNIYGHNTGKGYG 176
QY 179 -----VQRGLIVPHSSSEGSTVSYDLFDAQQYPTLIRIYDNTTISSTLSLSL 228

Db 177 YKSKFYSGFNGKVLFLHNKESFSDYDLFTGDLVSPFLKIYEDNKIESEKFLHDV 234

RESULT 14

Q8VVM1 ID Q8VVM1 PRELIMINARY; PRT; 225 AA.
AC Q8VVM1; MEDLINE=21259899; PubMed=11359827;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Exotoxin I.
GN SPEI.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M1;
RX MEDLINE=21259899; PubMed=11359827;
RA Prof. T., Arcus V.L., Handley V., Baker E.N., Fraser J.D.;
RT "Immunological and biochemical characterization of streptococcal
pyrogenic exotoxins I and J (SPE-I and SPE-J) from Streptococcus
pyogenes.";
RL J. Immunol. 166:6711-6719(2001).
DR EMBL; AF438524; AAL31571.1; -;
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; P:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 225 AA; 25654 MW; DB133667890ACDAF CRC64;

Query Match 24.2%; Score 294.5; DB 2; Length 225;
Best Local Similarity 32.4%; Pred. No. 5e-16;
Matches 72; Conservative 40; Mismatches 85; Indels 25; Gaps 8;
QY 25 NLKOIY-YNSKAITSEKSADOFNTLLFKGFTGHPWN---DLLVDLGSTAAATSEY 80
DB 8 NLNLSTYDPTVEVKINGEPPF-SGSLFYKNI-----PYGNSSIELKVELNSVEKAKFF 62
QY 81 EGSSVDLYGAYGYQCAGGTPNKTCACGGVTLHNNRLTEKKVPINLWIDG---KQTT 137
DB 63 SGRKVDIFLEYPSPCNSNIKNKNS---YGGITLSDGNRI-DKXNIPVNFIDGVQOKYSY 118
QY 138 VPIDKVKTSKVTVOELDLQARHYLHGKFGY-----NSDSFGGKVQGLIVPHS 188
DB 119 TDIYSTVTDKKEVTIQELDVKSRYLQKHFNITGYGDKVDFGRSSRFQSGFEGNIIFHL 178
QY 189 SEGSTVSVDLFDAGQGYPTDLRIYRDNNTTISSTLSISLYL 230
DB 179 NSGERISYNLFDTHGDRSMKLYSDNKTAYSQDLHDIYL 220

RESULT 15

Q9L921 ID Q9L921 PRELIMINARY; PRT; 225 AA.
AC Q9L921; MEDLINE=21871379; PubMed=11880405;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE 25.7 kDa protein.
OS Streptococcus equi.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.
OX NCBI_TaxID=1336;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CF32;
RA Artushin S.C., Timoney J.F., Sheoran A.S.;
RT "Identification and molecular characterization of mitogens from
Streptococcus equi.";
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF186180; AAF72808.1; -;
DR HSP; P13163; LSXT
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; P:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 225 AA; 25684 MW; EB43D47B26FB9F89 CRC64;
Query Match 24.1%; Score 293.5; DB 2; Length 225;
Best Local Similarity 32.4%; Pred. No. 6e-16;
Matches 72; Conservative 39; Mismatches 86; Indels 25; Gaps 8;
QY 25 NLKOIY-YNSKAITSEKSADOFNTLLFKGFTGHPWN---DLLVDLGSTAAATSEY 80
DB 8 NLNLSTYDPTVEVKINGEPPF-SGSLFYKNI-----PYGNSSIELKVELNSVEKAKFF 62
QY 81 EGSSVDLYGAYGYQCAGGTPNKTCACGGVTLHNNRLTEKKVPINLWIDG---KQTT 137
DB 63 SGRKVDIFLEYPSPCNSNIKNKNS---YGGITLSDGNRI-DKXNIPVNFIDGVQOKYSY 118
QY 138 VPIDKVKTSKVTVOELDLQARHYLHGKFGY-----NSDSFGGKVQGLIVPHS 188
DB 119 TDIYSTVTDKKEVTIQELDVKSRYLQKHFNITGYGDKVDFGRSSRFQSGFEGNIIFHL 178
QY 189 SEGSTVSVDLFDAGQGYPTDLRIYRDNNTTISSTLSISLYL 230
DB 179 NSGERISYNLFDTHGDRSMKLYSDNKTAYSQDLHDIYL 220
RESULT 16
Q8RR75 ID Q8RR75 PRELIMINARY; PRT; 218 AA.
AC Q8RR75; MEDLINE=21871379; PubMed=11880405;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Enterotoxin I (Fragment).
GN SEI.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21871379; PubMed=11880405;
RA Omoe K., Ishikawa M., Shimoda Y., Hu D.L., Ueda S., Shinagawa K.;
RT "Detection of seg, seh, and sei genes in Staphylococcus aureus
isolates and determination of the Enterotoxin Productivities of S.
aureus Isolates Harboring seg, seh, or sei Genes.";
RL J. Clin. Microbiol. 40:857-862(2002).
DR EMBL; AB060537; BAB85991.1; -;
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; P:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006123; Staph/Strep_toxin.

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DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR PFam; PF02876; Staph_strep_tox_C; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER
SQ SEQUENCE 218 AA; 24909 MW; 1017728FB71BF662 CRC64;

Query Match
Best Local Similarity 23.7%; Score 288.5; DB 2; Length 218;
Matches 70; Conservative 39; Mismatches 80; Indels 33; Gaps 8;

QY 23 LGNLKQIY---YNSKAITSEKSAQDLNTLLFKGFFTGHPWYNDLLVDLGLSTAATS 78
Db 6 VGNLRFYTKHDYIDLKGVTDKNLP-----IANQLEFS---TG---TNDLISESNWDEIS 55
QY 79 EYEGSSVDLYGAYGYCAGGTPNKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQTTV 138
Db 56 KFKGKKLIDFIDYNGPC-----KSKYMFQCATL-SQYVLSARKIPINLWVNGKHKT 108
QY 139 PIDKVTSKKEVTQVELDQARHYLHGKFGLYNSDSFG-GK-----VQRGILIVF 186
Db 109 STDKIATNKLVTAQIEDIVKURRLOBEYNYGHNTGKGEYKSYKFGYGFNGKVLV 168
QY 187 HSSGSGTYSYDLFDAQGYPTLLRIYRDNTTISSTLSISL 228
Db 169 HLNNEKSFYDLFTGDLGSPVSLKIVEDNKIIESEKFLHDV 210

RESULT 17
ID Q05157 PRELIMINARY; PRT; 239 AA..
AC Q05157;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Type C enterotoxin (Fragment).
OS Staphylococcus intermedius.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1285;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95-011195;
RA Edwards V.M., Deringer J.R., Callantine S.D., Deobald C.F.,
RA Berger P.H., Kapur V., Stauffacher C.V., Bohach G.A.;
RT "Characterization of the type C enterotoxin (SEC-canine) produced by
RT Staphylococcus intermedius pyoderma isolates."
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U91326; AAB50248.1; -.
DR HSP; P23313; 1UCK.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR PRINTS; PS00279; BACTELTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER
SQ SEQUENCE 239 AA; 27536 MW; D660644660DE4191 CRC64;

Query Match
Best Local Similarity 23.7%; Score 288.5; DB 2; Length 239;
Matches 81; Conservative 37; Mismatches 96; Indels 21; Gaps 9;

QY 11 DLKXSELQGTALGNLQIY--YNSKAITSEKSAQDLNTLLFKGFFTGHPWYNDLL 68
Db 10 DLKXSEFTGT-MGNWKLVDYYS---ATKVKSDVFLAHLIYNI-SDKLNKNDKVK 65

QY 69 VDLGSTAATSEYEGSSVDLYGAYGYC-----AGGTPNKTCMYGGVTLHDNNRLTE 121
Db 66 TELLNEDLAKKYKDEVDVYGSNYVNCYFSKDNVKGVTGKTKWYGGITKHEGNHFDN 125
QY 122 E--KKVPINLWIDGKQTTVPIDKVTSKKEVTQVELDQARHYLHGKFGLYNSDSFGGKV 179
Db 126 GNQLNVLIIRVY-ENKENTISFD-VQTDKKSVAQELDIKARNFLINKOLYEFNS--SPY 181
QY 190 QRGLIVHSSGSGTYSYDLFDAQGYPD--TLRIYRDNTTISSTLSISLILYT 232
Db 182 EFTGYIKFIESNDNTWYDMMPAPGDKFDQSKYLMYSDNKTVDKSKVIEVHLTT 236

RESULT 18
QY9ZZI PRELIMINARY; PRT; 225 AA.
ID Q99ZZI;
AC Q99ZZI;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Streptococcal exotoxin I.
DE SPEI OR SPY1007.
GN Streptococcus pyogenes.
OS Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RA MEDLINE=21192684; PubMed=11296296;
RA Ferreretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RA "Complete genome sequence of an M1 strain of Streptococcus pyogenes."
RL Proc. Natl. Acad. Sci. U.S.A. 98:4659-4663 (2001).
DR EMBL; AS006546; AAK3906.1; -.
DR HSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR PRINTS; PS00279; BACTELTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 225 AA; 25611 MW; CE0D6736CG11CC04 CRC64;

Query Match
Best Local Similarity 23.6%; Score 287.5; DB 16; Length 225;
Matches 71; Conservative 40; Mismatches 86; Indels 25; Gaps 8;

QY 25 NLKQIY-YNSKAITSEKSAQDLNTLLFKGFFTGHPWYNDLLVDLGLSTAATSEY 80
Db 8 NLRLNLYTDPTTEVKCKINEGPPF-SGSLFYKNI-----PYGNSSIELKVELANSVERKANFF 62
QY 81 EGSSVDLYGAYGYCAGGTPNKTCMYGGVTLHDNNRLTEKKVPINLWIDG---KQTT 137
Db 63 SGRVRDIFTLEYSPPCNSNIKKNS---YGGITLSDGNRI-DKNIIPVNI-FIDGVQOKSY 118
QY 138 VPIDKVTSKKEVTQVELDQARHYLHGKFGLY-----NSDSFGGKVQSGGLIVFHS 188
Db 119 TDLSTGTDKKEVTIQLDLVKSYIQLKHFNYFGDVKDFGSSRFQSGFEGNIIFHL 178
QY 189 SEGSTYSYDLFDAQGYPTLLRIYRDNTTISSTLSISL 230
Db 179 NSGERISYNLFDTHGDRSMKKYSDNKTAYSQDLHIDIYL 220
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DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 239 AA; 27371 MW; 69240BE23C44028A CRC64;

Query Match 23.3%; Score 284; DB 2; Length 239;
Best Local Similarity 30.4%; Pred. No. 3.8e-15;
Matches 69; Conservative 38; Mismatches 80; Indels 40; Gaps 6;

Qy 23 LGNLKQIYYNSKAIT--SSEKSAQDFLNTLLFKGFFTGHPWYNDLLVDLGSTAA---- 76
Db 24 VGVNLNRYGSPYEDHQSNPENNNHLSHQLVFS-----MDNSTVTABFKN 70

Qy 77 ---TSEYEGSVDLGYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEEKKVPINLWDG 133
Db 71 VDDVKEFNHADVYGLSYGYCL-----KNKIYGGVTL-AGDYLEKSRRIPLNLWNG 124

Qy 134 KQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLY-----NSDSFGGKQVOR 181
Db 125 EQHTISTDKVTNKLVTAQEIDTKLRYLQEEYNIYGFNDTKGRNYGNKSKFSSGFNA 184

Qy 182 GLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNTTISLSLSL 228
Db 185 GKILFHLNDGSSFYDLFTGTGQAESFLKYNKNTVETKFKFLDV 231

RESULT 22
Q99T47 PRELIMINARY; PRT; 239 AA.
ID Q99T47
AC Q99T47
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin SEM.
GN SEM OR SAV1829 OR SAL647.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878, 158879;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kaneshisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL; AF003363; BAB57991.1; -.
DR EMBL; AF003135; BAB42915.1; -.
DR PIR; D89969; D89969.
DR HSSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 239 AA; 27370 MW; 5F29665125705600 CRC64;

Query Match 23.2%; Score 282; DB 16; Length 239;
Best Local Similarity 29.7%; Pred. No. 5.6e-15;
Matches 68; Conservative 40; Mismatches 77; Indels 44; Gaps 6;

Qy 23 LGNLKQIYYNSKAIT--SSEKSAQDFLNTLLFKGFFTGHPWYNDLLVDLGSTAA-- 79
Db 24 VGVNLNRYGSPYEDHQSNPENNNHLSHQLV-----SMNSTVTAEF 68

Qy 80 -----YEGSVDLGYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEEKKVPINLWI 131
Db 69 KNVDVKKFNHADVYGLSYGYCL-----KNKIYGGVTL-AGDYLEKSRRIPLNLW 122

Qy 132 DGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLY-----NSDSFGGK 179
Db 123 NGEHQISTDKVTNKLVTAQEIDTKLRYLQEEYNIYGFNDTKGRNYGNKSKFSSGF 182

Qy 180 QRLGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNTTISLSLSL 228
Db 183 NAGKILFHLNDGSSFYDLFTGTGQAESFLKYNKNTVETKFKFLDV 231

RESULT 23
Q8NVW3 PRELIMINARY; PRT; 242 AA.
ID Q8NVW3
AC Q8NVW3
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Staphylococcal enterotoxin Seg.
GN SEG2 OR MW1937.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
DR EMBL; AP004828; BAB95802.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR008375; Staph_exotoxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PRINTS; PR01800; STAPHSTREP_TOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 242 AA; 28138 MW; FFC89B80E7A3BF5 CRC64;

Query Match 22.9%; Score 278.5; DB 16; Length 242;
Best Local Similarity 29.3%; Pred. No. 1.1e-14;
Matches 68; Conservative 34; Mismatches 69; Indels 61; Gaps 7;

Qy 17 ELQGTALGNLK---QIYYNSKAITSEKSAQDFLNTLLFKGFFTGHPWYNDLLVDLGS 73
Db 44 KLGQVSSGNFSTGHQLEYIDGKTYLSQ-----FHN----- 74

Qy 74 TAATSEYEGS-----SVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEEKKVPIN 128
Db 75 -----EYKAKLKHDKVDIFGISYGLC-----NTKMYGGITLANQN-LDKPRNIPIN 122
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QY 129 LWIDGKQTTVPIDKVKTSKKEVTQVELDLQARHLYHGKFGLYN-----SDSFG 176
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 123 LWVNGKQNTISTDKVSTQKKEVTAQAEIDIKLKYQLQNEINYGNFKTKKGQEVGYQSKEN 182

QY 177 GKVGRLIVFHSSGSGTSVSDLDFAQGGYPTDRLRIYRDNTTISSTLSISL 228
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 183 SGFNKGKITFHLNNEPSTYDLYFTGTGQAESFLKIYNDKNKTIDAENPHLDV 234

RESULT 24
Q8VLW7 PRELIMINARY; PRT; 256 AA.
AC Q8VLW7;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Staphylococcus enterotoxin Q.
GN ENTQ.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RN4282;
RX MEDLINE=9835824; PubMed=9720870;
RA Lindsay J.A., Ruzin A., Ross H.F., Kurepina N., Novick R.P.;
RT "The gene for toxic shock toxin is carried by a family of mobile
pathogenicity islands in Staphylococcus aureus.";
RL Mol. Microbiol. 29:527-543 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=RN4282;
RA Lindsay J.A., Kreiswirth B.N., Novick R.P.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=RN4282;
RA Barry P.C., Novick R.P.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR GO: 0005576; C:extracellular; IEA.
DR GO: 0015070; F:toxin activity; IEA.
DR GO: 0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph Strep toxin; 1.
DR Pfam; PF02876; Staph Strep toxin C; 1.
DR PRINTS; PR00279; BACTRTOXIN.
DR PRINTS; PR01800; STAPHSTREP_TOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 256 AA; 29734 MW; 9E2F13790823A7DF CRC64;

Query Match 22.9%; Score 278.5; DB 2; Length 256;
Best Local Similarity 29.3%; Pred. No. 1.2e-14;
Matches 69; Conservative 34; Mismatches 69; Indels 61; Gaps 7;

QY 17 ELQGTALGNLK---QIYYNSKAITSEKSADQFLNTLLFKGFTGHPWYNDLLVDLGS 73
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 58 KLGQVSGNFSSTSHQLEYIDKGYLSQ-----FHN----- 88

QY 74 TAATSEYGS-----SVDLYGAYGYQCAGGTFNKTACMYGVTLLHDNRRLTEEEKVPI 128
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 89 -----EYKRLKDKHVDIFGISYGLC-----NTKYMGGITLANQN-LDKPRNIPIN 136

QY 129 LWIDGKQTTVPIDKVKTSKKEVTQVELDLQARHLYHGKFGLYN-----SDSFG 176
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 137 LWVNGKQNTISTDKVSTQKKEVTAQAEIDIKLKYQLQNEINYGNFKTKKGQEVGYQSKEN 196
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QY 177 GKVGRLIVFHSSGSGTSVSDLDFAQGGYPTDRLRIYRDNTTISSTLSISL 228
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 183 SGFNKGKITFHLNNEPSTYDLYFTGTGQAESFLKIYNDKNKTIDAENPHLDV 248

RESULT 25
Q8NXJ6 PRELIMINARY; PRT; 266 AA.
AC Q8NXJ6;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin type C precursor.
GN SEC4 OR MW0759.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
acquired MRSA.";
RL Lancet 359:1819-1827 (2002).
DR EMBL; AP004824; BAB94624.1; -.
DR GO: 0005576; C:extracellular; IEA.
DR GO: 0015070; F:toxin activity; IEA.
DR GO: 0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph Strep toxin; 1.
DR Pfam; PF02876; Staph Strep toxin C; 1.
DR PRINTS; PR00279; BACTRTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 266 AA; 30670 MW; 4C654659AA48120F CRC64;

Query Match 22.9%; Score 278.5; DB 16; Length 266;
Best Local Similarity 31.1%; Pred. No. 1.2e-14;
Matches 76; Conservative 47; Mismatches 102; Indels 19; Gaps 9;

QY 1 SEKSEINEKDLRKKSBLQGTALGNLKQIYYNSKAITSE-KSADQFLNTLLFKGFT 59
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 27 AESQPDPTDELHKSSEFTGT-MGNMK--YLYDDHYVSATKVKSVDFLAHDLIYNISDK 83

QY 60 GHPWYNDLLVDLGSSTAATSEYGSVDLYGAYGYQC-----AGTPNKTACMYGCVT 112
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 84 KLRNYDKVKTLELNEIDLAKYKQDEVDVYGSNYYVNCYFSSKQNVGKVTGCKTMYGGIT 143

QY 113 LHDNNRLTEE--KKVINLWIDGKQTTVPIDKVKTSKKEVTQVELDLQARHLYHGKFGLY 170
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 144 KHEGHPDNGNLQNLIRVY-ENKNTISFE-VQTDKSVTAQELDIKARFLINKNLY 201

QY 171 NSDFGKGKVGRLIVFHSSGSGTSVSDLDFAQGGYPTDRLRIYRDNTTISSTLSISL 228
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 202 EFNS--SPYETGYTKFTIENNGNTFFYDMPAPGDKFDQSKYLMWYNDKNKTVDKRVKIEV 259

QY 229 YLYT 232
Db 260 HLTT 263

RESULT 26
Q06532 PRELIMINARY; PRT; 239 AA.
ID Q06532
AC Q06532;
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01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=740N;
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications."
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13375; AAA26619.1; -.
DR HSSP; P34071; 1SE2.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bact_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27651 MW; A21A954386AE8625 CRC64;

Query Match 22.8%; Score 277.5; DB 2; Length 239;
Best Local Similarity 31.3%; Pred. No. 1.3e-14;
Matches 76; Conservative 46; Mismatches 102; Indels 19; Gaps 9;

QY 2 EKSEINEKDLRKSELOQTALGNLKIYYNSKAITSSSE-KSADQFLNTLLFKGFFTG 60
Db 1 ESQDPTPDELHKSSEFTGT-MGNMK--LYDDHYVSATKVKSVDFLAHDLIYNISDKK 57
QY 61 HPWNLLVDLGSTAATSEYEGSSVDLYGAYGYQC-----AGTPTNKTACMYGGVTL 113
Db 58 LKNYDKVKTLELNEDEAKYKDEVDVYGSNYVNCYFSSKDNVGVKVTGGKTCMYGKIT 117
QY 114 HDNNRLTEE--KKVPINLWIDGKQTVPIDKVKTSKEVTQVQELDQARHYLHGKFGLYN 171
Db 118 HEGNFDNGNLQNLVIRY-ENKNTISFE-VQTDKKSVAQELDIKARNFLINKNLYE 175
QY 172 SDSFGGKVQGLIVFHSSEGSTVSYDLFDAQGYPD--TLRIYRDNTTISSTLSISLY 229
Db 176 FNS--SPYETGYIKFTIENNGNTFWYDMPAPGDKFDQSKYLMYNDNKTIVDSKRVKIEVH 233
QY 230 LYT 232
Db 234 LTT 236

RESULT 28
Q06533 PRELIMINARY; PRT; 234 AA.
ID Q06533
AC Q06533
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin-pyrogenic toxin (Fragment).
OS Staphylococcus.
OC Bacteria; Firmicutes; Bacillales.
OX NCBI_TaxID=1279;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94325995; PubMed=8049778;
RA Van den Bussche R.A., Lyon J.D., Bohach G.A.;
RL Mol. Phylogenet. Evol. 2:281-292(1993).
DR HSSP; P34071; 1SE2.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bact_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=740N;
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications."
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13375; AAA26619.1; -.
DR HSSP; P34071; 1SE2.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bact_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27642 MW; C77009F46BC8D645 CRC64;

Query Match 22.8%; Score 277.5; DB 2; Length 239;
Best Local Similarity 32.1%; Pred. No. 1.3e-14;
Matches 75; Conservative 45; Mismatches 95; Indels 19; Gaps 9;

QY 11 DLKSELOQTALGNLKIYYNSKAITSSSE-KSADQFLNTLLFKGFFTGHPWNLLV 69
Db 10 DLKSEFTGT-MDNMK--LYDDHYVSATKVKSVDFLAHDLIYNISDKKLNKYDKVT 66
QY 70 DLGSTAATSEYEGSSVDLYGAYGYQC-----AGTPTNKTACMYGGVTLHDNNRLTEE 122
Db 67 ELLNEDLAKYKDEVDVYGSNYVNCYFSSKDNVGVKVTGGKTCMYGKITKEGNHFDNG 126
QY 123 --KKVPINLWIDGKQTVPIDKVKTSKEVTQVQELDQARHYLHGKFGLYNSDSFGGKVQ 180
Db 127 NLQNLVIRY-ENKNTISFE-VQTDKKSVAQELDIKARNFLINKNLYEFNS--SPYE 182
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPD--TLRIYRDNTTISSTLSISLYLT 232
Db 183 TGYIKFTIENNGNTFWYDMPAPGDKFDQSKYLMYNDNKTIVDSKRVKIEVHLLT 236

RESULT 27
Q06533 PRELIMINARY; PRT; 239 AA.
ID Q06533
AC Q06533
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MNCopeland;
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications."
RL Infect. Immun. 61:4254-4262(1993).
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FT NON TER 1 1
FT NON TER 234 234
SQ SEQUENCE 234 AA; 27122 MW; D6A7B45FB9810052 CRC64;

Query Match 22.7%; Score 276.5; DB 2; Length 234;
Best Local Similarity 32.1%; Pred. No. 1.6e-14;
Matches 75; Conservative 45; Mismatches 95; Indels 19; Gaps 9;

Qy 11 DLKKSSELOGTALGNLKOIYYNSKAITSE-KSADQFLNTLLKFGFFTGHPWYNDLLV 69
Db 5 DLKKSSEFTGT-MGNMK--VLYDDNVYSATKVSVDKFLAHLDIYINISDKRLKXVDKVT 61

Qy 70 DLGSTAATSEYEGSSVDLYGAYGYQC-----AGTPNKTCMYGGVTLHDNNRLTEE 122
Db 62 ELLNEDLAKKYKDEVDVYGSNYVYVYFSSKDNVGVKGTGKTCMYGGITKEGNEHFDNG 121

Qy 123 --KKVPLNLDGKQTTVPIDKVKTSKEVTVQELDLOARHYLHGKFGLYNSDSFGKVKQ 180
Db 122 NLQNVLRVT-ENKRNITSE-VQTDKSVTAQELDIKARFLINKNLYEFNS--SPYE 177

Qy 181 RGLIVFHSSEGSTVSYDLFDAQOQYDP--TLRIYRDNTTISSTLSLSLYLT 232
Db 178 TGYIKFIENNFTFYWDMPAPGDKQSKYLMWYNDNKTVDSKSVKIEVHLTT 231

RESULT 29
Q93CC6 PRELIMINARY; PRT; 242 AA.
AC Q93CC6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin type I (Fragment).
OC Staphylococcus aureus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COL;
RA Yarwood J.M., McCormick J.K., Paustian M.L., Orwin P.M., Kapur V., Schlievert P.M.;
RL "Staphylococcus aureus pathogenicity island 3 (SapI3).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DB EMBL: AF410775; AAL04146.1;
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0015070; F:toxin activity; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact endotox.
DR InterPro: IPR006177; BctrI tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006125; Staph/Strep toxin.
DR InterPro: IPR008375; Staph exotoxin.
DR Pfam: PF01123; Staph strp toxin; 1.
DR Pfam: PF02876; Staph strp tox C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PRINTS: PR01800; STAPHEXOTOXN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 242 AA; 28184 MW; F6EEFD4AF8C30D85 CRC64;

Query Match 22.7%; Score 276.5; DB 2; Length 242;
Best Local Similarity 29.3%; Pred. No. 1.6e-14;
Matches 68; Conservative 34; Mismatches 69; Indels 61; Gaps 7;

Qy 17 ELQGTALGNLK---QYYNSKAITSEKSADQFLNTLLKFGFFTGHPWYNDLLVDLGS 73
Db 44 KLOGVSGNFTSHQLEYIDGKTYLSQ-----FHN----- 74

Qy 74 TAATSEYEGS---SVLDYGVYGYQCAGGTGPNKTCMYGGVTLHDNNRLTEEKKVPIN 128
Db 75 -----EYEAKRLDKHDKVDIFGYSGLC-----NTKYMYGGITLANQN-LDKPRNIPIN 122
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Qy 129 LWIDGKQTTVPIDKVKTSKEVTVQELDLOARHYLHGKFGLYN-----SDSFG 176
Db 123 LWVNGKQNTISTDKVSTQKKEVTAQELDIKURKYLQNEYIYNGFNKTKGQGYQSKFN 182

Qy 177 GKVRGLIVFHSSEGSTVSYDLFDAQOQYDPDRLRIYRDNTTISSTLSLSL 228
Db 183 SGFNKGKITFHLNNEPSFTYDLFTGTGQAESFLKIYDDNKTIIDTFNPHLDV 234

RESULT 30
Q7XOE8 PRELIMINARY; PRT; 207 AA.
AC Q7XOE8;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin type I (Fragment).
OC Staphylococcus aureus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AB-8802;
RA Blaiotta G., Pennacchia C., Casaburi A., Ercolini D., Fusco V., Villani F.;
RL "Detection of staphylococcal enterotoxin type G precursors on Staphylococcus spp. strains isolated from meat and dairy products.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DB EMBL: AY291444; AAP78524.1;
DR NON_TER 207 207
SQ SEQUENCE 207 AA; 23953 MW; AE71FC176ES5842C CRC64;

Query Match 22.6%; Score 275.5; DB 2; Length 207;
Best Local Similarity 34.4%; Pred. No. 1.6e-14;
Matches 72; Conservative 34; Mismatches 66; Indels 37; Gaps 10;

Qy 8 NEKDLRKSELOG-TALGNLKQIY-----YNSKAITSEKSADQFLNTLLKFGFFTGHP 62
Db 17 NIKDL---SYAQGDIGVGNLRNFYTKYDIDLKGVTDKNLP-----IANQLEFS---TG-- 64

Qy 63 WYNDLLVGLSTAATSEYEGSSVDLYGAYGYQCAGGTGPNKTCMYGGVTLHDNNRLTEE 122
Db 65 -TNDLISESNWDEISKEFGKXNDIFGIDYNGPC-----KTKMYGATL-SQYILNSA 116

Qy 123 KQVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLOARHYLHGKFGLYNSDSFG-GK--- 178
Db 117 RKIPINLWINGKHKTISTDKIATNKKLVTAQELDKLRYLQBEYNTYGHNNNGKGEYG 176

Qy 179 -----VORGLIVFHSSEGSTVSYDLF 199
Db 177 YKSFYSGFNKGVLFHLNDEKSFSDLP 205

RESULT 31
Q7XOE7 PRELIMINARY; PRT; 218 AA.
AC Q7XOE7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin type I (Fragment).
OC Staphylococcus aureus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AS14;
RA Blaiotta G., Pennacchia C., Casaburi A., Ercolini D., Fusco V., Villani F.;
RL "Detection of staphylococcal enterotoxin type G precursors on Staphylococcus spp. strains isolated from meat and dairy products.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
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DR EMBL: AY291445; AAF78526.1; -
FT NON TER 218 218
SQ SEQUENCE 218 AA; 24993 MW; 698BBBCE49754350 CRC64;

Query Match
  22.3%; Score 271.5; DB 2; Length 218;
Best Local Similarity 32.4%; Pred. No. 3.5e-14;
Matches 72; Conservative 37; Mismatches 76; Indels 37; Gaps 10;

Qy 8 NEKDLRKSELOG-TALGNLKOIY-----YNSKAITSEKSADQFLNTLLFKGFTGHP 62
Db 17 NIKDL---TYAGDIGVGNLRFYTKHDYIDLKGVTDKNLP-----IANQLEFS---TG-- 64

Qy 63 WYNLLVDLSTAATSEYSSVDLYGAYGYCQAGGTPNKTAQMGVGLHNNRLTEE 122
Db 65 -TNDLISESNWDEISFKGKGLDIFGIDYNGPC-----KSKYMYGGATL-SQYLSNA 116

Qy 123 KKVPIINWIDGKQTVPIIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFG-GK--- 178
Db 117 RKIPINLWNGKHKTISTDKIATNKLVLTAQEIIDVKLRYLQEBYNYGHNTGKGKEYG 176

Qy 179 -----VQSGLVFHSSEGSTVSVDLFDAGQGYPTLLRI 212
Db 177 YKSFYSGFNGKVLFLHNLNEKFSYDLFTYNGLPLVSFLKI 218

RESULT 32
Q7X0E9 PRELIMINARY; PRT; 218 AA.
AC Q7X0E9;
DT 01-OCT-2003 (TRENBLrel. 25, Created)
DT 01-OCT-2003 (TRENBLrel. 25, Last sequence update)
DE Enterotoxin type I (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R1;
RA Baiotta G., Pennacchia C., Casaburi A., Ercolini D., Fusco V.,
RA Villani F.;
RT "Detection of staphylococcal enterotoxin type G precursors on
RL Staphylococcus spp. strains isolated from meat and dairy products.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AY291443; AAF78522.1; -
FT NON TER 218 218
SQ SEQUENCE 218 AA; 24994 MW; 698329CE49754350 CRC64;

Query Match
  22.2%; Score 270.5; DB 2; Length 218;
Best Local Similarity 32.4%; Pred. No. 4.2e-14;
Matches 72; Conservative 37; Mismatches 76; Indels 37; Gaps 10;

Qy 8 NEKDLRKSELOG-TALGNLKOIY-----YNSKAITSEKSADQFLNTLLFKGFTGHP 62
Db 17 NIKDL---TYAGDIGVGNLRFYTKHDYIDLKGVTDKNLP-----IANQLEFS---TG-- 64

Qy 63 WYNLLVDLSTAATSEYSSVDLYGAYGYCQAGGTPNKTAQMGVGLHNNRLTEE 122
Db 65 -TNDLISESNWDEISFKGKGLDIFGIDYNGPC-----KSKYMYGGATL-SQYLSNA 116

Qy 123 KKVPIINWIDGKQTVPIIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFG-GK--- 178
Db 117 RKIPINLWNGKHKTISTDKIATNKLVLTAQEIIDVKLRYLQEBYNYGHNTGKGKEYG 176

Qy 179 -----VQSGLVFHSSEGSTVSVDLFDAGQGYPTLLRI 212
Db 177 YKSFYSGFNGKVLFLHNLNEKFSYDLFTYNGLPLVSFLKI 218

RESULT 33
Q8K6K5
ID Q8K6K5
AC Q8K6K5;
PRELIMINARY; PRT; 251 AA.
ID Q9F0L6 PRELIMINARY; PRT; 271 AA.
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DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Exotoxin type A-phage associated (spea precursor).
GN SPEA3 OR SPYM3 1301 OR SP50560.
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206;
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Cammelli D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SSI-1 / Serotype M3;
RA Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
RA Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
RA Hayashi H., Hamada S.;
RT "The genome of invasive Streptococcus pyogenes; a comparative analysis
RT of S. pyogenes SSI-1, SF370 and MGAS8232.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB014161; AAM79908.1; -
DR EMBL: AF005142; BAC63655.1; -
DR PIR: A60108; A60108.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0015070; F:toxin activity; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bactrl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_stp_toxin_1.
DR Pfam: PF02876; Staph_stp_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 251 AA; 29260 MW; 05E782CDA01BFCD5 CRC64;

Query Match
  22.0%; Score 268.5; DB 16; Length 251;
Best Local Similarity 32.1%; Pred. No. 7.4e-14;
Matches 76; Conservative 46; Mismatches 96; Indels 19; Gaps 10;

Qy 4 SEBINEKDLRKSELOGTAL-GNLKQIYY-YNSKAIT-SSKSADQFLNTLLFKGFTG 60
Db 25 SQEFAQQDPDFSQLHRSSLVKLNQNIYLYEGDPVTHENVKASVDQLLSDLIYN---VS 81

Qy 61 HPYNDLLVDLSTAATSEYSSVDLYGAYGYCQ-AGGTENKTAQMGVGLHNNRL 119
Db 82 GPNYDLKLTENQEMATLFDKNDIDYGVETHYLLCYLCENAESACIYGGVTHNEGNHL 141

Qy 120 TEKKVPIINWIDGKQTVPIIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKV 179
Db 142 ETPKKIIVKVSIDGIGQ-SLSFD-IEFNKQNTAQELDYKVKYLTNDKLYNGP--SKY 197

Qy 180 QRGLIVFHSSEGSTVSVDLFD----AQGYPTLLRIYRDNTTISTSTLSISLYLT 232
Db 198 ETGYIKFIPKNKESFWDFPSPPEFTQSKY----LMIYKDNETLDSNTSQIEVLYLT 250

RESULT 34
Q9F0L6
ID Q9F0L6 PRELIMINARY; PRT; 271 AA.
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QY 61 HPWYNDLLVLDLSTAATSEYEGSSVDLYGAYGYQC-----AGGTENKTAQMGVGTLL 113
Db 58 LKNVDKVTTELLNEDLAKYKDEVDVYGSYNYNCYFSSKDNVGVKVTGGKTCMYGKITK 117
QY 114 HNNRLTEEK--KVPINLWIDGKQTTPVIDKVKTSKEVTVOELDLQARHYLHGKFGLYN 171
Db 118 HEGNHFNDGKLNQVLRVY-ENKRNITSE-VOITDKSVTAQELDKARNELINKKNLYE 175
QY 172 SDSFGGKQVGLIVPHSSEGSTVSVDLPDAQGYPD--TLRIYRDNTTISSTLSISLY 229
Db 176 FNS--SPYETGYKRIENNGNFTWYDMPAPGDKPDKQKLYMYNDKNTVDSKSVKIEVH 233
QY 230 LYT 232
Db 234 LTT 236

RESULT 37
Q8NVW2 PRELIMINARY; PRT; 242 AA.
AC Q8NVW2;
DT 01-OCT-2002 (TREMELrel. 22, Created)
DT 01-OCT-2002 (TREMELrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Staphylococcus enterotoxin Sek.
GN SEK2 OR MW1938.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.,
RT "Genome and virulence determinants of high virulence community-
acquired MRSA."
RL Lancet 359:1819-1827 (2002).
DR EMBL; AF004828; BAB95803.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph_toxin.
DR Pfam; PF01123; Staph_stp_toxin.
DR Pfam; PF02876; Staph_stp_tox_C.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 242 AA; 27848 MW; FC377CB4C9BBB4E3 CRC64;

Query Match 21.7%; Score 264; DB 16; Length 242;
Best Local Similarity 30.0%; Pred. No. 1.6e-13;
Matches 67; Conservative 38; Mismatches 84; Indels 34; Gaps 9;

QY 23 LGNLKQIY----YNSKAITSEKSAQDFLTNTLLFKGFFTHPWNLDLVLGSLTAATS 78
Db 29 IDNLRNFYTKDFINLKDY----KNDTFPIANQLQF-----SNESY-DLISESKDFNFKFS 78
QY 79 EYEGSSVDLYGAYGYQCAGGTENKTAQMGVGTLLDNNRLTEKKVPINLWIDGKQVTV 138
Db 79 NFKGKLDVFGISYNGQC-----NTKYIYGVITA-TNEYLDKSRNIPINIWINGNHTKI 131
QY 139 PIDKVKTSKEVTVOELDLQARHYLHGKFGLY-----NSDSFGGK-----VORGLIVF 186
Db 132 STNKVSTNKKFVTAQELIDIKLRYLQEEYNIYGHNGTKGGEYGHKSKFYSGFNIGKVT 191
QY 187 HSESGSTVSVDLP-DAQGYPTTLRIYRDNTTISSTLSISL 228
Db 192 HLNNDTFSYDLFTGDDGLPKSFLEKDYEDNKTVESEKFLHDV 234
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RESULT 38

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Q93CC5 PRELIMINARY; PRT; 242 AA.
ID Q93CC5;
AC Q93CC5;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Sek.
GN SEK.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=COL;
RC Yarwood J.M., McCormick J.K., Faustian M.L., Orwin P.M., Kapur V.,
RA Schlievert F.M.;
RA "Staphylococcus aureus pathogenicity island 3 (SapI3).";
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410775; AAL04147.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph_toxin.
DR Pfam; PF01123; Staph_stp_toxin.
DR Pfam; PF02876; Staph_stp_tox_C.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 242 AA; 27727 MW; 207938B999DC9A9A CRC64;

Query Match 21.6%; Score 263; DB 2; Length 242;
Best Local Similarity 30.1%; Pred. No. 2e-13;
Matches 66; Conservative 35; Mismatches 92; Indels 26; Gaps 7;

QY 23 LGNLKQIYNYNSKAITSEKSAQDFLTNTLLFKGFFTHPWNLDLVLGSLTAATSEYEG 82
Db 29 IDNLRNFYTKDFVLDKVDKNDTPIANQLQF-----SNESY-DLISESKDFNFKFSFKG 82
QY 83 SSVLDYGAYGYQCAGGTENKTAQMGVGTLLDNNRLTEKKVPINLWIDGKQVTVPIDK 142
Db 83 KLDVFGISYNGQC-----NTKYIYGVITA-TNEYLDKSRNIPINIWINGNHTISTNK 135
QY 143 VKTSKEVTVOELDLQARHYLHGKFGLY-----NSDSFGGK-----VORGLIVFHSSE 190
Db 136 VSTNKKFVTAQELIDVLRKYLQEEYNIYGHNGTKGGEYGHKSKFYSGFNIGKVTFLNN 195
QY 191 GSTVSDYDLF-DAQGYPTTLRIYRDNTTISSTLSISL 228
Db 196 NDTFSYDLFTGDDGLPKSFLEKDYEDNKTVESEKFLHDV 234
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RESULT 39

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O54476 PRELIMINARY; PRT; 242 AA.
ID O54476;
AC O54476;
DT 01-JUN-1998 (TREMELrel. 06, Created)
DT 01-JUN-1998 (TREMELrel. 06, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Enterotoxin.
GN ENT.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
SEQUENCE FROM N.A.
RC STEAIN-RN4282; TRANSPON=Trn557;
RX MEDLINE=98385824; PubMed=9720870;
RA Lindsay J.A., Ruzin A., Ross H.F., Kurepina N., Novick R.P.;
```

"The gene for toxic shock toxin is carried by a family of mobile pathogenicity islands in *Staphylococcus aureus*.";
 Mol. Microbiol. 29:527-543 (1998).

DR EMBL; U93688; RAC28968.1; -;
 DR HSP; P13163; ISX1.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bctr1_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 SQ SEQUENCE 242 AA; 27720 MW; 28CB4F2EE6B66B9 CRC64;

Query Match 21.6%; Score 263; DB 2; Length 242;
 Best Local Similarity 30.1%; Pred. No. 2e-13;
 Matches 66; Conservative 35; Mismatches 92; Indels 26; Gaps 7;
 QY 23 LGNLKQIYYNKAITSSEKSDQFLNTLLFKGFTGHPWYNDLLVLDLGGSTAATSEYEG 82
 DB 29 IDNLRFYTKDFVLDKVDKNDTPIANQLQF-----SNESY-DLISEKDFNKSFKG 82
 QY 83 SSVLDYGAYGYQACGTPNKTACMGVTVLHNNRLTEKKVPINLWIDGKQTTVPIDK 142
 DB 83 KKLDFGIGSYNGQC-----NTRYIYGVTA-TNEYLDKSRNIPINWINGNHKTIISTNK 135
 QY 143 VKTSKKEVTQVELDQARHVLHCKFGLY-----NSDSFGK-----VQRLIVPHSSE 190
 DB 136 VSTNKKLVTAQELDVLRKYLQBEYIMYHNGTKGEEYGHKSKFYSGNIGKVPFLNN 195
 QY 191 GSTVSYDLF-DAQGQVPTLLRIYRDNNTTISLSLSL 228
 DB 196 NDTFSYDLFTYDGLPKSFLKIYEDNKTVESEKFLDV 234

RESULT 40
 Q06534 PRELIMINARY; PRT; 239 AA.
 AC Q06534;
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Enterotoxin (Fragment).
 OS *Staphylococcus aureus*.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94011313; PubMed=8406814;
 RA Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;
 RT "Characterization of novel type C staphylococcal enterotoxins:
 RT biological and evolutionary implications.";
 RL Infect. Immun. 61:4254-4262 (1993).
 DR EMBL; L13379; AAA26623.1; -;
 DR HSP; P34071; 1SE2.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bctr1_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER 1 1

SQ SEQUENCE 239 AA; 27517 MW; F354742619C8D196 CRC64;
 Query Match 21.2%; Score 258.5; DB 2; Length 239;
 Best Local Similarity 30.0%; Pred. No. 4.5e-13;
 Matches 73; Conservative 48; Mismatches 103; Indels 19; Gaps 9;
 QY 2 EKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSE-KSADQPLTNTLLFKGFTG 60
 DB 1 ESQDPPTPDELHKASKFTG-LMENMKVL--YDDRYVSATKVKSVKFLAHDLIYNSDKK 57
 QY 61 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGVQC-----AGGTPNKTACWYGGVTL 113
 DB 58 LKNYDKVKTLELLEDLAKKYDEVVDVYGSYNYVNCFFSSKDNVGVKGTGKTCMYGKITK 117
 QY 114 HDNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKKEVTQVELDQARHVLHCKFGLYN 171
 DB 118 HEGNFDNGNLQNVLIIRVY-ENKENTISFE-VQTDKKSVAQELDIKARSLINKKNLYE 175
 QY 172 SDSFGGKQVQGLIVPHSSEGSTVSYDLFDAQGQYD--TLRIYRDNNTTISLSLSLY 229
 DB 176 FNS--SPYETGYIKFIENNGNTFWYDMWPAPGKFDOSKYLMMYNDNKTVDKSKVLEHV 233
 QY 230 LYT 232
 DB 234 LTT 236
 RESULT 41
 P97163 PRELIMINARY; PRT; 236 AA.
 ID P97163;
 AC P97163; P97164;
 DT 01-MAY-1997 (T-EMBLrel. 03, Created)
 DT 01-MAY-1997 (T-EMBLrel. 03, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Type A exotoxin precursor (Fragment).
 GN SPEA.
 OS *Streptococcus pyogenes*.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MGAS156, and MGAS500;
 RX MEDLINE=92044323; PubMed=1940804;
 RA Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
 RT "Characterization and clonal distribution of four alleles of the speA
 RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
 RL J. Exp. Med. 174:1271-1274 (1991).
 DR EMBL; X61556; CAA43754.1; -;
 DR EMBL; X61557; CAA43755.1; -;
 DR EMBL; X61560; CAA43758.1; -;
 DR EMBL; X61555; CAA43753.1; -;
 DR EMBL; X61558; CAA43756.1; -;
 DR EMBL; X61559; CAA43757.1; -;
 DR EMBL; X61554; CAA43752.1; -;
 DR PIR; A60108; A60108.
 DR HSP; P08095; 1B1Z.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bctr1_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Signal.
 FT NON_TER 1 1


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FT SIGNAL      <1    22          POTENTIAL.
FT CHAIN       23   >236        TYPE A EXOTOXIN.
FT NON TER     236   236
SQ SEQUENCE    236 AA; 27454 MW; 3FB3F41ABDDC13A84 CRC64;

Query Match      20.9%; Score 254.5; DB 2; Length 236;
Best Local Similarity 32.0%; Pred. No. 9.3e-13;
Matches 74; Conservative 44; Mismatches 94; Indels 19; Gaps 10;

Qy 4 SEEINEKDLRKKSELOCTAL-GNLIKQIYY YNSKAIT-SSEKSADQFLTNTLFLKGFFTG 60
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 17 SQEVAQQDPDPSQLHRSSLVKNLQNLYFYLEGDPVTHENVKSVVDQLSLHDIYNN---VS 73
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 61 HPWINDLLVLGSTAASTSEYEGSSVDILYGAVGYQC--AGGTPNKATCMYGGVTLHDNNRL 119
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 74 GPNDVKUKTELNQEMATFLFKDRKNDVIDVEYHYLCYCENAEASACIYGGVTNHEGNHL 133
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 120 TEEKKVPINLMDGKQTIVPDKRVTKSKETVGTGELDLQARHYLHGFGFYNSDSFGKV 179
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 134 EIPKKVVVKSIDGIQ-SLSFD-IETNKOMVTAQELDVKVRKYLTDNKQLYTNGP--SKY 189
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

Qy 180 QRGGLIVFHSSSGSVTSVDLP-----AQGYEDTLIRIYRDNTTISSTLSLSI 226
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 190 ETGVIKFIPTPNKESFWDFPEPFPTQSKY----LMTYKKNETLDNSTSQI236
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT	42
ID	Q54779 PRELIMINARY; PRT; 236 AA.
AC	D54779; Q54613; Q54736; Q54740; Q54781;
DC	01-NOV-1996 (T-EMBLrel_01, Created)
DT	01-NOV-1996 (T-EMBLrel_01, Last sequence update)
DI	01-OCT-2003 (T-EMBLrel_25, Last annotation update)
DE	Type A exotoxin precursor (Fragment).
GN	SPEA.
OS	Streptococcus pyogenes.
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
CC	Streptococcus.
CX	NCB1_TaxID=1314;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=MGA524 AND MGA5158 AND MGA5485 AND MGA5491, and MGA5495;
RX	MEDLINE=92044323; PubMed=1940804;
RA	Neilson K., Schlievert P.M., Seldner R.K., Musser J.M.;
RT	"Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.";
KT	J. Exp. Med. 174:1271-1274(1991).
EL	EMBL; X61569; CAA43767.1; -
DR	EMBL; X61572; CAA43770.1; -
DR	EMBL; X61568; CAA43766.1; -
DR	EMBL; X61570; CAA43768.1; -
DR	EMBL; X61571; CAA43769.1; -
DR	PIR; A60108; A60108.
DR	HSSP; P08095; IBIZ.
DR	GO; GO:000576; Extracellular; IEA.
DR	GO; GO:0015070; F:toxin activity; IEA.
DR	GO; GO:0009405; Pathogenesis; IEA.
DR	InterPro; IPRO08992; Bact_endotox.
DR	InterPro; IPRO06177; Bctrl_tox.
DR	InterPro; IPRO06123; Staph/Strep.toxin.
DR	InterPro; IPRO06126; Staph/Strep tox.
DR	Pfam; PF01123; Stab_Strep_toxin; 1.
DR	Pfam; PF02876; Stab_Strep_cox_C; 1.
DR	PRINTS; PR00279; BACTRLTOXIN.
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW	Signal.
FT	NON TER 1 1
FT	<1 22 POTENTIAL,
FT	SIGNAL TYPE A EXOTOXIN.
FT	CHAIN 23 >236
FT	NON_TER 236

SEQ	SEQUENCE	236 AA; 27468 MW; 29DF2AD575623A84 CRC64;	
	Query Match	20.8%; Score 253.5; DB 2; Length 236;	
	Best Local Similarity	31.6%; Pred. No. 1.1e-12;	
	Matches	73; Conservative 45; Mismatches 94; Indels 19; Gaps 10;	
QY	4	SEBINEKDLRKSELOGTAL-GNLKQIYY-YNSKAIT-SSEKSADQFLNTLLFKGFFTG 60	
DB	17	SEVFAQQDPDSQLHRSSLVKNLQNIPLYEGDPVTHENVKSVQLLSHDLIYN---VS 73	
QY	61	HPWYNDLLVDLGSTAAATSSYEGSSVDLYGAYGYOC-AGGTENKTACMYGGVTLHDNNRL 119	
DB	74	GPNYDLKLTKELNQEMATLFDKDKNDIYGVVEYHLCYLCENAESACIYGGVTNHEGNHL 133	
QY	120	TEEKKVPINLWDIGKQTTVPIDKVKTSKEVTVQVELDQARHYLHGKFGLYNSDSFGGKV 179	
DB	134	ETPKIIVKVSIDGTQ-SLSFD-ISTNKQWTAQELDYKVRKYLTDKNQLYNGP--SKY 189	
QY	180	QRLGIIVFHSSSEGSTVSYDLFD---AQGYPTLLRIYRDNTTISTLSLI 226	
DB	190	ETGYIKFIPKNKESFWDFPPEPTQSKY----LMIYKDNELDSNTSQI 236	
	RESULT 43		
QY	Q9R931	PRELIMINARY; PRT; 222 AA.	
DB	Q9R931		
DT	01-MAY-2000 (TEMBLrel. 13, Created)		
DT	01-MAY-2000 (TEMBLrel. 13, Last sequence update)		
DT	01-OCT-2003 (TEMBLrel. 25, Last annotation update)		
DE	Exotoxin A (Fragment)		
GN	SPEA.		
OS	Streptococcus pyogenes.		
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;		
OC	Streptococcus.		
ON	NCBI_TaxID=1314;		
RX	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=D709.		
RX	MEDLINE=99137798; PubMed=9952369;		
RA	Bessen D.E., Izzo M.W., Fiorentino T.R., Caringal R.M.,		
RA	Hollinghead S.K., Beall B.;		
RT	"Genetic linkage of exotoxin alleles and emm gene markers for tissue		
RT	tropism in group A streptococci.";		
RL	J. Infect. Dis. 179:627-636(1999).		
DR	EWEL; AFG55698; RAD11624.1; -.		
DR	PIR; A60108; A60108.		
DR	HSP; P08095; IB1Z.		
DR	GO; GO:0005576; C:extracellular; IEA.		
DR	GO; GO:0015070; F:toxin activity; IEA.		
DR	GO; GO:0009405; F:pathogenesis; IEA.		
DR	InterPro; IPRO08992; Bact_endotox.		
DR	InterPro; IPRO06177; Bctr_l tox.		
DR	InterPro; IPRO06123; Staph/Strep_toxin.		
DR	InterPro; IPRO06126; Staph/Strep_tox.		
DR	InterPro; IPRO06173; Staph/Strep_tox.		
DR	Pfam; PF01123; Staph_strep_toxin; 1.		
DR	Pfam; PF02876; Staph_strep_toxin; 1.		
DR	PRINTS; PR00279; BACTRLTOXIN.		
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.		
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.		
FT	NON_TER	1	
FT	NON_TER	222	
SEQ	SEQUENCE	222 AA; 25759 MW; 48B57ADD91FBA3 CRC64;	
	Query Match	20.7%; Score 252.5; DB 2; Length 222;	
	Best Local Similarity	32.0%; Pred. No. 1.2e-12;	
	Matches	73; Conservative 44; Mismatches 92; Indels 19; Gaps 10;	
QY	4	SEBINEKDLRKSELOGTAL-GNLKQIYY-YNSKAIT-SSEKSADQFLNTLLFKGFFTG 60	
DB	5	SQVFAQQDPDSQLHRSSLVKNLQNIPLYEGDPVTHENVKSVQLLSHDLIYN---VS 61	

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QY 61 HPWNLDLVLDGTAATSEYEGSSVDLYGAYGYQC-AGGTPNKTACMYGGVTLHDNNRL 119
Db 62 GPNYDKLTELKQEWATLFRKNVDIYGVYVHLCYLCEAERSACTYGGVTHHEGNHL 121
QY 120 TEKKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKV 179
Db 122 EIPKIVKVSIDGQ-SLSFD-IETSKWVTAQELDYKVRKYLTNDKQLYTNGP--SKY 177

QY 180 ORGLIVPHSSEGSTVSVDLFD-----AQGPDPDTLLRIYRDNNTTISLSI 223
Db 178 ETGYIKFIPKNKESFWDFPPEFTQSKY----LMYKDNETLDSNT 221

RESULT 44
Q54696 PRELIMINARY; PRT; 236 AA.
AC Q54696;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN SBEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS156;
RX MEDLINE=320433; PubMed=1940804;
RA Nelson K., Schlievert P.M., Sclander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes."
RL J. Exp. Med. 174:1271-1274(1991).
DR EMBL, X61573; CAA43771.1; -.
DR FR; S18789; S18789.
DR HSP; P08095; IBLZ.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR Pfam; PF01123; Staph_strep_toxin_1.
DR Pfam; PF02876; Staph_strep_toxin_1.
DR PRINTS; PR00279; BACTELTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 2575 MW; 70FS4120E79127DF CRC64;

Query Match 20.6%; Score 251.5; DB 2; Length 236;
Best Local Similarity 31.7%; Pred. No. 1.6e-12;
Matches 72; Conservative 42; Mismatches 102; Indels 11; Gaps 7;

QY 4 SEINEKDLKKSELOGTAL-GNLKQIY--YVNSKAITSEKSAQOFLNTLLFKGFTG 60
Db 17 SQEVFAQDPNPQLHRSSLVKLNQIYFLYEGDPVHENVKSVQDLUSHDIYN--VS 73

QY 61 HPWNLDLVLDGTAATSEYEGSSVDLYGAYGYQC-AGGTPNKTACMYGGVTLHDNNRL 119
Db 74 GLNYDKLTELKKNRWSLTFKNKNVDIYGVYVHLCYCRNAKRACIYGGVTHHEGNHL 133

QY 120 TEKKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKV 179
Db 134 EIPKIVKVSIDGQ-SLSFD-IETSKWVTAQELDYKVRKYLTNDKQLYTNGP--SKY 189

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QY 180 ORGLIVPHSSEGSTVSVDLFDQAQGYPDTLRIYRDNNTTISLSI 226
Db 190 ETGYIKFISKDKETFWDFPPEFNFQVKYLMYKDNETLDSSTSQI 236

RESULT 45
Q54738 PRELIMINARY; PRT; 260 AA.
AC Q54738;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Superantigen SSA.
GN SSA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS 1842;
RX MEDLINE=94222556; PubMed=8168951;
RA Reda K.B., Kapur V., Mollick J.A., Lamphear J.G., Musser J.M.,
RA Rich R.R.;
RT "Molecular characterization and phylogenetic distribution of the
RT streptococcal superantigen gene (ssa) from Streptococcus pyogenes."
RL Infect. Immun. 62:1867-1874(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS 1842;
RX MEDLINE=96178607; PubMed=8606073;
RA Reda K.B., Kapur V., Goela D., Lamphear J.G., Musser J.M., Rich R.R.;
RT "Phylogenetic distribution of streptococcal superantigen SSA allelic
RT variants provides evidence for horizontal transfer of ssa within
RT Streptococcus pyogenes."
RL Infect. Immun. 64:1161-1165(1996).
DR EMBL; U4793; AAB02149.1; -.
DR HSP; P01552; ISEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR Pfam; PF01123; Staph_strep_toxin_1.
DR Pfam; PF02876; Staph_strep_toxin_1.
DR PRINTS; PR00279; BACTELTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 260 AA; 29836 MW; C122141693B42AD6 CRC64;

Query Match 20.6%; Score 251; DB 2; Length 260;
Best Local Similarity 31.2%; Pred. No. 2e-12;
Matches 72; Conservative 44; Mismatches 97; Indels 18; Gaps 9;

QY 10 KDLKKSELOGTALGNLQIYYNSKAITSEKSAQOFLNTLLFKGFTGHPWNLDLV 69
Db 35 EQLNKSQFTG-VGNLRCL-YDNHFVEGTNVASTGQLLQHLDFPKDLKLNYSVKT 92

QY 70 DLGTAATSEYEGSSVDLYGAYGYQCAGTPN-----KACMYGGVTLHDNNRLTEKK 124
Db 93 EFNKDLAAKKNKVDIFGNTYNYCYSEGSCKNAKATCMYGGVTHEHRNQI--EGK 150

QY 125 VPINLMT---DGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQR 181
Db 151 FP-NITVKVYEDNENILSPD-IITNKKQVTVQELDCDKTRKILVSRKNLYEFNN--SPYET 206

QY 182 GLIVPHSSEGSTVSVDLFDQAQGYPD--TLRIYRDNNTTISLSI 230
Db 207 GYIKFISSGDSFWMYDMPAPGAIFQSKYLMYNDNKTVSSSAIAIEVHL 257

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RESULT 46
Q54971 PRELIMINARY; PRT; 260 AA.
ID AC Q54971;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE Superantigen.
GN SSA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Weiler;
RX MEDLINE=94222556; PubMed=8168951;
RA Reda K.B., Kapur V., Mollick J.A., Lamphear J.G., Musser J.M.,
EA Rich R.R.;
RT "Molecular characterization and phylogenetic distribution of the
RT streptococcal superantigen gene (ssa) from Streptococcus pyogenes."
RL Infect. Immun. 62:1867-1874(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.pyogenes;
RX MEDLINE=96178602; PubMed=8606073;
RA Reda K.B., Kapur V., Goela D., Lamphear J.G., Musser J.M., Rich R.R.;
RT "Phylogenetic distribution of streptococcal superantigen SSA allelic
RT variants provides evidence for horizontal transfer of ssa within
RT Streptococcus pyogenes."
RL Infect. Immun. 64:1161-1165(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=S.pyogenes; STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206;
RA Beres S.B., Syiva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.P., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence."
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=S.pyogenes; STRAIN=SSI-1 / Serotype M3;
RA Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
RA Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
RA Hayashi H., Hamada S.;
RT "The genome of invasive Streptococcus pyogenes; a comparative analysis
RT of S. pyogenes SSI-1, SF370 and MGAS8232."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U48794; AAB02150.1; -.
DR EMBL; U48792; AAB02148.1; -.
DR EMBL; AE014155; AAM79527.1; -.
DR EMBL; AP005144; BAC64214.1; -.
DR HSP; P01552; ISEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR Pfam; PF02876; Staph_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Complete proteome.
KW SEQUENCE 260 AA; 29767 MW; EA1FB7CCAE80F99B CRC64;

Query Match 20.6%; Score 251; DB 2; Length 260;
Best Local Similarity 31.2%; Pred. No. 2e-12; Indels 18; Gaps 9;
Matches 72; Conservative 44; Mismatches 97; Indels 18; Gaps 9;

OY 10 KDLRKSELOQTALGNLKIYYVNSKAITSSKSDAQFLNTLLPKGFTGHPWYNLLV 69
DB 35 EQLNKSQFTG-VMGNLRCL-YDNHFVEGTNVRSTGQLLQHLIPIKDLKKNYDSVKT 92
OY 70 DLGSTAATSEYEGSSVDLYGAYGYQCAGTNP-----KTACMYGCVTLHNNRLTEKK 124
DB 93 EFNKSLATKYKNDVDFGNSYNYCYSEGNCKNAKKTCTMGYGVTEHHRNQI--EGK 150
OY 125 VPINLMI---DGKQTVPIDKVTKSKVTVQELDQARHYLHGKFGLYNSDSFGKVOR 181
DB 151 FP-NITVKYVENENILSPD-ITNNKQTVQELDCKTRKILVSRKNLYEFNN--SPYET 206
OY 182 GLIVFHSSEGSTVSVDLPDAQOQYD--TLRIYRDNTTISTSLISLYL 230
DB 207 GVTKFTIESSGDSFWYDMMPAPGAIFDQSKYLMYNDNKTVSSSAIAIEVHL 257

RESULT 47
Q54739 PRELIMINARY; PRT; 260 AA.
ID AC Q54739;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE SUPERANTIGEN SSA (Streptococcal superantigen SSA-phase associated)
DE (SSA precursor).
GN SSA OR SPYM3 0920 OR SPS1119.
OS Streptococcus pyogenes, and

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OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314, 198466;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.pyogenes;
RX MEDLINE=94222556; PubMed=8168951;
RA Reda K.B., Kapur V., Mollick J.A., Lamphear J.G., Musser J.M.,
RA Rich R.R.;
RT "Molecular characterization and phylogenetic distribution of the
RT streptococcal superantigen gene (ssa) from Streptococcus pyogenes."
RL Infect. Immun. 62:1867-1874(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=S.pyogenes;
RX MEDLINE=96178602; PubMed=8606073;
RA Reda K.B., Kapur V., Goela D., Lamphear J.G., Musser J.M., Rich R.R.;
RT "Phylogenetic distribution of streptococcal superantigen SSA allelic
RT variants provides evidence for horizontal transfer of ssa within
RT Streptococcus pyogenes."
RL Infect. Immun. 64:1161-1165(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=S.pyogenes; STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206;
RA Beres S.B., Syiva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.P., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence."
RL Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=S.pyogenes; STRAIN=SSI-1 / Serotype M3;
RA Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
RA Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
RA Hayashi H., Hamada S.;
RT "The genome of invasive Streptococcus pyogenes; a comparative analysis
RT of S. pyogenes SSI-1, SF370 and MGAS8232."
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U48794; AAB02150.1; -.
DR EMBL; U48792; AAB02148.1; -.
DR EMBL; AE014155; AAM79527.1; -.
DR EMBL; AP005144; BAC64214.1; -.
DR HSP; P01552; ISEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR Pfam; PF02876; Staph_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Complete proteome.
KW SEQUENCE 260 AA; 29767 MW; EA1FB7CCAE80F99B CRC64;

Query Match 20.6%; Score 251; DB 16; Length 260;
Best Local Similarity 31.2%; Pred. No. 2e-12;
Matches 72; Conservative 44; Mismatches 97; Indels 18; Gaps 9;

OY 10 KDLRKSELOQTALGNLKIYYVNSKAITSSKSDAQFLNTLLPKGFTGHPWYNLLV 69
DB 35 EQLNKSQFTG-VMGNLRCL-YDNHFVEGTNVRSTGQLLQHLIPIKDLKKNYDSVKT 92
OY 70 DLGSTAATSEYEGSSVDLYGAYGYQCAGTNP-----KTACMYGCVTLHNNRLTEKK 124
DB 93 EFNKSLATKYKNDVDFGNSYNYCYSEGNCKNAKKTCTMGYGVTEHHRNQI--EGK 150
OY 125 VPINLMI---DGKQTVPIDKVTKSKVTVQELDQARHYLHGKFGLYNSDSFGKVOR 181
DB 151 FP-NITVKYVENENILSPD-ITNNKQTVQELDCKTRKILVSRKNLYEFNN--SPYET 206
OY 182 GLIVFHSSEGSTVSVDLPDAQOQYD--TLRIYRDNTTISTSLISLYL 230
DB 207 GVTKFTIESSGDSFWYDMMPAPGAIFDQSKYLMYNDNKTVSSSAIAIEVHL 257

RESULT 47
Q54739 PRELIMINARY; PRT; 260 AA.
ID AC Q54739;
DT 01-NOV-1996 (TRENBLrel. 01, Created)
DT 01-NOV-1996 (TRENBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
DE SUPERANTIGEN SSA (Streptococcal superantigen SSA-phase associated)
DE (SSA precursor).
GN SSA OR SPYM3 0920 OR SPS1119.
OS Streptococcus pyogenes, and

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DR	EMBL; X61585; CAA43763.1; -.
DR	EMBL; X61586; CAA43764.1; -.
DR	Pir; A60108; A60108.
DR	HSP; P08095; IBIZ.
DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0015070; F:toxin activity; IEA.
DR	GO; GO:0003405; P:pathogenesis; IEA.
DR	InterPro; IPR008992; Bact_endotox.
DR	InterPro; IPR006177; Bctr1_cox.
DR	InterPro; IPR006123; Staph/Strep_toxin.
DR	InterPro; IPR006126; Staph/Strept_tox.
DR	InterPro; IPR006173; Staph tox OB.
DR	pfam; PF01123; Staph_stip_toxin; 1.
DR	pfam; PF02876; Staph_stip_tox_C; 1.
DR	PRINTS; PR00279; BACTELTOXIN
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW	Signal.
	NON_TER 1 1
FT	SIGNAL <1 22 POTENTIAL.
FT	CHAIN 23 >236 TYPE A EXOTOXIN.
FT	NON_TER 236 236
SEQ	SEQUENCE 236 AA; 27484 MW; 2EF7F41AAC853600 CRC64;
Query Match 20.4%; Score 248.5; DB 2; Length 236;	
Best Local Similarity 31.6%; Pred.No.2.8e-12;	
Matches 73; Conservative 44; Mismatches 95; Indels 19; Gaps 10;	
QY	4 SEINEKDKRKSELOGTAL-GNLKOIYY-YNSKAIT-SSEKSADQLNTLLFKGFFTG 60
DB	17 SOEVFAQQDPDSQLRRSLVKNLQNIYFLYEGDPVTNENKSVDOQLSHDLIYN--VS 73
QY	61 HPWINDLLVLGSTAATSEYGSSVDLYGAYGYQC-AGGTPNKTACMYGGVTLHDNNRL 119
DB	74 GPNYDKLTKELNQENMATLFKQKVDIYSVEYVHLVCLENASRSACIYGVVINHEGNHL 133
QY	120 TREKKVPINLWDIGKQTTPIDIKVTSKKEVTVQVELDLOARHYLHKGFLYNSDSFGKV 179
DB	134 EIPKTIWKVKSIDGIO-SLSFD-IETNKMWTAQELDLYKVRKYLTDNKQLYTNGP--SKY 189
QY	180 ORGLIVFHSSGTSVSYDFD---AQOGVPTLLRIYRDNTTISSTLSLI 226
DB	190 ETGYIKFIPIKNESFWDFEPPEFTQSKEY----LMYKDNETLDNTSQI 236
RESULT 52	
Q8RR77	PRELIMINARY; PRT; 233 AA.
ID	Q8RR77
IC	Q8RR77
AD	Q8RR77
DT	01-JUN-2002 (TrEMBLrel. 21, Created)
DT	01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 21, Last annotation update)
DE	Enterotoxin G (Fragment).
GN	SEG.
OS	Staphylococcus aureus.
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_Taxid=1280;	
RN	[1]
RN	SEQUENCE FROM N.A.
RP	MEDLINE=21871379; PubMed=11880405;
RA	Omoce K., Ishikawa M., Shimoda Y., Hu D.L., Ueda S., Shinagawa K.;
RX	"Detection of seg, seh, and sei genes in Staphylococcus aureus
RT	isolates and Determination of the enterotoxin Productivities of S.
RT	aureus isolates Harboring seg, seh, or sei Genes.";
RL	J. Clin. Microbiol. 40:857-862(2002).
DR	EMBL; AB060535; BAB85989.1; -.
DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0015070; F:toxin activity; IEA.
DR	GO; GO:0003405; P:pathogenesis; IEA.
DR	InterPro; IPR008992; Bact_endotox.
DR	InterPro; IPR006177; Bctr1_cox.
DR	InterPro; IPR006123; Staph/Strep_toxin.
DR	InterPro; IPR006173; Staph tox OB.

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DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PS00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 233 AA; 27040 MW; ECE85287D63BF60D CRC64;

Query Match
Best Local Similarity 19.8%; Score 241; DB 2; Length 233;
Matches 72; Conservative 48; Mismatches 88; Indels 42; Gaps 12;

QY 3 KSEINEKDLRKSEKLGQALGNLKOIYY---YNSKAITSSSEKSDQFLNTLLFKGFFT 59
DB 5 KLDELNKVSDYKNN--KGT-MGNVMNLYTSPVVEGRGVNSR-----QFLSHDLIFP---I 54

QY 60 GHPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYOCA-----GGTPNKKTACM 107
DB 55 EYKSYNEVTELENTLANNYKDKVDIFGVPIFYTCIIPKSEPDINQNFEG-----CCM 109

QY 108 YGGVTLH--DNNRLTEBKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHG 165
DB 110 YGGLTFNSSNER---DKLITVQVTTIDNRQSLG--FTITTNKNMVTIQELDYKARHWLTK 164

QY 166 KFGLYNSDSFGKVGQRLIVFHSSEGSTVSVDLFDAGQGYPDT---LLRIYRDNNTTISST 222
DB 165 EKLYEFD--GSAPESGYIKFTEKNNTSFWDFLPKKELVPFVYKFLNIYGNKVVDSK 222

QY 223 SLISLYLYT 232
DB 223 SIRMEVFLNT 232

RESULT 53
Q9EZM3 PRELIMINARY; PRT; 258 AA.
AC Q9EZM3
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE SGL29P.
GN SGL29P.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20571956; PubMed=11123352;
RA Jarrard S., Peyrat M.A., Lim A., Tristram A., Bes M., Mougel C.,
RA Etienne J., Vandenesch F., Bonneville M., Lina G.;
RT "egc, A highly prevalent operon of enterotoxin gene, forms a putative
RT nursery of superantigens in Staphylococcus aureus.";
RL J. Immunol. 166:669-677(2001).
DR EMBL; AF285760; AAC36957.1; -.
DR HSP; P01552; ISB8.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006173; Bact_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PS00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR PROSITE; PS00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 258 AA; 29956 MW; A85619E2FE21E3B7 CRC64;

Query Match
Best Local Similarity 19.8%; Score 241; DB 2; Length 259;
Matches 72; Conservative 48; Mismatches 88; Indels 42; Gaps 12;

QY 3 KSEINEKDLRKSEKLGQALGNLKOIYY---YNSKAITSSSEKSDQFLNTLLFKGFFT 59
DB 5 KLDELNKVSDYKNN--KGT-MGNVMNLYTSPVVEGRGVNSR-----QFLSHDLIFP---I 54

QY 60 GHPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYOCA-----GGTPNKKTACM 107
DB 55 EYKSYNEVTELENTLANNYKDKVDIFGVPIFYTCIIPKSEPDINQNFEG-----CCM 109

QY 108 YGGVTLH--DNNRLTEBKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHG 165
DB 110 YGGLTFNSSNER---DKLITVQVTTIDNRQSLG--FTITTNKNMVTIQELDYKARHWLTK 164

QY 166 KFGLYNSDSFGKVGQRLIVFHSSEGSTVSVDLFDAGQGYPDT---LLRIYRDNNTTISST 222
DB 165 EKLYEFD--GSAPESGYIKFTEKNNTSFWDFLPKKELVPFVYKFLNIYGNKVVDSK 247

QY 223 SLISLYLYT 232
DB 248 SIRMEVFLNT 257

RESULT 54
Q936G4 PRELIMINARY; PRT; 259 AA.
AC Q936G4
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin-like protein.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M;
RX MEDLINE=95050273; PubMed=7961465;
RA Lin W.S., Cunneen T., Lee C.Y.;
RT "Sequence analysis and molecular characterization of genes required
RT for the biosynthesis of type 1 capsular polysaccharide in
RT Staphylococcus aureus.";
RL J. Bacteriol. 176:7005-7016(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=M;
RA Luong T.T., Shu O., Bush K., Lee C.Y.;
RT "The Type 1 Capsular Polysaccharide of Staphylococcus aureus is carried
RT in a Staphylococcal Cassette Chromosome Genetic Element.";
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U10927; AAL26674.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bact_tox.
DR InterPro; IPR005566; Lipoclin_cyFABP.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PS00279; BACTRLTOXIN.
DR PROSITE; PS00213; LIPOCALIN; 1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_2; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 259 AA; 29981 MW; 783E1E4FEF057EDB CRC64;

Query Match
Best Local Similarity 19.6%; Score 238.5; DB 2; Length 259;
Matches 70; Conservative 43; Mismatches 106; Indels 25; Gaps 9;

QY 1 KSEINEKDLRKSEKLGQALGNLKOIYY---YNSKAITSSSEKSDQFLNTLLFKGFFT 58

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Db 24 AETQNDPNISELNKSQY---TGSWHNIWLYNSDPVNAKKIKLSKDFLSHEFIVPINN 79
QY 59 TGHFWYNDLLDVGTAATSEVSGSSVDLYGAYGYQC-----AGTGNKTACM 107
Db 80 PSH--YDVVKELKOSTWASSFDGKEVDIFGVNVPDQCYFLNENIQDSNOGAGSKTTCM 137
QY 108 YGVTLHDNNRLTEKKVPINLMI-DGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGK 166
Db 138 YGGITLNNEN--TNNRIQIVVKKVENDSVTLSPD-INIDKETVTIQELDYKVRNKLISK 194
QY 167 FGLYNSDSFGKVGQGLVHFSSSEGSTVSYDLFDAQGYPTLLRIYRDNTTISLSI 226
Db 195 INLYHLG--GTSYETGYIKFIENGRRYTYWMPDPGFTQSKYLMYIRGNETVESAKTEI 252
QY 227 SLYL 230
Db 253 EVHL 256

RESULT 55
Q9RQ05 PRELIMINARY; PRT; 209 AA.
AC Q9RQ05; (T-EMBLrel. 13, Created)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
DE Mitogenic exotoxin Z (Fragment).
GN SMEZ-2.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2035;
RX MEDLINE=99093428; PubMed=9874566;
RA Prof. T. Moffatt S.L., Berkahn C.J., Fraser J.D.;
RT "Identification and characterization of novel superantigens from
ST Streptococcus pyogenes";
RL J. Exp. Med. 189:189-192(1999).
DR EMBL; AF086626; AAD52087.1; --
DR PDB; 1ET6; 24-MAY-00.
DR PDB; 1EU3; 24-MAY-00.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR Pfam; PF01123; Staph_tox_OB.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24131 MW; 52BF7911BB100152 CRC64;

Query Match 18.2%; Score 222; DB 2; Length 209;
Best Local Similarity 29.1%; Fred. No. 3.4e-10;
Matches 58; Conservative 40; Mismatches 65; Indels 36; Gaps 6;
QY 50 NTLLFKGFTGHPWYNDLLVD-----LGSTAATSEVSGSSVDLYGAY----- 91
Db 6 NSLLRNISTIVVEYSIDVIDEKTSHNLVTKLDVDRDARDFINSEWDEYAANDFKTGDK 65
QY 92 -----YGYOCAGGTGPNKTACMYGVTLDHNNRLTEKKVPINLWIDGKQTTVPIDK 142
Db 66 IAVFSVPFDWNYLSG---KVTAYTYGGITPYQKTSI--PKNIPVNLWINGKQISVPEYNE 120
QY 143 VKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKVGQGLVHFSSSEGS--TVSYDLFDA 201
Db 121 ISTNKTVTVAQEIDLKVRKFLIAQHQLYSS---GSSYKSGKLVFHTNDNSDKYSFDLYV 177

QY 202 QGOVPTLLRIYRDNTTIS 220
Db 178 GYRDKESIFKVKDKNSFN 196
RESULT 56
Q9LAE0 PRELIMINARY; PRT; 209 AA.
AC Q9LAE0; (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DE Mitogenic exotoxin Z-4 (Fragment).
GN SMEZ-4.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9893;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof. T. Moffatt S.L., Weller K.D., Paterson A., Martin D.,
Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143654; AAF66655.1; --
DR HGSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR Pfam; PF01123; Staph_tox_OB.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24108 MW; 67EC279BBC4A8247 CRC64;

Query Match 18.0%; Score 219; DB 2; Length 209;
Best Local Similarity 29.1%; Fred. No. 6e-10;
Matches 58; Conservative 39; Mismatches 66; Indels 36; Gaps 6;
QY 50 NTLLFKGFTGHPWYNDLLVD-----LGSTAATSEVSGSSVDLYGAY----- 91
Db 6 NSLLRNISTIVVEYSIDVIDEKTSHNLVTKLDVDRDARDFINSEWDEYAANDFKTGDK 65
QY 92 -----YGYOCAGGTGPNKTACMYGVTLDHNNRLTEKKVPINLWIDGKQTTVPIDK 142
Db 66 IAVFSVPFDWNYLSG---KVTAYTYGGITPYQKTSI--PKNIPVNLWINGKQISVPEYNE 120
QY 143 VKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKVGQGLVHFSSSEGS--TVSYDLFDA 201
Db 121 ISTNKTVTVAQEIDLKVRKFLIAQHQLYSS---GSSYKSGKLVFHTNDNSDKYSFDLYV 177
QY 202 QGOVPTLLRIYRDNTTIS 220
Db 178 GYRDKESIFKVKDKNSFN 196

RESULT 57
Q9LAD8 PRELIMINARY; PRT; 209 AA.
AC Q9LAD8; (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DE Mitogenic exotoxin Z-7 (Fragment).
GN SMEZ-7.

OS	Streptococcus pyogenes.
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC	Streptococcus.
OX	NCBI_TaxID=13114;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=11574;
RX	MEDLINE=20273982; PubMed=10811869;
RA	Proft T., Mofatt S.L., Weller K.D., Paterson A., Martin D.,
RA	Fraser J.D.;
RT	"The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT	Mosaic Structure, and Significant Antigenic Variation.";
RL	J. Exp. Med. 191.1:1765-1776(2000).
DR	EMBL; AF143657; AAF66657.1; -.
DR	HSSP; P13463; ISXT.
DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0015070; F:toxin activity; IEA.
DR	GO; GO:0009405; P:pathogenesis; IEA.
DR	InterPro; IPR008992; Bact_endotox.
DR	InterPro; IPR006177; Bctr1_tox.
DR	InterPro; IPR006123; Staph_Strep_toxin.
DR	InterPro; IPR006173; Staph_tox_OB.
DR	Pfam; PF01123; Staph_Strep_toxin; 1.
DR	Pfam; PF02876; Staph_Strep_tox_C; 1.
DR	PRINTS; PR00279; BACTRUTOXIN
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT	NON_TER
FT	SEQUENCE 209 AA; 24064 MW; 67E977CD5AA934F7 CRC64;
QY	Query Match
QY	Best Local Similarity 29.1%; Score 219; DB 2; Length 209;
QY	Matches 58; Conservative 39; Mismatches 66; Indels 36; Gaps 6;
DB	50 NTLLEKGFCTGHPWYNDLLVD-----LGSAAATSEYEGSSVDLYGAY----- 91
DB	6 NSLLRNIIYTTIVYBSYSTDIVDFKSHNLVTKLDVDRDFFINSEMDEYAAANDFKAGDK 65
QY	92 -----YGYQCAGGTPNKTCAGYGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDK 142
DB	66 IAVFVSPFDWNYLSEG---KVTATYGGIIPYKTSI--PKNIPVNLWINGKQISVPYNE 120
QY	143 VQTSKKEVTVQELDLQARHYLHGKFGHLYNDSGCGKQKGLIVFHSSEGS--TVSVLDLFD 201
DB	121 ISTNKTNTTVAQEI DLKVRKFLIAQHQLYSS--GSSYKSGKGLVFTNDNDNSKYSDFLE 177
QY	202 QGOYPTDLLRIYRDNTTIS 220
DB	178 GYRDKESIFRVYKONKSFN 196
RESULT 58	
Q9LAC6	Q9LAC6 PRELIMINARY; PRT; 209 AA.
ID	Q9LAC6
AC	Q9LAC6
DT	01-OCT-2000 (TrEMBLrel. 15, Created)
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Mitogenic exotoxin Z-20 (Fragment).
GN	SMEZ-20.
OS	Streptococcus pyogenes.
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC	Streptococcus.
OX	NCBI_TaxID=13114;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=10989;
RX	MEDLINE=20273982; PubMed=10811869;
RA	Proft T., Mofatt S.L., Weller K.D., Paterson A., Martin D.,
RA	Fraser J.D.;
RT	"The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT	Mosaic Structure, and Significant Antigenic Variation.";
RL	J. Exp. Med. 191.1:1765-1776(2000).
DR	EMBL; AF143670; AAF66669.1; -.

Query Match 17.8%; Score 217; DB 2; Length 209;
Best Local Similarity 29.1%; Pred. No. 8.7e-10;
Matches 58; Conservative 38; Mismatches 67; Indels 36; Gaps 6;

QY 50 NTLFKGFTGHPWYNDLLVD-----LGSTAATSEYEGSSVDLYGAY----- 91
Db 6 NSLLRNIYSTIYVESDTVIDFKTSHNLVTKKLDVRDARDFFINSEMDYAAANDFKAGDK 65

QY 92 -----YGVOCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDK 142
Db 66 IAVFSVPFDWNYLSKG---KVTATYTGGITPYQKTSI--PKNIPVNLWINGKQISVPYNE 120

QY 143 VKTSKEVTVQELDLQARHLYHGKFLGYNSSDFGKVGQRLIVFHSSEGS--TVSYDLFDA 201
Db 121 ISTNKTITVAQEIDLKVRKFLIAHQHLYSS---GSSYKSGKLVFHTNDNSDKYSLDLFT 177

QY 202 QGQYPTLLRIYRDNTTIS 220
Db 178 GYRDKESIFKVKDKNSFN 196

RESULT 60
Q9LAE1 PRELIMINARY; PRT; 209 AA.
AC Q9LAE1
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin 2-3 (Fragment).
GN SMEZ-3.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11681;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation."
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143653; AAF66654.1; -.
DR HSP; P13163; LSXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph_toxOB.
DR Pfam; PF01123; Staph_toxOB.
DR Pfam; PF02876; Staph_toxOB.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 209 AA; 24071 MW; FADAFCDIAA87271 CRC64;

Query Match 17.7%; Score 215; DB 2; Length 209;
Best Local Similarity 29.1%; Pred. No. 1.3e-09;
Matches 58; Conservative 38; Mismatches 67; Indels 36; Gaps 6;

QY 50 NTLFKGFTGHPWYNDLLVD-----LGSTAATSEYEGSSVDLYGAY----- 91
Db 6 NSLLRNIYSTIYVESDTVIDFKTSHNLVTKKLDVRDARDFFINSEMDYAAANDFKAGDK 65

QY 92 -----YGVOCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDK 142
Db 66 IAVFSVPFDWNYLSKG---KVTATYTGGITPYQKTSI--PKNIPVNLWINGKQISVPYNE 120

QY 143 VKTSKEVTVQELDLQARHLYHGKFLGYNSSDFGKVGQRLIVFHSSEGS--TVSYDLFDA 201
Db 121 ISTNKTITVAQEIDLKVRKFLIAHQHLYSS---GSSYKSGKLVFHTNDNSDKYSLDLFT 177

QY 202 QGQYPTLLRIYRDNTTIS 220
Db 178 GYRDKESIFKVKDKNSFN 196

RESULT 62
Q9LAC5 PRELIMINARY; PRT; 209 AA.
AC Q9LAC5
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin 2-22 (Fragment).
GN SMEZ-22.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10463;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation."
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143672; AAF66671.1; -.
DR HSP; P13163; LSXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph_toxOB.
DR Pfam; PF01123; Staph_toxOB.
DR Pfam; PF02876; Staph_toxOB.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 209 AA; 24075 MW; 3611E7C456D6EDE8 CRC64;

Query Match 17.8%; Score 217; DB 2; Length 209;
Best Local Similarity 29.1%; Pred. No. 8.7e-10;
Matches 58; Conservative 38; Mismatches 67; Indels 36; Gaps 6;

QY 50 NTLFKGFTGHPWYNDLLVD-----LGSTAATSEYEGSSVDLYGAY----- 91
Db 6 NSLLRNIYSTIYVESDTVIDFKTSHNLVTKKLDVRDARDFFINSEMDYAAANDFKAGDK 65

QY 92 -----YGVOCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDK 142
Db 66 IAVFSVPFDWNYLSKG---KVTATYTGGITPYQKTSI--PKNIPVNLWINGKQISVPYNE 120

QY 143 VKTSKEVTVQELDLQARHLYHGKFLGYNSSDFGKVGQRLIVFHSSEGS--TVSYDLFDA 201
Db 121 ISTNKTITVAQEIDLKVRKFLIAHQHLYSS---GSSYKSGKLVFHTNDNSDKYSLDLFT 177

QY 202 QGQYPTLLRIYRDNTTIS 220
Db 178 GYRDKESIFKVKDKNSFN 196

RESULT 61
Q9LAC4 PRELIMINARY; PRT; 209 AA.
AC Q9LAC4
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin 2-22 (Fragment).
GN SMEZ-22.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10463;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation."
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143672; AAF66671.1; -.
DR HSP; P13163; LSXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph_toxOB.
DR Pfam; PF01123; Staph_toxOB.
DR Pfam; PF02876; Staph_toxOB.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 209 AA; 24075 MW; 3611E7C456D6EDE8 CRC64;

Query Match 17.7%; Score 215; DB 2; Length 209;
Best Local Similarity 29.1%; Pred. No. 1.3e-09;
Matches 58; Conservative 38; Mismatches 67; Indels 36; Gaps 6;

QY 50 NTLFKGFTGHPWYNDLLVD-----LGSTAATSEYEGSSVDLYGAY----- 91
Db 6 NSLLRNIYSTIYVESDTVIDFKTSHNLVTKKLDVRDARDFFINSEMDYAAANDFKAGDK 65

QY 92 -----YGVOCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDK 142
Db 66 IAVFSVPFDWNYLSKG---KVTATYTGGITPYQKTSI--PKNIPVNLWINGKQISVPYNE 120

QY 143 VKTSKEVTVQELDLQARHLYHGKFLGYNSSDFGKVGQRLIVFHSSEGS--TVSYDLFDA 201
Db 121 ISTNKTITVAQEIDLKVRKFLIAHQHLYSS---GSSYKSGKLVFHTNDNSDKYSLDLFT 177

QY 202 QGQYPTLLRIYRDNTTIS 220
Db 178 GYRDKESIFKVKDKNSFN 196

RESULT 62
Q9LAC5 PRELIMINARY; PRT; 209 AA.
AC Q9LAC5
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin 2-22 (Fragment).
GN SMEZ-22.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10463;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation."
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143672; AAF66671.1; -.
DR HSP; P13163; LSXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph_toxOB.
DR Pfam; PF01123; Staph_toxOB.
DR Pfam; PF02876; Staph_toxOB.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 209 AA; 24075 MW; 3611E7C456D6EDE8 CRC64;

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DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-21 (Fragment)
GN SMEZ-21
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11247;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143671; AAF66670.1; -
DR HSSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN_
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER
FT SEQUENCE 209 AA; 24106 MW; 67FD2696FA4BC55A CRC64;

Query Match 17.5%; Score 213; DB 2; Length 209;
Best Local Similarity 28.8%; Pred. No. 1.8e-09;
Matches 57; Conservative 39; Mismatches 67; Indels 36; Gaps 6;

QY 50 NTLFKGFFTHGHPWYNDLLVD-----LGSTAATSEYEGSGVDLYGAY----- 91
Db 6 NSLLRNISTVVEYSSTVIDTIDKTSNHLNLTCKLDVRDARDFTINSEMDYEAANDFKTDGK 65

QY 92 -----GYQCAGGTENKTCMYGGVTLHDNNLTTEEKVPINLWIDGKQTTVPIDK 142
Db 66 IAVSFVDFDWNLYSEG---KVIATYGGITPQKTSI--PKIPVNLWINGKQISVPYNE 120

QY 143 VKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRLIVFHSSEGS--TVSYDLFDA 201
Db 121 ISTNKTITVTAQEIIDLKVRKFLIAHQHLYSS---GSSYKSGKLVFHTNDSKYSFDLFT 177

QY 202 QGYPTLLRIYRDNTIS 220
Db 178 YRKESIFKVKYDNKSNF 196

RESULT 63
QY 01-OCT-2003 (TrEMBLrel. 15, Created)
AC QY01AD9 PRELIMINARY; PRT; 209 AA.
DT 01-OCT-2003 (TrEMBLrel. 15, Last annotation update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-5 (Fragment).
GN SMEZ-5.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11244;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143663; AAF66663.1; -
DR HSSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN_
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER
FT SEQUENCE 209 AA; 24079 MW; 24CA3885469CB99B CRC64;

Query Match 17.3%; Score 211; DB 2; Length 209;
Best Local Similarity 28.3%; Pred. No. 2.7e-09;
Matches 56; Conservative 43; Mismatches 75; Indels 24; Gaps 8;

QY 29 IYVNSKAITSSSEKSAQDFLTNTLFP---KGFTGHPWYNDLLDGLSTAAATSEYEGSV 85
Db 17 VVEYSSTVI--DFKTSNHLNLTCKLDVRDARDFTINSEMDYEAANDFKDGDKI 66

QY 86 DLVGAYY--GYQCAGGTENKTCMYGGVTLHDNNLTTEEKVPINLWIDGKQTTVPIDK 143
Db 67 AMFSVPDFDWNLYSEG---KVIATYGGITPQKTSI--PKIPVNLWINGKQISVPYNEI 121

QY 144 KTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRLIVFHSSEGS--TVSYDLFDA 202
Db 122 STNKTITVTAQEIIDLKVRKFLIAHQHLYSS---GSSYKSGKLVFHTNDSKYSFDLFT 178

QY 203 QGYPTLLRIYRDNTIS 220
Db 179 YRKESIFKVKYDNKSNF 196

RESULT 64
QY 01-OCT-2003 (TrEMBLrel. 15, Created)
AC QY01AD2 PRELIMINARY; PRT; 209 AA.
DT 01-OCT-2003 (TrEMBLrel. 15, Last annotation update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-13 (Fragment).
GN SMEZ-13.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95/31;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143663; AAF66663.1; -
DR HSSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN_

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DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER 1
 SQ SEQUENCE 209 AA; 24072 MW; 984C1B4614589A1E CRC64;

Query Match 17.2%; Score 210; DB 2; Length 209;
 Best Local Similarity 28.8%; Pred. No. 3.2e-09;
 Matches 57; Conservative 39; Mismatches 68; Indels 36; Gaps 6;

QY 50 NTLFLFGFFTGHPYNDLLVD-----LGSTAATSEYEGSSVDLYGAY----- 91
 Db 6 NSLLRNIYSTIVYEYSDTVIDFTKSHNLVTKLDVRDARDFINSEMDVAANDFKAGDK 65
 QY 92 -----YGYOCAGGTPNKTCACMYGGVTLHDNNRLTEEEKYPINLWIDGKQTTVPIDK 142
 Db 66 IAVSFVDFDNNYLSEG---KVIATYTGGITPYQKTSI--PKNIPVNLWIDGKQLISVPYNE 120
 QY 143 VKTSKKEVTVQELDLQARHYLHGKFLGYNDSFGKGQVQRGLIVFHSSEGS-TVSYDLFDA 201
 Db 121 ISNTKTTVAQEIIDLKVRKELIAHQHLYSS--GSSYKSKGLVFHTDNDSDKYSLDLFYV 177
 QY 202 QGQYPTLLRIYRDNTIS 220
 Db 178 GYRDKESIFKVKYDKNKSFN 196

RESULT 65
 Q9LAD6 PRELIMINARY; PRT; 209 AA.

ID Q9LAD6 AC Q9LAD6; AC Q9LAD6;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Mitogenic exotoxin Z-9 (fragment).
 GN SMEZ-9.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RP [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=11299;
 RX MEDLINE=20273982; PubMed=10811859;
 RA Proft T., Moffatt S.L., Weiler K.D., Paterson A., Martin D.,
 RA "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 RL Mosaic Structure, and Significant Antigenic Variation.";
 RL J. Exp. Med. 191:1765-1776(2000).
 DR EMBL; AF143659; AAF66659.1; -.
 DR HSSP; P31663; ISXI.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bctrl_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER 1
 SQ SEQUENCE 209 AA; 24213 MW; B21587BA343B5DD5 CRC64;

Query Match 17.2%; Score 210; DB 2; Length 209;
 Best Local Similarity 29.1%; Pred. No. 3.2e-09;
 Matches 59; Conservative 37; Mismatches 68; Indels 36; Gaps 6;

QY 50 NTLFLFGFFTGHPYNDLLVD-----LGSTAATSEYEGSSVDLYGAY----- 91
 Db 6 NSLLRNIYSTIVYEYSDTVIDFTKSHNLVTKLDVRDARDFINSEMDVAANDFKAGDK 65
 QY 92 -----YGYOCAGGTPNKTCACMYGGVTLHDNNRLTEEEKYPINLWIDGKQTTVPIDK 142

Db 66 IAVSVVFDNNYLSKG---KVTATYVGGITPYQKTGI--PKNIPVNWNIRNKIPIVPYNQ 120

Qy 143 VKTSKEVTVQEILDQARHYLHGKFGLYNSDSFGGKVQRGLIVFHSSEGS-TVSYDLFDA 201
: : ||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
Db 121 ISTNKITVTAQEIIDLKVRFLIAHQHLYSS--GSSVKSGRLVFHTNDNSDKYSFDLFYT 177
: :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Qy 202 GQQYPDTLLRIYRDNTTIS 220
: :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Db 178 GYADKESIFKIYKDNKSFN 196
: :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 66

Q8NZ89 PRELIMINARY; PRT; 233 AA.

ID Q8NZ89 AC Q8NZ89
AC Q8NZ89; AC Q8NZ89
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z.
GN SNEZ_OR SPYM18_2064.
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
CX NCBI_TaxID=186103;
CN [1]

RN RP SEQUENCE FROM N.A.
RC STRAIN=MCA58232 / Serotype M18;
RX MEDLINE=2197593; PubMed=1917108;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4568-4673 (2002).

DR EMEL; AEO10110; AAL98535.1; -
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPRO08992; Bact_endotox.
DR InterPro; IPRO06177; BctR_tox.
DR InterPro; IPRO06123; Staph_Strep_toxin.
DR InterPro; IPRO06173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW complete proteome.
SQ SEQUENCE 233 AA; 26859 MW; 23R07CC9C0AE866 CRC64;

Query Match 17.2%; Score 209.5; DB 16; Length 233;
Best Local Similarity 26.6%; Pred.No.4e-09;
Matches 58; Conservative 43; Mismatches 70; Indels 47; Gaps 8;

Qy 34 SKAITSEKSADQFLN---TLLEKFQFTGHPPYNDLLVD-----LGSTATSE 79
: :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Db 19 SRPVIGLEVDDNSSLRNRYSTIMYE-----YSTVIDFKTSHNLVTKKLVDARDDF 70
: :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Qy 80 YEGSSVDLYGAY-----YGQCAGGTPTAKCYGGVTLHDNNRLTEEK 123
: :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Db 71 FINSEWDEVANDPKGDXTAMFSVPFDNYLSEG---KVIATYGGMTPTYQTISI--PK 125

Qy 124 KVFINLWDGKQTTPIDKVKTSKEVTVQVELDQARHYLHGKFGLYNSDSFGGKVQRGL 183
: :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Db 126 NIPVNLWINGKQISVPEYNISTNKTITVAOEIDLKVRFLIAHQHLYSS---GSSYKSGK 182
: :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Qy 184 IVFHSSEGS-TVSYDLFDAQGQYPDTLLRIYRDNTTIS 220
: :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

Db 183 LVFHTNDNSKYSLDLFYGYRKESIFKYKDNKSFN 220
: :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

RESULT 67

Q7WY99 PRELIMINARY; PRT; 207 AA.
 ID Q7WY99
 AC Q7WY99; (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DE Mitogenic exotoxin Z (Fragment).
 GN SWEZ-16.
 OS Streptococcus canis.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1329;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Igwe E.I., Gertz B.;
 RT "Streptococcal superantigen genes in human pathogenesis group G
 streptococcus."
 RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ564198; CAD91900.1; -
 FT NON TER 1
 FT NON TER 207
 SQ SEQUENCE 207 AA; 24034 MW; C9D5C7B1603BDFC4 CRC64;

Query Match 17.2%; Score 209; DB 2; Length 207;
 Best Local Similarity 28.6%; Pred. No. 3.8e-09;
 Matches 57; Conservative 38; Mismatches 68; Indels 36; Gaps 6;

QY 50 NTLFLKGFTHPWYNDLLVD-----LGSTAATSEYEGSSVDLYGAY----- 91
 Db 5 NSLRNIYSTIVVEYSDTVDFKTSNLTVKLDVRDARDFFINSEMDEYAANDFKAGDR 64
 QY 92 -----YGYCAGGTGPNKTCMGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDK 142
 Db 65 IAVFSPFDWNLYSKG---KVTATYTGITPYQKTSI--PKNIPVNLWINRKQISVPYNE 119
 QY 143 VKTSKEVTVOELDLQARHVLHGKFLGNSDSFGGKVORGLIVFHSSEGS-TVSYDLFDA 201
 Db 120 ISTNKTIVTAQEDLKVRFKLSIQYQLYSS---GSNYKSGKLIVFHTNDNSDKYSLDLFYT 176
 QY 202 QGQYPTLLRIYRDNTTIS 220
 Db 177 GYRDKESIFKVKDKNSFN 195

RESULT 68

Q9LAC9 PRELIMINARY; PRT; 209 AA.
 ID Q9LAC9
 AC Q9LAC9;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Mitogenic exotoxin Z-16 (Fragment).
 GN SWEZ-16.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Profit T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
 Fraser J.D.;
 RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 Mosaic Structure, and Significant Antigenic Variation."
 RL J. Exp. Med. 191:1765-1776(2000).
 DR EMBL; AF143666; AAF66666.1; -
 FT NON TER 1
 FT NON TER 209
 SQ SEQUENCE 209 AA; 24214 MW; 5755ED7340D77527 CRC64;

Query Match 16.9%; Score 206; DB 2; Length 209;
 Best Local Similarity 35.6%; Pred. No. 6.8e-09;
 Matches 42; Conservative 30; Mismatches 40; Indels 6; Gaps 3;

DR InterPro; IPR006123; Staph/Strep toxin.
 DR InterPro; IPR006173; Staph tox_OB.
 DR Pfam; PF01123; Staph_Strp_toxin; 1.
 DR Pfam; PF02876; Staph_Strp_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON TER 1
 FT NON TER 209
 SQ SEQUENCE 209 AA; 24172 MW; A1DB8FA187098BA5 CRC64;

Query Match 17.0%; Score 207; DB 2; Length 209;
 Best Local Similarity 28.6%; Pred. No. 5.6e-09;
 Matches 57; Conservative 38; Mismatches 68; Indels 36; Gaps 6;

QY 50 NTLFLKGFTHPWYNDLLVD-----LGSTAATSEYEGSSVDLYGAY----- 91
 Db 6 NSLRNIYSTIVVEYSDTVDFKTSNLTVKLDVRDARDFFINSEMDEYAANDFKAGDR 65
 QY 92 -----YGYCAGGTGPNKTCMGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDK 142
 Db 66 IAVFSPFDWNLYSKG---KVTATYTGITPYQKTSI--PKNIPVNLWINRKQISVPYNE 120
 QY 143 VKTSKEVTVOELDLQARHVLHGKFLGNSDSFGGKVORGLIVFHSSEGS-TVSYDLFDA 201
 Db 121 ISTNKTIVTAQEDLKVRFKLSIQYQLYSS---GSSYKSGKLIVFHTNDNSDKYSLDLFYT 177
 QY 202 QGQYPTLLRIYRDNTTIS 220
 Db 178 GYRDKESIFKVKDKNSFN 196

RESULT 69

Q9LAC7 PRELIMINARY; PRT; 209 AA.
 ID Q9LAC7
 AC Q9LAC7;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Mitogenic exotoxin Z-18 (Fragment).
 GN SWEZ-18.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Profit T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
 Fraser J.D.;
 RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
 Mosaic Structure, and Significant Antigenic Variation."
 RL J. Exp. Med. 191:1765-1776(2000).
 DR EMBL; AF143666; AAF66666.1; -
 FT NON TER 1
 FT NON TER 209
 SQ SEQUENCE 209 AA; 24214 MW; 5755ED7340D77527 CRC64;

Query Match 16.9%; Score 206; DB 2; Length 209;
 Best Local Similarity 35.6%; Pred. No. 6.8e-09;
 Matches 42; Conservative 30; Mismatches 40; Indels 6; Gaps 3;

QY 104 TACMGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDKTKSVTVQELDLQARHVL 163

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Db      84 TAYTYGGITVYQKTSI--PKNIPVNLWINRKQIPVPYNOISTNKTVTVAQIEDLKVRFEL 141
QY      164 HGKFGLYNSDFGKVGQRLVPHSHSSEGS-TVSYDLFDAQGGVDPDLLRIYRDNNTTIS 220
Db      142 IAQHOLYSS---GSSYKSGKLIVFHTNDNSDKISFDLFTYTGKDYKESIFKYVKNKSNFN 196

RESULT 70
Q9LAD4 PRELIMINARY; PRT; 209 AA.
ID Q9LAD4
AC Q9LAD4
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-11 (Fragment).
GN SMEZ-11.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OC NCBI_TaxID=1314;
RN [1]_TaxID=1314;
RP SEQUENCE FROM N.A.
RC STRAIN=9779;
RX MEDLINE=20273982; PubMed=10811869;
RA Profit T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
RL EMBL; AF143661; AAF66661.1; -.
DR HSSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Stap/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Stap_Strep_toxin; 1.
DR Pfam; PF02876; Stap_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24194 MW; E12EF47B3B8D95DE CRC64;

Query Match 16.9%; Score 206; DB 2; Length 209;
Best Local Similarity 29.1%; Pred. No. 6.8e-09;
Matches 58; Conservative 36; Mismatches 69; Indels 36; Gaps 6;

QY 50 NTLFKGFTGHPWYNDLLVD-----LGSTAATSEYEGSSVDLYGAY----- 91
Db 6 NSLLRNIVSTIVYSDTVDFKTSNLTVKLDVRDARDFFINSEMDEYAANDFKAGDR 65

QY 92 -----YGYQCAGGTPTNCTACMYGVTLDHNNRLTEKKVPINLWIDGKQTTVPIDK 142
Db 66 IAVFSVPDMNYLSKG---KVTATYGGITVYQKTSI--PKNIPVNLWINRKQIPVPYNO 120

QY 143 VKTSKEVTVOELDIQARHYLHGKFGLYNSDFGKVGQRLVPHSHSSEGS-TVSYDLFDA 201
Db 121 ISTNKTVTVAQIEDLKVAKFLISQHLQYSS---GSSYKSGKLIVFHTNDNSDKYSLDLFT 177

QY 202 QGQYDPDLLRIYRDNNTTIS 220
Db 178 GYRDKESIFKYVKNKSNFN 196

RESULT 71
Q9LAC8 PRELIMINARY; PRT; 209 AA.
ID Q9LAC8
AC Q9LAC8
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DE Mitogenic exotoxin Z-11 (Fragment).
GN SMEZ-11.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OC NCBI_TaxID=1314;
RN [1]_TaxID=1314;
RP SEQUENCE FROM N.A.
RC STRAIN=10438;
RX MEDLINE=20273982; PubMed=10811869;
RA Profit T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
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DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-17 (Fragment).
GN SMEZ-17.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OC NCBI_TaxID=1314;
RN [1]_TaxID=1314;
RP SEQUENCE FROM N.A.
RC STRAIN=11686;
RX MEDLINE=20273982; PubMed=10811869;
RA Profit T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
RL EMBL; AF143661; AAF66661.1; -.
DR HSSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Stap/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Stap_Strep_toxin; 1.
DR Pfam; PF02876; Stap_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24181 MW; A333F466398D9DC2 CRC64;

Query Match 16.8%; Score 205; DB 2; Length 209;
Best Local Similarity 28.6%; Pred. No. 8.2e-09;
Matches 57; Conservative 37; Mismatches 69; Indels 36; Gaps 6;

QY 50 NTLFKGFTGHPWYNDLLVD-----LGSTAATSEYEGSSVDLYGAY----- 91
Db 6 NSLLRNIVSTIVYSDTVDFKTSNLTVKLDVRDARDFFINSEMDEYAANDFKAGDR 65

QY 92 -----YGYQCAGGTPTNCTACMYGVTLDHNNRLTEKKVPINLWIDGKQTTVPIDK 142
Db 66 IAVFSVPDMNYLSKG---KVTATYGGITVYQKTSI--PKNIPVNLWINRKQIPVPYNO 120

QY 143 VKTSKEVTVOELDIQARHYLHGKFGLYNSDFGKVGQRLVPHSHSSEGS-TVSYDLFDA 201
Db 121 ISTNKTVTVAQIEDLKVAKFLISQHLQYSS---GSSYKSGKLIVFHTNDNSDKYSLDLFT 177

QY 202 QGQYDPDLLRIYRDNNTTIS 220
Db 178 GYRDKESIFKYVKNKSNFN 196

RESULT 72
Q9LAC3 PRELIMINARY; PRT; 209 AA.
ID Q9LAC3
AC Q9LAC3
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-24 (Fragment).
GN SMEZ-24.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OC NCBI_TaxID=1314;
RN [1]_TaxID=1314;
RP SEQUENCE FROM N.A.
RC STRAIN=10438;
RX MEDLINE=20273982; PubMed=10811869;
RA Profit T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
```

	Mosaic Structure, and Significant Antigenic Variation."	
RT	J. Exp. Med. 191:1765-1776(2000).	
RL	EMBL; AF143674; AAF66672.1; -.	
RR	HSSP; F13163; 1SXT.	
DR	GO; GO:0005576; C:extracellular; IEA.	
DR	GO; GO:0015070; P:toxin activity; IEA.	
DR	GO; GO:0009405; P:pathogenesis; IEA.	
DR	InterPro; IPR008992; Bact_endotox.	
DR	InterPro; IPR006177; Bctr1_tox.	
DR	InterPro; IPR006123; Staph/Strep toxin.	
DR	InterPro; IPR006173; Staph tox OB.	
DR	Pfam; PF01123; Stap_strp_toxin; 1.	
DR	Pfam; PF02876; Bac_Strp_tox_C; 1.	
DR	PRINTS; PR00279; BACTRTOXIN_1.	
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.	
DR	NON_TER	
SQ	SEQUENCE 209 AA; 24137 MW; 301587A9A995F715 CRC64;	
FT		
	Query Match	
	Best Local Similarity 28.6%; Score 205; DB 2; Length 209;	
	Matches 57; Conservative 37; Mismatches 69; Indels 36; Gaps	
QY	50 NTLAFKGFTHGHPWYNLLVD-----LGSTAATSEYGSSVDLYGAY----- 91	
DB	: :: : : :	:
DB	6 NSLLRNXYSTIVYEYSOTVIDFKTSHNLVTKKLDVRDARDFFINSEMDEYAANDFKAGDK 65	
QY	92 -----YQCACGGTPNKTCAMGYGVVLTDDNNLRTSEEKVPIINLWDIGKTVPIDK 142	
DB	: :: : : :	:
DB	66 IAVFSVPDMNWLISKG---KVTATYTGITPYQTSI--PKNIPLNLNRKOIPVFNQ 120	
QY	143 VKTSKEVTVOELDLQARHYHLGHFGILNSDSFCGKVQRGLIVFHSGES-TVSYDLFDA 201	
DB	: :: : : :	:
DB	121 ISTNKTTVTAQEIDLKYRKFLIAHQHLYSS---GSSYKSKGLVFHTNDSDKYSLDLFYT 177	
QY	202 QCGYPDTLLRIYRDNTTIS 220	
DB	: :: :~::~	:
DB	178 GYRDKESIIFYKNCKSFN 196	
RESULT 73		
Q9SLH8	PRELIMINARY; PRT; 256 AA.	
ID	Q9SLH8	
AC	Q9SLH8;	
DT	01-MAY-2000 (TREMBLrel. 13, Created)	
TT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)	
DE	01-OCT-2003 (TREMBLrel. 25, Last annotation update)	
TE	SpeX protein precursor.	
DE	SPEX.	
CN	Streptococcus pyogenes.	
OS	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;	
OC	Streptococcus.	
OX	NCBI TaxID=1314;	
RN	[1]	
RP	SEQUENCE FROM:N.A.	
RC	STRAIN=12714 type 12;	
RX	MEDLINE=20374978; PubMed=10913699;	
RA	Gerlach D., Fleischer B., Wagner M., Schmidt K.H., Vettermann S., Reichardt W.;	
RA	"Purification and Biochemical Characterization of a Basic Superantigen (SPeX/SME23)";	
RT	FEMS Microbiol. Lett. 188:153-163(2000).	
RL	EMBL; AJ245405; CAB51744.1; -.	
DR	HSSP; F13163; 1SXT.	
DR	GO; GO:0005576; C:extracellular; IEA.	
DR	GO; GO:0015070; P:toxin activity; IEA.	
DR	GO; GO:0009405; P:pathogenesis; IEA.	
DR	InterPro; IPR008992; Bact_endotox.	
DR	InterPro; IPR006177; Bctr1_tox.	
DR	InterPro; IPR006123; Staph/Strep toxin.	
DR	InterPro; IPR006173; Staph tox OB.	
DR	Pfam; PF01123; Stap_strp_toxin; 1.	
DR	Pfam; PF02876; Staph_strp_tox_C; 1.	
DR	PRINTS; PR00279; BACTRTOXIN_1.	

Search completed: August 12, 2004, 13:32:30
Job time : 26.2698 secs

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OM protein - protein search, using sw model

Run on: August 12, 2004, 13:21:44 ; Search time 29.2786 Seconds
(without alignments)
2248.525 Million cell updates/sec

Title: US-09-900-766-2
Perfect score: 1218
Sequence: 1 SEKSEINEKDLKKSELOG.....RDNTTISLSLSLYVT 233

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : A Geneseq_29Jan04:*

1: Geneseqp1980s:*

2: Geneseqp1990s:*

3: Geneseqp2000s:*

4: Geneseqp2001s:*

5: Geneseqp2002s:*

6: Geneseqp2003as:*

7: Geneseqp2003bs:*

8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1218	100.0	233	6	ABP58455 Engineere
2	1218	100.0	672	6	ABP58454 Engineere
3	1130	92.8	233	6	ABP58457 Engineere
4	1113	91.4	245	2	AAW35375 Staphyloc
5	1107	90.9	233	6	ABP58456 Staphyloc
6	1107	90.9	257	4	AAU14103 Peptide s
7	1107	90.9	257	6	ABO10268 S. aureus
8	1093	89.7	230	4	AAAB67339 Staphyloc
9	1091	89.6	245	2	AAW35374 Staphyloc
10	1072	88.0	248	6	ABU79072 S. aureus
11	1048	86.0	230	2	AAW45012 Staphyloc
12	1044	85.7	230	5	ABP78235 Staphyloc
13	1035	85.0	230	2	AAAR13204 Staphyloc
14	960	78.8	233	2	AAAR13203 Staphyloc
15	948	77.8	233	6	ABP58458 Staphyloc
16	948	77.8	257	4	AAU14104 Peptide s
17	948	77.8	257	6	ABO10269 S. aureus
18	948	77.8	257	7	ADD44368 Staphyloc
19	944	77.5	233	2	AAW08738 Staphyloc
20	942	77.3	233	2	AAW45011 Staphyloc
21	941	77.3	233	2	AAW35373 Staphyloc
22	941	77.3	233	4	AAAB67338 Staphyloc
23	935	76.8	257	6	ABU79068 S. aureus
24	933	76.6	233	5	ABP76234 Staphyloc
25	925	75.9	257	5	ABP79501 Staphyloc

FT FT /note= "wild-type Lys substituted by Ser"
 Misc-difference 452
 FT FT /note= "wild-type Asp substituted by Ser"
 Region 459..565
 FT FT /note= "574 variable light chain"
 FT FT /note= "wild-type Phe substituted by Ser"
 Misc-difference 469
 FT FT /note= "wild-type Thr substituted by Lys"
 Misc-difference 504
 FT FT /note= "wild-type Thr substituted by Lys"
 Misc-difference 522
 FT FT /note= "wild-type Ile substituted by Ser"
 Misc-difference 532
 FT FT /note= "wild-type Phe substituted by Leu"
 Misc-difference 536
 FT FT /note= "wild-type Thr substituted by Ser"
 Misc-difference 537
 FT FT /note= "wild-type Leu substituted by Val"
 Misc-difference 542
 FT FT /note= "wild-type Leu substituted by Ala"
 Region 566..572
 FT FT /note= "C242 constant light chain"
 XX XX
 PN WO2003002143-A1.
 XX XX
 XX 09-JAN-2003.
 XX XX
 XX 19-JUN-2002; 2002WO-SE001188.
 XX XX
 XX 28-JUN-2001; 2001SE-00002327.
 XX XX
 PA (ACTI-) ACTIVE BIOTECH AB.
 XX XX
 PI Forsberg G, Erlandsson E, Antonsson P, Walse B;
 XX WPI; 2003-201467/19.
 DR
 XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
 PT receptor and four regions to determine binding to class II major
 PT histocompatibility complex, antibody to cancer associated cell surface
 PT structure.
 XX
 PS Claim 12; Fig 10; 102pp; English.
 XX
 CC The present sequence is a conjugate of a bacterial superantigen and an
 CC antibody moiety, and has been designed to target and destroy cancer
 CC cells. The bacterial superantigen is SEA/E-120 (see also ABP58455), which
 CC was derived from staphylococcal enterotoxin E (SEE) by the incorporation
 CC of the following amino acid substitutions to reduce seroreactivity whilst
 CC maintaining production levels and biological activity: R20G, N21T, S24G,
 CC R27K, K79E, K81E, K83S and D227S. SEA/E-120 was genetically fused to the
 CC Fab moiety of the tumour reactive antibody 574. Substitutions were made
 CC in the 574 sequence to obtain higher yields: in the heavy chain, H41P,
 CC S44G, L69T and V113G; and in the light chain, F10S, T45K, I63S, F73L,
 CC T77S, L78V and L83A. An expression vector comprising DNA encoding the
 CC conjugate can be used to transform host cells for recombinant production
 CC of the conjugate. The conjugate is useful for treating cancer, including
 CC cancer of the lung, breast, colon, kidney, pancreas, ovary, stomach,
 CC cervix and prostate (claimed)
 XX
 SQ Sequence 672 AA;
 Query Match 100.0%; Score 1218; DB 6; Length 672;
 Best Local Similarity 100.0%; Pred. No. 3,2e-114;
 Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSDAQFLTNTLLFKGFTG 60
 Db 226 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSDAQFLTNTLLFKGFTG 285
 QY 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYYGQCAGGTPNKTAACMYGGVTLHDNNRLT 120
 Db 286 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYYGQCAGGTPNKTAACMYGGVTLHDNNRLT 345

QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 Db 346 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLRLRIYRDNNTTISSTLSLSLYLYTT 233
 Db 406 RGLIVFHSSEGSTVSVDLFDAGQYPTDLRLRIYRDNNTTISSTLSLSLYLYTT 458

RESULT 3
 ABP58457
 ID ABP58457 standard; protein; 233 AA.
 XX
 AC ABP58457;
 XX
 DT 14-APR-2003 (first entry)
 XX
 XX Engineered superantigen SEA/E-18 for human cancer therapy.
 DE
 XX Superantigen; staphylococcal enterotoxin; antibody; cancer; tumour;
 KW cytostatic; vaccine; SEA/E-18; mutant; mutein.
 XX
 OS Staphylococcus sp.
 OS Synthetic.
 OS
 PN WO2003002143-A1.
 XX
 PD 09-JAN-2003.
 XX
 XX 19-JUN-2002; 2002WO-SE001188.
 XX
 XX 28-JUN-2001; 2001SE-00002327.
 XX
 PA (ACTI-) ACTIVE BIOTECH AB.
 XX
 PI Forsberg G, Erlandsson E, Antonsson P, Walse B;
 XX WPI; 2003-201467/19.
 DR
 XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
 PT receptor and four regions to determine binding to class II major
 PT histocompatibility complex, antibody to cancer associated cell surface
 PT structure.
 XX
 PS Example 3; Fig 3; 102pp; English.
 XX
 CC The present sequence is the protein sequence of engineered staphylococcal
 CC superantigen SEA/E-18. The superantigen is based on staphylococcal
 CC enterotoxin E (SEE, see ABP58456) except for 4 amino acid residues close
 CC to the N-terminal that were from enterotoxin A and one substitution in
 CC the C-terminal part, D227A. Models of new superantigen variants were
 CC constructed using the SEA/E-18 model as the template. These include the
 CC new engineered superantigen SEA/E-120 (see ABP58455), which has been
 CC genetically fused to the Fab moiety of the tumour reactive antibody 574
 CC to form a conjugate (see ABP58454) polypeptide. The conjugate is a
 CC claimed example of novel conjugates of the invention comprising an
 CC engineered bacterial superantigen and an antibody moiety. The conjugates
 CC are designed to target and destroy cancer cells, including cancer of the
 CC lung, breast, colon, kidney, pancreas, ovary, stomach, cervix and
 CC prostate (claimed)
 XX
 SQ Sequence 233 AA;
 Query Match 92.8%; Score 1130; DB 6; Length 233;
 Best Local Similarity 91.4%; Pred. No. 5.9e-106;
 Matches 233; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSDAQFLTNTLLFKGFTG 60
 Db 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSDAQFLTNTLLFKGFTG 60
 QY 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYYGQCAGGTPNKTAACMYGGVTLHDNNRLT 120

Db 61 HPWYNDLLVLDGSKDNTKYGKGVLDLYGAYYGYOCAGGTPNKTCMYGGVTLHDNNRLT 120
 Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 Qy 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNNTTSISLSLYLTT 233
 Db 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNNTTSISLSLYLTT 233

RESULT 4

AAW35375
 ID AAW35375 standard; peptide; 245 AA.
 AC AAW35375;
 XX
 DT 20-APR-1998 (first entry)
 XX
 DE Staphylococcus enterotoxin SEE modified superantigen.
 XX
 KW SEE; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment;
 KW cancer; infection; autoimmune disease; antibody; modified.
 XX
 OS Staphylococcus sp.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 20 /label= R20G
 FT /note= "wild-type Arg is replaced by Gly"
 FT Misc-difference 21 /label= N21T
 FT /note= "wild-type Asn is replaced by Thr"
 FT Misc-difference 24 /label= S24G
 FT /note= "wild-type Ser is replaced by Gly"
 FT Misc-difference 27 /label= R27K
 FT /note= "wild-type Arg is replaced by Lys"
 FT
 XX
 PN WO9736932-A1.
 XX
 PD 09-OCT-1997.
 XX
 XX 26-MAR-1997; 97WO-SE000537.
 XX
 XX 29-MAR-1996; 96SE-00001245.
 PR 12-AUG-1996; 96US-00695692.
 XX
 XX (PHAA) PHARMACIA & UPJOHN AB.
 XX
 XX Antonsson P, Hansson J, Björk P, Dohlsten M, Kalland T;
 PI Abrahmsen L, Forsberg G;
 XX
 XX WPI; 1997-503052/46.
 XX
 XX Conjugate of target seeking moiety and modified superantigen - useful for
 PT activating the immune system to treat cancer, viral infections, parasitic
 PT infestations and autoimmune diseases.
 XX
 XX Claim 5; Page: 58pp; English.
 XX

XX This is a modified Staphylococcus enterotoxin SEE superantigen. The wild-
 CC type SEE superantigen is modified to be used in a novel conjugate. The
 CC novel conjugate comprises a target seeking moiety and a modified wild
 CC type superantigen. This modified superantigen retains its ability to
 CC activate a subset of T cells, even though 1 or more wild-type amino acid
 CC residues in at least 1 region which functions in determining binding to T
 CC cell receptor (TCR) and activation of a subset of T cells has/have been
 CC replaced. Such a modified superantigen can optionally be used as part of
 CC a conjugate with a target seeking moiety for activating the immune
 CC system to treat a mammalian disease. A pharmaceutical composition can be
 CC prepared comprising a modified antibody (preferably a Fab fragment fused

CC to a peptide moiety providing activation of T cells in Vbeta specific
 CC manner) in which cysteines providing for interchain cysteine linkages in
 CC the native antibody have been replaced (preferably by serine residues) to
 CC prohibit cysteine formation. The modified wild-type superantigen is used
 CC for treating cancer, viral infections, parasitic infestations and
 CC autoimmune disease. The modified wild type superantigen has a lower
 CC immunogenicity and reactivity with neutralising antibodies and has fewer
 CC side-effects when used as a drug, compared to wild type superantigen.
 CC Note: This sequence is not provided in the specification. It has been
 CC created by modifying the wild-type SEE superantigen sequence in Pages 38-
 CC 39 of the specification
 XX
 SQ Sequence 245 AA;

Query Match 91.4%; Score 1113; DB 2; Length 245;
 Best Local Similarity 86.9%; Pred. No. 3.3e-104;
 Matches 213; Conservative 8; Mismatches 12; Indels 12; Gaps 1;
 Qy 1 SEKSEINEKDLRKKSELOQTALGNLKOIYYNKAITSSEKSADQFLNTLLFKGFFTG 60
 Db 1 SEKSEINEKDLRKKSELOQTALGNLKOIYYNKAITSSEKSADQFLNTLLFKGFFTG 60
 Qy 61 HPWYNDLLVLDGSKDNTKYGKGVLDLYGAYYGYOCAGGTPNKTCMYGGVTLHDNNRLT 120
 Db 61 HPWYNDLLVLDGSKDNTKYGKGVLDLYGAYYGYOCAGGTPNKTCMYGGVTLHDNNRLT 120
 Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 Qy 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNNTTSISLSLYLTT 228
 Db 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNNTTSISLSLYLTT 228
 Qy 229 YLYTT 233
 Db 241 YLYTT 245

RESULT 5

ABP58456
 ID ABP58456 standard; protein; 233 AA.
 XX
 AC ABP58456;
 XX
 DT 14-APR-2003 (first entry)
 XX
 DE Staphylococcal enterotoxin E.
 XX
 KW Superantigen; staphylococcal enterotoxin E; antibody; cancer; tumour;
 KW cytostatic; vaccine.
 XX
 OS Staphylococcus sp.
 XX
 PN WO2003002143-A1.
 XX
 XX 09-JAN-2003.
 PD
 XX 19-JUN-2002; 2002WO-SE001188.
 XX
 XX 28-JUN-2001; 2001SE-00002327.
 PR
 XX (ACTI-) ACTIVE BIOTECH AB.
 XX
 XX Forsberg G, Erlandsson E, Antonsson P, Walse B;
 XX WPI; 2003-201467/19.
 XX
 XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
 XX receptor and four regions to determine binding to class II major
 XX histocompatibility complex, antibody to cancer associated cell surface
 XX structure.
 XX

PS Example 3; Fig 4; 102pp; English.

CC The present sequence is the protein sequence of staphylococcal

CC enterotoxin SEE. The invention provides novel conjugates (see ABP58454)

CC for human cancer therapy. These comprise an engineered bacterial

CC superantigen, such as novel SEA/3-120 (see ABP58455), which is based on

CC SEE, and an antibody moiety, such as tumour reactive antibody 514. The

CC superantigen is engineered to reduce seroreactivity whilst maintaining

CC biological activity and production levels. The conjugates are designed to

CC target and destroy cancer cells, including cancer of the lung, breast,

CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)

XX Sequence 233 AA;

SQ

Query Match 90.9%; Score 1107; DB 6; Length 233;

Best Local Similarity 89.7%; Pred. No. 1.3e-103;

Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLQIYYVNSKAITSEKSDAQFLNTLLFKGFTG 60

DB 1 SEKSEINEKDLRKSELQRLNALSNLQIYYVNSKAITENKESDDQFLNTLLFKGFTG 60

QY 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120

DB 61 HPWYNDLLVDLGSDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120

QY 121 BEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180

DB 121 BEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180

QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNNTTISSTLSISLYLYTT 233

DB 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNNTTINSENHIDLILYLYTT 233

RESULT 6

ID AAU14103 standard; peptide; 257 AA.

XX AAU14103;

AC AAU14103;

XX

DT 21-NOV-2001 (first entry)

XX

DE Peptide sequence from Staphylococcus aureus enterotoxin type E.

XX

KW Anti-retroviral; DP178-like; DP107-like; enterotoxin type E;

KW antifusogenic; antiviral; HIV transmission.

XX

OS Staphylococcus aureus.

XX

FN WO200151673-A2.

XX

PD 19-JUL-2001.

XX

PF 05-JUL-2000; 2000WO-US035727.

XX

PR 09-JUL-1999; 99US-00350841.

XX

PA (TRIM-) TRIMERIS INC.

XX

PI Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;

XX

DR WPI; 2001-442157/47.

XX

PT Identifying a compound that inhibits the formation of or disrupts a

PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral

PT or intracellular modulatory activity, by detecting the formation of a

PT DP107/DP178 complex.

XX

PS Disclosure; Fig 41; 259pp; English.

XX

CC The present invention relates to peptides which exhibit anti-retroviral

CC activity. The peptides of the invention (AAU12559-AAU14009) comprise

CC

CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to

CC amino acids 639-673 of the transmembrane protein gp41 from human

CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide

CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention

CC also relates to a method of identifying compounds that inhibit the

CC formation of or disrupts a DP107/DP178 complex. The method comprises

CC detecting the formation of a DP107/DP178 complex, both in the presence or

CC absence of a test compound, in a reaction mixture containing DP107 and

CC DP178 peptides. The method is useful for identifying compounds, including

CC small molecule compounds, which may themselves exhibit antifusogenic,

CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like

CC peptides are useful to inhibit human and non-human retroviral,

CC particularly HIV, transmission to uninfected cells. The present sequence

CC represents a peptide sequence from Staphylococcus aureus enterotoxin type

XX E

SQ Sequence 257 AA;

Query Match 90.9%; Score 1107; DB 4; Length 257;

Best Local Similarity 89.7%; Pred. No. 1.5e-103;

Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLQIYYVNSKAITSEKSDAQFLNTLLFKGFTG 60

DB 25 SEKSEINEKDLRKSELQRLNALSNLQIYYVNSKAITENKESDDQFLNTLLFKGFTG 84

QY 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120

DB 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 121 BEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180

DB 145 BEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204

QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNNTTISSTLSISLYLYTT 233

DB 205 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNNTTINSENHIDLILYLYTT 257

RESULT 7

ABO10268

ID ABO10268 standard; protein; 257 AA.

XX ABO10268;

AC ABO10268;

XX

DT 19-AUG-2003 (first entry)

XX

DE S. aureus enterotoxin E.

XX

KW HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;

KW Epstein-Barr virus infection; heptad repeat motif.

XX

OS Staphylococcus aureus.

XX

FN US6518013-B1.

XX

PD 11-FEB-2003.

XX

PF 07-JUN-1995; 95US-00485546.

XX

PR 07-JUN-1993; 93US-00073028.

PR 07-JUN-1994; 94US-00255208.

PR 20-DEC-1994; 94US-00360107.

XX

PA (TRIM-) TRIMERIS INC.

XX

PI Barney SO, Lambert DM, Petteway SR;

XX

DR WPI; 2003-465599/44.

XX

PT Inhibiting transmission of Epstein-Barr virus to a cell, by contacting

PT the cell with a peptide consisting of a region of Epstein-Barr virus

PT protein.

PT

XX Example; Fig 41; 716pp; English.

PS The invention relates to inhibiting (M) transmission of an Epstein-Barr virus to a cell, comprising contacting the cell with an effective concentration of a peptide consisting of a region of 16-39 consecutive amino acids of an Epstein-Barr virus protein for an effective period of time, where the region is recognised by one or more of ALIMOT15, 107x1784 or PIZ1P sequence search motifs, the peptide further comprises an amino terminal X, and a carboxy terminal Z in which X comprises an amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic group or macromolecular carrier group, and Z comprises a carboxyl group, amido group, hydrophobic group, or macromolecular carrier group, and fusion of the virus to the cell is inhibited. The peptides were identified by analysing the structure/motifs present in the HIV-1 glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat motif containing peptides were used to design the motifs cited above, which in turn were used to analyse proteins from other pathogenic organisms and HIV isolates, looking for DP107/178 structural analogues. The method is useful for inhibiting transmission of Epstein-Barr virus to a cell and Epstein-Barr virus infection. The present sequence is a protein from a pathogenic organism analysed for regions analogous to DP107 or DP178

XX SQ Sequence 257 AA;

Query Match 90.9%; Score 1107; DB 6; Length 257;
Best Local Similarity 89.7%; Pred. No. 1.5e-103;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDKRKSELOQTALGNLKOIYYNSKAITSEKSADQFLTNLLFKGFTG 60
Db 25 SEKSEINEKDKRKSELOQTALGNLKOIYYNSKAITSEKSADQFLTNLLFKGFTG 84
QY 61 HPYNLLVDLGSATSEYEGSSVDLYGAYGYQCAGTGNKTKACMGVTLHNNLT 120
Db 85 HPYNLLVDLGSADATNKYKGVLDLYGAYGYQCAGTGNKTKACMGVTLHNNLT 144
QY 121 EEKVPINLWDGQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVQ 180
Db 145 EEKVPINLWDGQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVQ 204
QY 181 RGLIVFHSSEGSTSVSYDLFDAQGYPTDLLRIYRDNNTTSSLSISLYTT 233
Db 205 RGLIVFHSSEGSTSVSYDLFDAQGYPTDLLRIYRDNNTTSSLSISLYTT 257

RESULT 8
AAB67339
ID AAB67339 standard; peptide; 230 AA.
XX AC AAB67339;
XX AC AAB67339;
XX DT 23-APR-2001 (first entry)
XX DE Staphylococcus aureus enterotoxin E protein.
XX DE Tumour; cancer; immune; enterotoxin.
XX OS Staphylococcus aureus.
XX PN US6180097-B1.
XX PD 30-JAN-2001.
XX PF 30-OCT-1998; 98US-00183437.
XX PR 03-OCT-1989; 89US-00416530.
XX PR 17-JAN-1990; 90US-00466577.
XX PR 17-JAN-1991; 91WO-US000342.
XX PR 01-JUN-1992; 92US-00891718.
XX PR 02-MAR-1993; 93US-00025144.
XX PR 31-JAN-1994; 94US-00189424.

PR 19-JUN-1995; 95US-00491746.
XX (TERM/) TERNAN D S.
XX Terman DS;
XX WPI; 2001-158657/16.
XX Tumor cell capable of stimulating antitumor immune reactivity in vitro or in vivo comprises exogenous nucleic acids encoding a superantigen and a costimulatory molecule.
XX Disclosure; Fig 2; 16pp; English.
XX The present invention relates to a tumour cell capable of stimulating antitumor immune reactivity in vitro or in vivo contains and expresses an exogenous nucleic acid molecule encoding a superantigen or its active fragment and an exogenous nucleic acid molecule encoding a costimulatory molecule that activates T cells in conjunction with an antigenic stimulus. The invention may be used for cancer therapy by stimulating an anticancer immune response in vivo or ex vivo
XX Sequence 230 AA;

Query Match 89.7%; Score 1093; DB 4; Length 230;
Best Local Similarity 89.6%; Pred. No. 3.3e-102;
Matches 206; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 4 SEENEDLKKSELOQTALGNLKOIYYNSKAITSEKSADQFLTNLLFKGFTGHPW 63
Db 1 SEENEDLKKSELOQTALGNLKOIYYNSKAITSEKSADQFLTNLLFKGFTGHPW 60
QY 64 YNDLLVDLGSATSEYEGSSVDLYGAYGYQCAGTGNKTKACMGVTLHNNLTTEK 123
Db 61 YNDLLVDLGSADATNKYKGVLDLYGAYGYQCAGTGNKTKACMGVTLHNNLTTEK 120
QY 124 KVPINLWDGQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVQRL 183
Db 121 KVPINLWDGQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVQRL 180
QY 184 IVFHSSEGSTSVSYDLFDAQGYPTDLLRIYRDNNTTSSLSISLYTT 233
Db 181 IVFHSSEGSTSVSYDLFDAQGYPTDLLRIYRDNNTTSSLSISLYTT 230

RESULT 9
AAW35374
ID AAW35374 standard; peptide; 245 AA.
XX AC AAW35374;
XX AC AAW35374;
XX DT 20-APR-1998 (first entry)
XX DE Staphylococcus enterotoxin SEE wild-type superantigen.
XX DE SEE; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment;
XX KW cancer; infection; autoimmune disease; antibody.
XX OS Staphylococcus sp.
XX Key Location/Qualifiers
XX FH Misc-difference 20 /note= "can be mutated at this position"
XX FT Misc-difference 21 /note= "can be mutated at this position"
XX FT Misc-difference 24 /note= "can be mutated at this position"
XX FT Misc-difference 27 /note= "can be mutated at this position"
XX PN WO9736932-A1.
XX PD 09-OCT-1997.

XX PF 26-MAR-1997; 97WO-SE000537.
XX PR 29-MAR-1996; 96SE-00001245.
XX PR 12-AUG-1996; 96US-00695692.
XX PA (PHAA) PHARMACIA & UPJOHN AB.
XX PI Antonsson P, Hansson J, Bjoerk P, Dohlsten M, Kalland T;
XX PI Abrahamsen L, Forsberg G;
XX DR WPI; 1997-503052/46.
XX PR Conjugate of target seeking moiety and modified superantigen - useful for
XX PT activating the immune system to treat cancer, viral infections, parasitic
XX PT infestations and autoimmune diseases.
XX XX Claim 4; Page 38-39; 58pp; English.
XX XX This is the wild-type Staphylococcus enterotoxin SEE superantigen. This
XX CC SEE superantigen can be modified to be used in a novel conjugate. The
XX CC novel conjugate comprises a target seeking moiety and a modified wild
XX CC type superantigen. The modified superantigen retains its ability to
XX CC activate a subset of T cells, even though 1 or more wild-type amino acid
XX CC residues in at least 1 region which functions in determining binding to T
XX CC cell receptor (TCR) and activation of a subset of T cells has/have been
XX CC replaced. Such a modified superantigen can optionally be used as part of
XX CC a conjugate with a target seeking moiety, for activating the immune
XX CC system to treat a mammalian disease. A pharmaceutical composition can be
XX CC prepared comprising a modified antibody (preferably a Fab fragment fused
XX CC to a peptide moiety providing activation of T cells in beta specific
XX CC manner) in which cysteines providing for interchain cysteine linkages in
XX CC the native antibody have been replaced (preferably by serine residues) to
XX CC prohibit cysteine formation. The modified wild-type superantigen is used
XX CC for treating cancer, viral infections, parasitic infestations and
XX CC autoimmune disease. The modified wild type superantigen has a lower
XX CC immunogenicity and reactivity with neutralising antibodies and has fewer
XX CC side-effects when used as a drug, compared to wild type superantigen
XX SQ Sequence 245 AA;
Query Match 89.6%; Score 1091; DB 2; Length 245;
Best Local Similarity 85.3%; Pred. No. 5,7e-102;
Matches 209; Conservative 9; Mismatches 15; Indels 12; Gaps 1;
Qy 1 SEKSEINEKDLRKKSEIQGTALGNLKOIYYNYSKATTSSEKSDQFLNTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKKSEIQGTALGNLKOIYYNYSKATTSSEKSDQFLNTLLFKGFFTG 60
Qy 61 HPWYNDLLVDLGSAATSEYEGSSVDLYGAVYGCAGGTENKTCACMYGGVTLHDNNRLT 120
Db 61 HPWYNDLLVDLGSAATSEYEGSSVDLYGAVYGCAGGTENKTCACMYGGVTLHDNNRLT 120
Qy 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDQARHYLKGKFLYNSDSFGGKVQ 180
Db 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDQARHYLKGKFLYNSDSFGGKVQ 180
Qy 181 RGLVHFHSSSEGSTVSVDLFDAGQVPTDLLRIYDNT-----TISSTLSLSL 228
Db 181 RGLVHFHSSSEGSTVSVDLFDAGQVPTDLLRIYDNTINSENLIHDIYLTINSENLIHDL 240
Qy 229 YLYTT 233
Db 241 YLYTT 245
RESULT 10
ID ABU79072
XX ABU79072 standard; protein; 248 AA.
XX AC ABU79072;
XX DT 18-JUN-2003 (first entry)

XX DE S. aureus SEE (staphylococcus enterotoxin E) protein.
XX XX Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis;
XX KW Gene therapy; mammalian cell receptor; tumour associated lipid; anergy;
XX KW T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;
XX KW APC; antitumour.
XX OS Staphylococcus aureus.
XX XX US2002177551-A1.
XX PD 28-NOV-2002.
XX PF 30-MAY-2001; 2001US-00870759.
XX PR 31-MAY-2000; 2000US-0208128P.
XX PA (TERM/) Terman D S.
XX PI Terman DS;
XX DR WPI; 2003-361759/34.
XX DR N-PSDB; AC646498.
XX PT A mammalian cell receptor, useful in the treatment of cancer by binding
XX PT to tumor associated lipids where the binding induces anergy or apoptosis
XX PT in T cells and antigen presenting cells.
XX PS Disclosure; Page; 167pp; English.
XX XX The invention relates to a mammalian cell receptor, useful in the
XX CC treatment of cancer, which binds to tumour associated lipids and induces
XX CC anergy or apoptosis in the T cells and antigen presenting cells (APCs).
XX CC Also included are a mammalian cell useful in the treatment of cancer
XX CC where the receptor which binds tumour associated lipids and induces
XX CC cellular inactivation or death is deleted or functionally deactivated,
XX CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal
XX CC (by allowing tumour associated lipids to contact immunocytes in which
XX CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,
XX CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
XX CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
XX CC deleted), a construct useful in the treatment of cancer comprising a
XX CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
XX CC useful in the treatment of cancer (where an adaptor protein which
XX CC inhibits T cell activation by tumour associated antigens is deleted or
XX CC functionally deactivated), a composition useful in the treatment of
XX CC cancer (comprising a lipid raft conjugated to a superantigen), producing
XX CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
XX CC allowing tumour associated lipids to contact immunocytes, in which
XX CC receptors for the lipids are inactivated or deleted to produce a
XX CC tumouricidal immunocyte population, and administering the tumouricidal
XX CC activated immunocytes to the host), producing (M3) a tumouricidal APC
XX CC population ex vivo in a mammal (by allowing a tumour associated lipid to
XX CC contact APCs, in which receptors for the tumour associated lipids are
XX CC inactivated or deleted to produce a tumouricidally activated population,
XX CC and administering APCs to the host), producing a tumouricidal T cell
XX CC population ex vivo in a mammal (by allowing a tumour associated lipids to
XX CC contact T cells, in which adaptor proteins, which inhibit T cell
XX CC activation by tumour associated antigens, are deleted or functionally
XX CC deactivated to produce a tumouricidal population of T cells, and
XX CC administering the tumouricidally activated T cells to the host, or
XX CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
XX CC administering the tumouricidally activated T cells to the host), treating
XX CC (M5) cancer in a mammal (by administering a lipid binding molecule which
XX CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
XX CC a tumouricidal T cell population in vivo in a mammal (by allowing a
XX CC tumour associated antigen to contact immunocytes in which adaptor
XX CC proteins which inhibit T cell activation by tumour associated antigens
XX CC are deleted or functionally deactivated) and producing (M7) a
XX CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
XX CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
XX CC receptors, methods and compositions are useful for treating cancers and

CC tumours. Bacterial superantigens are co-administered or administered as
 CC fusion constructs with anti-tumour proteins or motifs. The present
 CC sequence represents a bacterial superantigen protein (e.g. a
 CC staphylococcal enterotoxin). Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format from the US patent office website at
 CC "seqdata.uspto.gov/sequence.html?DocID=20020177551"
 XX
 XX Sequence 248 AA;

Query Match 88.0%; Score 1072; DB 6; Length 248;
 Best Local Similarity 90.2%; Pred. No. 4.9e-100; Indels 0; Gaps 0;
 Matches 202; Conservative 9; Mismatches 13;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSADQFLNTLLFKGFFTG 60
 Db 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSADQFLNTLLFKGFFTG 84
 QY 61 HPWYNLLVDLGGTAATSEYEGSSVDLYGAYYQYQAGGTPNKTACMYGGVTLHNNRLT 120
 Db 85 HPWYNLLVDLGGTAATSEYEGSSVDLYGAYYQYQAGGTPNKTACMYGGVTLHNNRLT 144
 QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNNTISSTLS 224
 Db 205 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNNTISSTLS 248

RESULT 11
 AAR45012
 ID AAR45012 standard; protein; 230 AA.
 XX
 AC AAR45012;
 DT 25-MAR-2003 (revised)
 DT 08-JUN-1994 (first entry)
 XX
 XX Staphylococcal enterotoxin SEE.
 DE
 DE Staphylococcal enterotoxin; SE; cancer; tumour; agent;
 KW autoimmune disease; toxicity; Protein A; perfusion system.
 KW
 XX Staphylococcus aureus.
 OS
 XX Key Location/Qualifiers
 FT FT Misc-difference 120
 FT /note= "Given in the specification as J, no further
 FT details given"
 FT Misc-difference 121
 FT /note= "Given in the specification as J, no further
 FT details given"
 FT Misc-difference 123
 FT /note= "Given in the specification as O, no further
 FT details given"
 FT Misc-difference 124
 FT /note= "Given in the specification as U, no further
 FT details given"
 XX
 PN W09324136-A1.
 XX
 XX 09-DEC-1993.
 PD
 PF 01-JUN-1993; 93WO-US005213.
 XX
 XX 01-JUN-1992; 92US-00891718.
 XX
 XX (TERM/) Terman D S.
 PA (STON/) STONE J L.
 XX
 XX Terman DS, Stone JL;
 PP

XX
 DR WPI; 1993-405418/50.
 XX
 PT Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
 PT in a patient or for the treatment of auto-immune diseases.
 XX
 PS Disclosure; Fig 1; 90pp; English.
 XX
 CC The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer in
 CC a patient. These SEs, and homologues of them, can be used as tumouricidal
 CC agents for treating cancers and autoimmune disease. They exhibit
 CC tumouricidal activity and toxicity identical to that observed for the
 CC Protein A perfusion system. They may be administered by i.v. injection.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 230 AA;

Query Match 86.0%; Score 1048; DB 2; Length 230;
 Best Local Similarity 85.7%; Pred. No. 1.2e-97; Indels 0; Gaps 0;
 Matches 197; Conservative 12; Mismatches 21;
 QY 4 SEEINEXDLRKSELOQTALGNLKOIYYNKAITSSEKSADQFLNTLLFKGFFTGHPW 63
 Db 1 SEEINEXDLRKSELOQTALGNLKOIYYNKAITSSEKSADQFLNTLLFKGFFTGHPW 60
 QY 64 YNDLLVDLGGTAATSEYEGSSVDLYGAYYQYQAGGTPNKTACMYGGVTLHNNRLTEK 123
 Db 61 YNDLLVDLGGTAATSEYEGSSVDLYGAYYQYQAGGTPNKTACMYGGVTLHNNRLTEK 120
 QY 124 KVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 183
 Db 121 XVXBKWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 QY 184 IVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNNTISSTLSISLYTT 233
 Db 181 IVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNNTISSTLSISLYTT 230

RESULT 12
 ABB76235
 ID ABB76235 standard; protein; 230 AA.
 XX
 AC ABB76235;
 XX
 DT 09-AUG-2002 (first entry)
 XX
 XX Staphylococcus aureus enterotoxin E.
 DE
 DE Enterotoxin E; SEE; superantigen; antigen; tumour; cancer; antitumour;
 KW therapy.
 KW
 XX Staphylococcus aureus.
 OS
 XX Key Location/Qualifiers
 FT FT Misc-difference 120
 FT /note= "Given as 'J' in the specification"
 FT Misc-difference 121
 FT /note= "Given as 'J' in the specification"
 FT Misc-difference 123
 FT /note= "Given as 'O' in the specification"
 FT Misc-difference 124
 FT /note= "Given as 'U' in the specification"
 FT Misc-difference 125
 FT /note= "Given as 'V' in the specification"
 XX
 PN US2002051765-A1.
 XX
 XX 02-MAY-2002.
 PD
 XX 19-DEC-2000; 2000US-00741503.
 XX
 XX 03-OCT-1989; 89US-00416530.
 PP

PR 17-JAN-1990; 90US-00466577.
 PR 17-JAN-1991; 91WO-US000342.
 PR 01-JUN-1992; 92US-00891718.
 PR 02-MAR-1993; 93US-00025144.
 PR 31-JAN-1994; 94US-00189424.
 PR 19-JUN-1995; 95US-00491746.
 XX (TERM/) Terman D S.
 PA
 XX
 PI Terman DS;
 XX
 DR WPI; 2002-415198/44.
 XX

PT Reagent for treating cancer without the need for e.g. radiotherapy,
 PT comprises a specific V beta subset of T cells sensitized to a growing
 PT tumor and stimulated with superantigens.
 XX

PS Disclosure; Fig 2; 17pp; English.
 XX

CC The present sequence is the protein sequence of enterotoxin E (SEE) of
 CC Staphylococcus aureus. Similarity is shown, in several stretches of
 CC sequence, between staphylococcal enterotoxins, streptococcal pyrogenic
 CC exotoxins and staphylococcal exfoliative toxins (see AB076234-44). In the
 CC present invention, synthetic polypeptides useful in tumour therapy and in
 CC blocking or destroying autoreactive T and B lymphocyte populations are
 CC characterised by substantial structural homology to staphylococcal
 CC enterotoxin A and enterotoxin B, and to streptococcal pyrogenic
 CC exotoxins, with statistically significant sequence homology and
 CC similarity (Z value of Lipman and Pearson algorithm in Monte Carlo
 CC analysis exceeding 6) to include alignment of cysteine residues and
 CC similar hydropathy profiles. These superantigens are used to treat solid
 CC tumours, including their metastases, without radiation, surgery or
 CC standard chemotherapeutic agents. A claimed method of human cancer
 CC treatment involves contacting haematopoietic cells from a patient with
 CC one or more superantigens ex vivo to generate stimulated cells, selecting
 CC a specific V beta subset of cells, and reintroducing these cells into the
 CC patient to induce an in vivo therapeutic, tumouricidal reaction
 XX

SQ Sequence 230 AA;

Query Match 85.7%; Score 1044; DB 5; Length 230;
 Best Local Similarity 85.7%; Pred. No. 3e-97;
 Matches 197; Conservative 11; Mismatches 22; Indels 0; Gaps 0;

QY 4 SEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSDQPLNTLLFKGFTGHPW 63
 DB 1 SEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSDQPLNTLLFKGFTGHPW 60
 QY 64 YNDLLVDLGGSTAATSEYEGSSVDLYGAYGYOCAGTGNKTACMYGGVTLHDNNLTTEEX 123
 DB 61 YNDLLVDKSGKDANKYKGVLDLYGAYGYOCAGTGNKTACMYGGVTLHDNNLTTEEX 120
 QY 124 KVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRL 183
 DB 121 XVQXKXKWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRL 180
 QY 184 IVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYLYTT 233
 DB 181 IVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYLYTT 230

RESULT 13

AAR13204
 ID AAR13204 standard; protein; 230 AA.
 XX
 AC AAR13204;

DT 15-OCT-1991 (first entry)

DE Staphylococcal enterotoxin E.

XX SEE; cancer treatment; pyrogen; tumouricide.
 KW
 XX

OS Staphylococcus aureus.

PN WO9110680-A.

PD 25-JUL-1991.

PF 17-JAN-1990; 90US-00466577.

PR 17-JAN-1990; 90US-00466577.

PA (TERM/) Terman D S.

PI Terman DS;

DR WPI; 1991-237984/32.

PT Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumoricidal activity as
 PT Staphylococcal protein A without potential toxic reactions.
 XX

PS Disclosure; Fig 1; 74pp; English.

CC SEE was isolated and purified from S. aureus. It can be used for treating
 CC cancer, activating cytokine mediators and procoagulant systems,
 CC augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be
 CC administered intravenously, optionally with ibuprofen to attenuate toxic
 CC reaction to SEE. Synthetic polypeptides having structural homology to
 CC Staphylococcal exotoxins are claimed, provided the homology includes
 CC statistically significant sequence homology, alignment of Cysteine
 CC residues and similar hydropathy profiles. See AAR13203-R13211
 XX

SQ Sequence 230 AA;

Query Match 85.0%; Score 1035; DB 2; Length 230;
 Best Local Similarity 84.3%; Pred. No. 2.5e-96;
 Matches 194; Conservative 14; Mismatches 22; Indels 0; Gaps 0;

QY 4 SEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSDQPLNTLLFKGFTGHPW 63
 DB 1 SEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSDQPLNTLLFKGFTGHPW 60
 QY 64 YNDLLVDLGGSTAATSEYEGSSVDLYGAYGYOCAGTGNKTACMYGGVTLHDNNLTTEEX 123
 DB 61 YNDLLVDKSGKDANKYKGVLDLYGAYGYOCAGTGNKTACMYGGVTLHDNNLTTEEX 120
 QY 124 KVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRL 183
 DB 121 XVQXKXKWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRL 180
 QY 184 IVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYLYTT 233
 DB 181 IVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYLYTT 230

RESULT 14

AAR13203
 ID AAR13203 standard; protein; 233 AA.
 XX
 AC AAR13203;

DT 15-OCT-1991 (first entry)

DE Staphylococcal enterotoxin A.

XX SEA; cancer treatment; pyrogen; tumouricide.
 KW
 XX

OS Staphylococcus aureus.

PN WO9110680-A.

PD 25-JUL-1991.

PF 17-JAN-1990; 90US-00466577.

XX 17-JAN-1990; 90US-00465577.
XX (TERM/) Terman D S.
XX Terman DS;
XX WPI; 1991-237984/32.
XX
XX Treating cancer with enterotoxin from Staphylococcus aureus -
PT administered by IV injection, having same tumoricidal activity as
PT Staphylococcal protein A without potential toxic reactions.
XX
XX Disclosure; Fig 1; 74pp; English.
XX
XX SEA was isolated and purified from S.aureus. It can be used for treating
CC cancer, activating cytokine mediators and procoagulant systems,
CC augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be
CC administered intravenously, optionally with ibuprofen to attenuate toxic
CC reaction to SEA. Synthetic polypeptides having structural homology to
CC Staphylococcal exotoxins are claimed, provided the homology includes
CC statistically significant sequence homology, alignment of Cysteine
CC residues and similar hydropathy profiles. See also AAR13204-R13211
XX
XX Sequence 233 AA;
SQ

Query Match 78.8%; Score 960; DB 2; Length 233;
Best Local Similarity 77.3%; Pred. No. 1e-88;
Matches 180; Conservative 21; Mismatches 32; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSELOGTALGNLKOIYYNKAITSSEKSAQDLTNTLLPKGFTG 60
DB 1 SEKSEINEKDLRKKSELOGTALGNLKOIYYNEKAKTENKESHQDFLOHILFKGFTG 60
QY 61 HPWYNDLLVDLGSTATSEYEGSSVDLYGAYYGQACGTPNKTACMYGGVTLHNNRLT 120
DB 61 HSWYNDLLVDLGSKDITVDYKKGKVDLYGAYYGQACGTPNKTACMYGGVTLHNNRLT 120
QY 121 EEKVPINLWIDGKQTTVPIDIKVTSKKEVTVOELDLQARHLYHGKFLYNSDSFGKVQ 180
DB 121 EEKVPINLWIDGKQNTVPLETVKTKNKNVTVOELDLQARRYLQEKYLYNSDVDFGKVQ 180
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDILLRIYRDNNTTISSTLSISLYLTT 233
DB 181 RGLIVFHTSTEPSVNYDLFDAGQGYNTLLRIYRDNKNTINSENMHIDIYLYTS 233

RESULT 15
ABP58458
ID ABP58458 standard; protein; 233 AA.
XX
XX ABP58458;
XX
XX 14-APR-2003 (first entry)
XX
XX Staphylococcal enterotoxin A.
XX
XX Superantigen; staphylococcal enterotoxin A; antibody; cancer; tumour;
XX cytostatic; vaccine.
XX
XX Staphylococcus sp.
XX
XX WO2003002143-A1.
XX
XX 09-JAN-2003.
XX
XX 19-JUN-2002; 2002WO-SE001185.
XX
XX 28-JUN-2001; 2001SE-00002327.
XX
XX (ACTI-) ACTIVE BIOTECH AB.
XX
XX Forsberg G, Erlandsson E, Antonsson P, Walse B;
PI

XX WPI; 2003-201467/19.
XX
XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
PT receptor and four regions to determine binding to class II major
PT histocompatibility complex, antibody to cancer associated cell surface
PT structure.
XX
XX Example 3; Fig 3; 102pp; English.
XX
XX The present sequence is the protein sequence of staphylococcal
CC enterotoxin A (SEA). The invention provides novel conjugates (see
CC ABP58454) for human cancer therapy. These comprise an engineered
CC bacterial superantigen, such as novel SEA/E-120 (see ABP58453), and an
CC antibody moiety, such as tumour reactive antibody 574. Bacterial
CC enterotoxins such as SEA, SEE, SED and SEH were used in the molecular
CC modelling of the engineered superantigens. The superantigens were
CC engineered to reduce seroreactivity whilst maintaining biological
CC activity and production levels. The novel conjugates were designed to
CC target and destroy cancer cells, including cancer of the lung, breast,
XX colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
XX
XX Sequence 233 AA;
SQ

Query Match 77.8%; Score 948; DB 6; Length 233;
Best Local Similarity 76.4%; Pred. No. 1.7e-87;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSELOGTALGNLKOIYYNKAITSSEKSAQDLTNTLLFKGFTG 60
DB 1 SEKSEINEKDLRKKSELOGTALGNLKOIYYNEKAKTENKESHQDFLOHILFKGFTG 60
QY 61 HPWYNDLLVDLGSTATSEYEGSSVDLYGAYYGQACGTPNKTACMYGGVTLHNNRLT 120
DB 61 HSWYNDLLVDLGSKDITVDYKKGKVDLYGAYYGQACGTPNKTACMYGGVTLHNNRLT 120
QY 121 EEKVPINLWIDGKQTTVPIDIKVTSKKEVTVOELDLQARHLYHGKFLYNSDSFGKVQ 180
DB 121 EEKVPINLWIDGKQNTVPLETVKTKNKNVTVOELDLQARRYLQEKYLYNSDVDFGKVQ 180
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDILLRIYRDNNTTISSTLSISLYLTT 233
DB 181 RGLIVFHTSTEPSVNYDLFDAGQGYNTLLRIYRDNKNTINSENMHIDIYLYTS 233

RESULT 16
AAU14104
ID AAU14104 standard; peptide; 257 AA.
XX
XX AAU14104;
XX
XX 21-NOV-2001 (first entry)
XX
XX Peptide sequence from Staphylococcus aureus enterotoxin A.
XX
XX Anti-retroviral; DP178-like; DP107-like; enterotoxin A; antifusogenic;
XX antiviral; HIV transmission.
XX
XX Staphylococcus aureus.
XX
XX WO200151673-A2.
XX
XX 19-JUL-2001.
XX
XX 05-JUL-2000; 2000WO-US035727.
XX
XX 09-JUL-1999; 99US-00350841.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
XX WPI; 2001-442157/47.
XX
XX

XX Identifying a compound that inhibits the formation of or disrupts a
 PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral
 PT or intracellular modulatory activity, by detecting the formation of a
 XX DP107/DP178 complex.
 PS Disclosure; Fig 42; 259pp; English.
 XX The present invention relates to peptides which exhibit anti-retroviral
 CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
 CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
 CC amino acids 639-673 of the transmembrane protein gp41 from human
 CC immunodeficiency virus 1 (HIV-1) isolate LA1. The DP107 peptide
 CC corresponds to amino acids 558-595 of gp41 from HIV-1LA1. The invention
 CC also relates to a method of identifying compounds that inhibit the
 CC formation of or disrupts a DP107/DP178 complex. The method comprises
 CC detecting the formation of a DP107/DP178 complex, both in the presence or
 CC absence of a test compound, in a reaction mixture containing DP107 and
 CC DP178 peptides. The method is useful for identifying compounds, including
 CC small molecule compounds, which may themselves exhibit antifusogenic,
 CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
 CC peptides are useful to inhibit human and non-human retroviral,
 CC particularly HIV, transmission to uninfected cells. The present sequence
 CC represents a peptide sequence from *Staphylococcus aureus* enterotoxin A
 XX Sequence 257 AA;

Query Match 77.8%; Score 948; DB 4; Length 257;
 Best Local Similarity 76.4%; Pred. No. 1.9e-87;
 Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOGTALGNLQIYYNKAITSSEKSAQFLNTLLFKGFFTG 60
 Db 25 SEKSEINEKDLRKSELOGTALGNLQIYYNKAITSSEKSHQDFLOHTILFKGFFTD 84
 QY 61 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYYGQACGTPNKTACMYGGVTLHDNNRLT 120
 Db 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYYGQACGTPNKTACMYGGVTLHDNNRLT 144
 QY 121 BEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGGKVQ 180
 Db 145 BEKVPINLWIDGKQNTVPLETVTNKKNVTVOELDQARHYLQEKYLNYSVDVDFGKVQ 204
 QY 181 RGLIVPHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNNTTISSTLSISLYLYTT 233
 Db 205 RGLIVFHTSTEPSVNYDLFGAQGYSNLLRIYRDNKNTINSENHIDIYLYTS 257

RESULT 17
 ABO10269
 XX ABO10269 standard; protein; 257 AA.
 XX ABO10269;
 DT 19-AUG-2003 (first entry)
 XX S. aureus enterotoxin A.
 DE HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;
 KW Epstein-Barr virus infection; heptad repeat motif.
 XX *Staphylococcus aureus*.
 OS US6518013-B1.
 PN 11-FEB-2003.
 XX 07-JUN-1995; 95US-00485546.
 XX 07-JUN-1993; 93US-00073028.
 PR 07-JUN-1994; 94US-00255208.
 PR 20-DEC-1994; 94US-00360107.
 XX

PA (TRIM-) TRIMERIS INC.
 XX Barney SO, Lambert DM, Petteway SR;
 PI WPI; 2003-465599/44.
 DR Inhibiting transmission of Epstein-Barr virus to a cell, by contacting
 PT the cell with a peptide consisting of a region of Epstein-Barr virus
 PT protein.
 XX Example; Fig 42; 716pp; English.
 CC The invention relates to inhibiting (M) transmission of an Epstein-Barr
 CC virus to a cell, comprising contacting the cell with an effective
 CC concentration of a peptide consisting of a region of 18-39 consecutive
 CC amino acids of an Epstein-Barr virus protein for an effective period of
 CC time, where the region is recognised by one or more of ALIMOTI5,
 CC 107x178x4 or PZIP sequence search motifs, the peptide further comprises
 CC an amino terminal X, and a carboxy terminal Z in which X comprises an
 CC amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic
 CC group or macromolecular carrier group, and Z comprises a carboxyl group,
 CC amido group, hydrophobic group, or macromolecular carrier group, and
 CC fusion of the virus to the cell is inhibited. The peptides were
 CC identified by analysing the structure/motifs present in the HIV-1
 CC glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat
 CC motif containing peptides were used to design the motifs cited above,
 CC which in turn were used to analyse proteins from other pathogenic
 CC organisms and HIV isolates, looking for DP107/178 structural analogues.
 CC The method is useful for inhibiting transmission of Epstein-Barr virus to
 CC a cell and Epstein-Barr virus infection. The present sequence is a
 CC protein from a pathogenic organism analysed for regions analogous to
 CC DP107 or DP178
 XX Sequence 257 AA;
 SQ
 Query Match 77.8%; Score 948; DB 6; Length 257;
 Best Local Similarity 76.4%; Pred. No. 1.9e-87;
 Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOGTALGNLQIYYNKAITSSEKSAQFLNTLLFKGFFTG 60
 Db 25 SEKSEINEKDLRKSELOGTALGNLQIYYNKAITSSEKSHQDFLOHTILFKGFFTD 84
 QY 61 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYYGQACGTPNKTACMYGGVTLHDNNRLT 120
 Db 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYYGQACGTPNKTACMYGGVTLHDNNRLT 144
 QY 121 BEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGGKVQ 180
 Db 145 BEKVPINLWIDGKQNTVPLETVTNKKNVTVOELDQARHYLQEKYLNYSVDVDFGKVQ 204
 QY 181 RGLIVPHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNNTTISSTLSISLYLYTT 233
 Db 205 RGLIVFHTSTEPSVNYDLFGAQGYSNLLRIYRDNKNTINSENHIDIYLYTS 257
 RESULT 18
 ADD44368
 ID ADD44368 standard; protein; 257 AA.
 XX ADD44368;
 XX 15-JAN-2004 (first entry)
 DT *Staphylococcus aureus* enterotoxin A protein.
 DE enterotoxin A; ent A; food poisoning; bacterium; food; milk; fruit juice;
 KW ice cream.
 XX *Staphylococcus aureus*.
 OS WO2003080865-A1.
 PN
 XX

PD 02-OCT-2003.
 XX
 XX 26-MAR-2002; 2002WO-IB001150.
 XX
 XX 26-MAR-2002; 2002WO-IB001150.
 XX
 XX (COUL) COUNCIL SCI & IND RES.
 XX
 XX Padmapriya BP, Ramesh A, Chandrashekar A, Varadaraj MC;
 XX
 XX WPI; 2003-779273/73.
 XX
 XX N-PSDB; ADD44369.
 XX
 XX Novel oligonucleotide primers directed against enterotoxin A gene of
 PT Staphylococcus aureus and heat stable enterotoxin gene of Yersinia
 PT enterocolitica, useful for detecting food poisoning causing bacteria.
 XX
 XX Example 2; Page 14-15; 34pp; English.
 XX
 XX The invention relates to novel oligonucleotide primers directed against
 CC enterotoxin A gene (ent A) of Staphylococcus aureus and heat stable
 CC enterotoxin A gene (yst) of bacteria Yersinia enterocolitica. The novel
 CC oligonucleotide primers are useful for simultaneously detecting food
 CC poisoning bacterial species Staphylococcus aureus and/or Yersinia
 CC enterocolitica in food systems e.g., milk, fruit juices and ice creams,
 CC without prior enrichment for preventing food poisoning outbreak. The PCR
 CC detection method is useful for detecting the bacteria strains in quantity
 CC as low as one cell. The method can be directly used for detecting
 CC bacterial strains. The oligonucleotide primers allow quick and highly
 CC sensitive detection of the food poisoning bacterial species. This
 CC sequence represents the protein derived from the enterotoxin A gene from
 CC Staphylococcus aureus of the invention.
 XX
 XX Sequence 257 AA;
 Query Match 77.8%; Score 948; DB 7; Length 257;
 Best Local Similarity 76.4%; Pred. No. 1.9e-87;
 Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOQTALGNLQIYYNKAITSSEKSAQDLTNTLLPKGFTG 60
 DB 25 SEKSEINEKDLRKSELOQTALGNLQIYYNKAITSSEKSHDQFLQHTILPKGFTD 84
 QY 61 HPYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGTGNKTCACMYGGVTLHDNNRLT 120
 DB 85 HSYNDLLVDLGFSDKIDVYKYGKVDLYGAYGYQCAGTGNKTCACMYGGVTLHDNNRLT 144
 QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHLYHGKFLGYNDSFGKQV 180
 DB 145 EEKKVPINLWLDGKQNTVPLETVKTKNKNVTQELDLQARRYLQEKYNLNSDVFQKQV 204
 QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTDRLRIYRNTTISSTLSISLYLTT 233
 DB 205 RGLIVFHTSTPNSVNYDLFGAQGYQNTLLRIYRDNKTINSENHDIYLYTS 257

RESULT 19

AAW06738
 ID AAW06738 standard; protein; 233 AA.

XX AAW06738;

XX 08-MAR-1997 (first entry)

XX Staphylococcus enterotoxin A.

XX Enterotoxin A; superantigen; antigen; cytokine; chemokine; T cell;
 XX lymphocyte; monocyte; natural killer cell; gene therapy; cancer; vaccine;
 XX adjuvant.

XX Staphylococcus sp.

XX WO9636366-A1.

XX 21-NOV-1996.
 XX
 XX 20-MAY-1996; 96WO-US007432.
 XX
 XX 18-MAY-1995; 95US-00446918.
 XX
 XX 29-DEC-1995; 95US-00580806.
 XX
 XX (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
 XX
 XX Dow SW, Elmslie RE, Potter TA;
 XX
 XX WPI; 1997-011857/01.
 XX
 XX N-PSDB; AAT45699.
 XX
 XX Recombinant molecule encoding superantigen and opt. cytokine or
 PT chemokine - controls activity of effector cells (T cells, monocytes,
 PT natural killer cells), used for gene therapy of cancer.
 XX
 XX Example 1; Page 98-99; 131pp; English.
 XX
 XX A cDNA clone (AAT45699) codes for staphylococcal enterotoxin A (AAW06738)
 CC superantigen. Nucleic acids encoding superantigens (see also AAW06737,
 CC AAW06739), esp. truncated forms of the superantigen lacking the leader
 CC peptide, can be used in the gene therapy of cancer, infectious diseases
 CC and immunological disorders. The nucleic acid, optionally in combination
 CC with cytokine or chemokine nucleic acids, is delivered to an animal using
 CC e.g. liposomes. It acts by controlling the activity of effector cells,
 CC such as T-cells, macrophages, monocytes and/or natural killer cells.
 CC Localised prodrn. of an effective but non-toxic amount of encoded proteins
 CC allows safe treatment of the animal
 XX
 XX Sequence 233 AA;
 Query Match 77.5%; Score 944; DB 2; Length 233;
 Best Local Similarity 76.3%; Pred. No. 4.3e-87;
 Matches 177; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
 QY 2 EKSEINEKDLRKSELOQTALGNLQIYYNKAITSSEKSAQDLTNTLLPKGFTGH 61
 DB 2 EKSEINEKDLRKSELOQTALGNLQIYYNKAITSSEKSHDQFLQHTILPKGFTDH 61
 QY 62 PWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGTGNKTCACMYGGVTLHDNNRLTE 121
 DB 62 SWYNDLLVDLGFSDKIDVYKYGKVDLYGAYGYQCAGTGNKTCACMYGGVTLHDNNRLTE 121
 QY 122 EKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHLYHGKFLGYNDSFGKQV 181
 DB 122 EKVPINLWLDGKQNTVPLETVKTKNKNVTQELDLQARRYLQEKYNLNSDVFQKQV 181
 QY 182 GLIVFHSSEGSTVSYDLFDAQGYPTDRLRIYRNTTISSTLSISLYLTT 233
 DB 182 GLIVFHTSTPNSVNYDLFGAQGYQNTLLRIYRDNKTINSENHDIYLYTS 233

RESULT 20

AAW45011

ID AAW45011 standard; protein; 233 AA.

XX AAW45011;

XX 25-MAR-2003 (revised)

XX 08-JUN-1994 (first entry)

XX Staphylococcal enterotoxin SEA.

XX Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
 XX autoimmune disease; toxicity; Protein A; perfusion system.

XX Staphylococcus aureus.

XX Key Location/Qualifiers

XX Misc-difference 49

```

FT /note= "Given in the specification as O, no further
FI details given"
XX
XX WO3224136-A1.
XX
XX 09-DEC-1993.
XX
XX 01-JUN-1993; 93WO-US005213.
XX
XX 01-JUN-1992; 92US-00891718.
XX
XX (TERM/) TERMAN D S.
XX
XX (STON/) STONE J L.
XX
XX Terman DS, Stone JL;
XX
XX WPI; 1993-405418/50.
XX
XX Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
XX in a patient or for the treatment of auto-immune diseases.
XX
XX Disclosure; Fig 1; 90pp; English.
XX
XX The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
XX which may be used in the methods of the invention for treating cancer in
XX a patient. These SEs, and homologues of them, can be used as tumouricidal
XX agents for treating cancers and autoimmune disease. They exhibit
XX tumouricidal activity and toxicity identical to that observed for the
XX Protein A perfusion system. They may be administered by i.v. injection.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 233 AA;
SQ
Query Match 77.3%; Score 942; DB 2; Length 233;
Best Local Similarity 76.0%; Pred. No. 6.8e-87;
Matches 177; Conservative 21; Mismatches 35; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOQTALGNLQIYYNKAITSSEKSADQFLNTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHQFLXHTILFKGFFD 60
QY 61 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYOCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 61 HSWYNDLLVDFDSDKDIDVKYKGVLDLYGAYGYOCAGGTPNKTCMYGGVTLHDNNRLT 120
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQASHYLGKFGLYNSDSFGKQV 180
DB 121 BEKKVPINLWLDGKQNTVPLETVKTKKQNTVQELDPQARRYLOEKYNLYNSDVFQKQV 180
QY 181 RGLIVFHSSEGSTVSVDLFDQAQGYPTLLRIYRDNTTISSTLSISLYTT 233
DB 181 RGLIVFHTSTEPSVNYDLFQAQGYSNLTLRIYRDNKTINSENHDIYLYTS 233
RESULT 21
AAR35373
ID AAR35373 standard; peptide; 233 AA.
XX
XX AAR35373;
XX
XX 20-APR-1998 (first entry)
XX
XX Staphylococcus enterotoxin SEA wild-type superantigen.
XX
XX SE5; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment;
XX cancer; infection; autoimmune disease; antibody.
XX
XX Staphylococcus sp.
XX
XX WO9736932-A1.
XX
XX 09-OCT-1997.
XX

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PF 26-MAR-1997; 97WO-SE000537.
XX
XX 29-MAR-1996; 96SE-00001245.
XX
XX 12-AUG-1996; 96US-00695692.
XX
XX (PHAA ) PHARMACIA & UPJOHN AB.
XX
XX Antonsson P, Hansson J, Bjoerk P, Dohlisten M, Kalland T;
XX Abrahmsen L, Forsberg G;
XX
XX WPI; 1997-503052/46.
XX
XX Conjugate of target seeking moiety and modified superantigen - useful for
XX activating the immune system to treat cancer, viral infections, parasitic
XX infestations and autoimmune diseases.
XX
XX Claim 8; Page 36-37; 58pp; English.
XX
XX This is the wild-type Staphylococcus enterotoxin SEA superantigen. This
XX SEA superantigen can be modified to be used in a novel conjugate. The
XX novel conjugate comprises a target seeking moiety and a modified wild
XX type superantigen. The modified superantigen retains its ability to
XX activate a subset of T cells, even though 1 or more wild-type amino acid
XX residues in at least 1 region which functions in determining binding to T
XX cell receptor (TCR) and activation of a subset of T cells has/have been
XX replaced. Such a modified superantigen can optionally be used as part of
XX a conjugate with a target seeking moiety, for activating the immune
XX system to treat a mammalian disease. A pharmaceutical composition can be
XX prepared comprising a modified antibody (preferably a Fab fragment fused
XX to a peptide moiety providing activation of T cells in Vbeta specific
XX manner) in which cysteines providing for interchain cysteine linkages in
XX the native antibody have been replaced (preferably by serine residues) to
XX prohibit cysteine formation. The modified wild-type superantigen is used
XX for treating cancer, viral infections, parasitic infestations and
XX autoimmune disease. The modified wild type superantigen has a lower
XX immunogenicity and reactivity with neutralising antibodies and has fewer
XX side-effects when used as a drug, compared to wild type superantigen
XX
XX Sequence 233 AA;
SQ
Query Match 77.3%; Score 941; DB 2; Length 233;
Best Local Similarity 76.0%; Pred. No. 8.6e-87;
Matches 177; Conservative 21; Mismatches 35; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOQTALGNLQIYYNKAITSSEKSADQFLNTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHQFLQHTILFKGFFD 60
QY 61 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYOCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 61 HSWYNDLLVDFDSDKDIDVKYKGVLDLYGAYGYOCAGGTPNKTCMYGGVTLHDNNRLT 120
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQASHYLGKFGLYNSDSFGKQV 180
DB 121 BEKKVPINLWLDGKQNTVPLETVKTKKQNTVQELDLQARRYLOEKYNLYNSDVFQKQV 180
QY 181 RGLIVFHSSEGSTVSVDLFDQAQGYPTLLRIYRDNTTISSTLSISLYTT 233
DB 181 RGLIVFHTSTEPSVNYDLFQAQGYSNLTLRIYRDNKTINSENHDIYLYTS 233
RESULT 22
AAB67338
ID AAB67338 standard; peptide; 233 AA.
XX
XX AAB67338;
XX
XX 23-APR-2001 (first entry)
XX
XX Staphylococcus aureus enterotoxin A protein.
XX
XX Tumour; cancer; immune; enterotoxin.
XX

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OS Staphylococcus aureus.
 XX US6180097-B1.
 XX 30-JAN-2001.
 XX 30-OCT-1998; 98US-00183437.
 XX 03-OCT-1989; 89US-00416530.
 XX 17-JAN-1990; 90US-00466577.
 XX 17-JAN-1991; 91WO-US000342.
 XX 01-JUN-1992; 92US-00891718.
 XX 02-MAR-1993; 93US-00025144.
 XX 21-JAN-1994; 94US-00189424.
 XX 19-JUN-1995; 95US-00491746.
 XX (TERM/) TERNAN D S.
 XX Terman DS;
 XX WPI; 2001-158657/16.
 XX Disclosure; Fig 2; 16pp; English.
 XX The present invention relates to a tumour cell capable of stimulating
 CC antitumor immune reactivity in vitro or in vivo contains and expresses an
 CC exogenous nucleic acid molecule encoding a superantigen or its active
 CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
 CC molecule that activates T cells in conjunction with an antigenic
 CC stimulus. The invention may be used for cancer therapy by stimulating an
 CC anticancer immune response in vivo or ex vivo
 XX Sequence 233 AA;
 XX
 XX Query Match 77.3%; Score 941; DB 4; Length 233;
 XX Best Local Similarity 76.0%; Pred. No. 8.6e-87;
 XX Matches 177; Conservative 21; Mismatches 35; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNSTRATSSKSAOFTNLILFKGFTG 60
 DB 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNSTRATSSKSAOFTNLILFKGFTD 60
 QY 61 HPWYNDLLVDFSGKIDVYKGGKVDLYGAYGYOCAGTGNKTKMYGGVTLHDNNRLT 120
 DB 61 HSWYNDLLVDFSGKIDVYKGGKVDLYGAYGYOCAGTGNKTKMYGGVTLHDNNRLT 120
 QY 121 EEKVPINLWIDGKQTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
 DB 121 EEKVPINLWIDGKQTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
 QY 181 RGLIVFHSSEGSVSYDLFDAGQVDPDILLRYRNTNITSSLSLSLYLYTT 233
 DB 181 RGLIVFHTSTEPSVNYDLFDAGQVSNLTLRYRNTNITSSLSLSLYLYTS 233
 RESULT 23
 ID ABU79068
 XX ABU79068 standard; protein; 257 AA.
 XX AC ABU79068;
 XX 18-JUN-2003 (first entry)
 XX S. aureus SEA (staphylococcus enterotoxin A) protein.
 XX Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis;
 XX gene therapy; mammalian cell receptor; tumour associated lipid; energy;
 XX T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;
 XX APC; antitumour.

XX OS Staphylococcus aureus.
 XX US2002177551-A1.
 XX 28-NOV-2002.
 XX 30-MAY-2001; 2001US-00870759.
 XX 31-MAY-2000; 2000US-0208128P.
 XX (TERM/) TERNAN D S.
 XX Terman DS;
 XX WPI; 2003-361759/34.
 XX N-PSDB; ACA64694.
 XX A mammalian cell receptor, useful in the treatment of cancer by binding
 PT to tumour associated lipids where the binding induces energy or apoptosis
 PT in T cells and antigen presenting cells.
 XX Disclosure; Page; 167pp; English.
 XX The invention relates to a mammalian cell receptor, useful in the
 CC treatment of cancer, which binds to tumour associated lipids and induces
 CC energy or apoptosis in the T cells and antigen presenting cells (APCs).
 CC Also included are a mammalian cell useful in the treatment of cancer
 CC where the receptor which binds tumour associated lipids and induces
 CC cellular inactivation or death is deleted or functionally deactivated,
 CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal
 CC (by allowing tumour associated lipids to contact immunocytes in which
 CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,
 CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
 CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
 CC deleted), a construct useful in the treatment of cancer comprising a
 CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
 CC useful in the treatment of cancer (where an adaptor protein which
 CC inhibits T cell activation by tumour associated antigens is deleted or
 CC functionally deactivated), a composition useful in the treatment of
 CC cancer (comprising a lipid raft conjugated to a superantigen), producing
 CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
 CC allowing tumour associated lipids to contact immunocytes, in which
 CC receptors for the lipids are inactivated or deleted to produce a
 CC tumouricidal immunocyte population, and administering the tumouricidal
 CC activated immunocytes to the host), producing (M3) a tumouricidal APC
 CC population ex vivo in a mammal (by allowing a tumour associated lipid to
 CC contact APCs, in which receptors for the tumour associated lipids are
 CC inactivated or deleted to produce a tumouricidally activated population,
 CC and administering APCs to the host), producing a tumouricidal T cell
 CC population ex vivo in a mammal (by allowing a tumour associated lipids to
 CC contact T cells, in which adaptor proteins, which inhibit T cell
 CC activation by tumour associated antigens, are deleted or functionally
 CC deactivated to produce a tumouricidal population of T cells, and
 CC administering the tumouricidally activated T cells to the host, or
 CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
 CC administering the tumouricidally activated T cells to the host), treating
 CC (M5) cancer in a mammal (by administering a lipid binding molecule which
 CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
 CC a tumouricidal T cell population in vivo in a mammal (by allowing a
 CC tumour associated antigen to contact immunocytes in which adaptor
 CC proteins which inhibit T cell activation by tumour associated antigens
 CC are deleted or functionally deactivated) and producing (M7) a
 CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
 CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
 CC receptors, methods and compositions are useful for treating cancers and
 CC tumours. Bacterial superantigens are co-administered or administered as
 CC fusion constructs with anti-tumour proteins or motifs. The present
 CC sequence represents a bacterial superantigen protein (e.g. a
 CC staphylococcal enterotoxin). Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format from the US patent office website at
 CC "seqdata.uspto.gov/sequence.html?DocID=20020177551"

XX SQ Sequence 257 AA;
Query Match 76.8%; Score 935; DB 6; Length 257;
Best Local Similarity 75.5%; Pred. No. 4e-86;
Matches 176; Conservative 21; Mismatches 36; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOGTALGNLQIYYNYSKAITSEKSDAQFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOGTALGNLQIYYNYSKAITSEKSDAQFLNTLLFKGFFTG 84
QY 61 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYYGYQCAGTGNKTCMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDPDSKDIDVKYKGVLDYGYGYQCAGTGNKTCMYGGVTLHDNNRLT 144
QY 121 BEKVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 145 BEKVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNNTTISSTLSISLYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQQGNSNTLLRIYRDNNTTINSENHIDIYLYTS 257
RESULT 24
ID ABB76234 standard; protein; 233 AA.
XX AC ABB76234;
XX DT 09-AUG-2002 (first entry)
XX DE Staphylococcus aureus enterotoxin A.
XX KW Enterotoxin A; SEA; superantigen; antigen; tumour; cancer; antitumour;
XX KW therapy.
XX OS Staphylococcus aureus.
XX FH Key Location/Qualifiers
FT Misc-difference 49 /note= "amino acid residue given as 'O' in the
FT specification"
XX PN US2002051765-A1.
XX PD 02-MAY-2002.
XX PF 19-DEC-2000; 2000US-00741503.
XX PR 03-OCT-1989; 89US-00416530.
XX PR 17-JAN-1990; 90US-00466577.
XX PR 17-JAN-1991; 91WO-US000342.
XX PR 01-JUN-1992; 92US-00891718.
XX PR 02-MAR-1993; 93US-00025144.
XX PR 31-JAN-1994; 94US-00189424.
XX PR 19-JUN-1995; 95US-00491746.
XX FA (TERM/) TERMAN D S.
XX FI Terman DS;
XX WPI; 2002-415198/44.
XX DR WPI; 2002-415198/44.
XX PT Reagent for treating cancer without the need for e.g. radiotherapy,
XX PT comprises a specific V beta subset of T cells sensitized to a growing
XX PT tumor and stimulated with superantigens.
XX PS Disclosure; Fig 2; 17pp; English.
XX CC The present sequence is the protein sequence of enterotoxin A (SEA) of
XX CC Staphylococcus aureus. Similarity is shown, in several stretches of
XX CC sequence, between staphylococcal enterotoxins, streptococcal pyrogenic

CC exotoxins and staphylococcal exfoliative toxins (see ABB76234-44). In the
CC present invention, synthetic polypeptides useful in tumour therapy and in
CC blocking or destroying autoreactive T and B lymphocyte populations are
CC characterised by substantial structural homology to staphylococcal
CC enterotoxin A and enterotoxin B, and to streptococcal pyrogenic
CC exotoxins, with statistically significant sequence homology and
CC similarity (Z value of Lipman and Pearson algorithm in Monte Carlo
CC analysis exceeding 6) to include alignment of cysteine residues and
CC similar hydropathy profiles. These superantigens are used to treat solid
CC tumours, including their metastases, without radiation, surgery or
CC standard chemotherapeutic agents. A claimed method of human cancer
CC treatment involves contacting haematopoietic cells from a patient with
CC one or more superantigens ex vivo to generate stimulated cells, selecting
CC a specific V beta subset of cells, and reintroducing these cells into the
CC patient to induce an in vivo therapeutic, tumoricidal reaction
XX Sequence 233 AA;
SQ Query Match 76.6%; Score 933; DB 5; Length 233;
Best Local Similarity 75.5%; Pred. No. 5.6e-86;
Matches 176; Conservative 21; Mismatches 36; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOGTALGNLQIYYNYSKAITSEKSDAQFLNTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELOGTALGNLQIYYNYSKAITSEKSDAQFLNTLLFKGFFTG 60
QY 61 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYYGYQCAGTGNKTCMYGGVTLHDNNRLT 120
DB 61 HSWYNDLLVDPDSKDIDVKYKGVLDYGYGYQCAGTGNKTCMYGGVTLHDNNRLT 120
QY 121 BEKVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 121 BEKVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNNTTISSTLSISLYLYTT 233
DB 181 RGLIVFHTSTEPSVNYDLFGAQQGNSNTLLRIYRDNNTTINSENHIDIYLYTS 233
RESULT 25
ID ABB79501 standard; protein; 257 AA.
XX AC ABB79501;
XX DT 23-SEP-2002 (first entry)
XX DE Staphylococcal enterotoxin A vaccine, periplasmic (A489270P).
XX KW Enterotoxin A; superantigen; antigen; toxin; vaccine; A489270P;
XX KW attenuation; mutant; mutein.
XX OS Staphylococcus sp.
XX OS Synthetic.
XX FH Key Location/Qualifiers
FT Peptide 1..25 /label= Signal_peptide
FT Protein 26..257 -/label= Mature_protein
FT Misc-difference 72 /note= "wild-type Leu substituted by Arg"
FT Misc-difference 94 /note= "wild-type Asp substituted by Arg"
FT Misc-difference 116 /note= "wild-type Tyr substituted by Ala"
XX PN US6399332-B1.
XX PD 04-JUN-2002.
XX PF 01-SEP-1998; 98US-00144776.
XX

PR 25-JUN-1997; 97US-00882431.
 PA (USSA) US SEC OF ARMY.
 XX
 PI Ulrich RG, Olson MA, Bavari S;
 XX
 DR WPI; 2002-546281/58.
 DR N-PSDB; ABN84222.
 XX
 PT Novel isolated and purified superantigen toxin DNA fragment which has
 PT been genetically altered, useful for producing vaccine for treatment of
 PT superantigen toxin-associated bacterial diseases.
 XX
 PS Claim 4; Col 33-35; 46pp; English.
 XX
 CC The present sequence is the protein sequence of staphylococcal
 CC enterotoxin A (SEA) vaccine, periplasmic (A489270P). The vaccine
 CC comprises 3 amino acid substitutions introduced into the SEA sequence:
 CC L48R, Y89A and D70R. These mutations reduce the binding of the toxin to
 CC major histocompatibility complex (MHC) Class II and/or T cell receptors.
 CC The full-length expressed product is secreted into the periplasmic space
 CC of *Escherichia coli* host cells, and the leader peptide is recognised and
 CC cleaved by a native mechanism. The vaccine is used to protect against
 CC superantigen toxin infections. Superantigen attributes are absent, but
 CC the superantigen is effectively recognised by the immune system and an
 CC appropriate antibody response is produced. In examples from the
 CC invention, attenuated superantigen toxins were shown to protect animals
 CC against challenge with wild-type toxin. Methods of producing and using
 CC the altered superantigen toxins as vaccines, and in diagnosis and
 CC therapy, are provided. A multivalent vaccine consisting of altered
 CC superantigen toxins from SEA, SEB, SEC-1, TST-1 and streptococcal SPEA
 CC is predicted to provide protective immunity against the majority of
 CC bacterial superantigen toxins
 XX
 SQ Sequence 257 AA;
 XX
 Query Match 75.9%; Score 925; DB 5; Length 257;
 Best Local Similarity 75.1%; Pred. No. 4.2e-85;
 Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKQIYYNKAITSSEKSAOQFTNTLLFKGFTTG 60
 DB 25 SEKSEINEKDLRKSELOQTALGNLKQIYYNKAITSSEKSAOQFTNTLLFKGFTTG 84
 QY 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYOCAGGTPNKTACMYGGVTLHNNRLT 120
 DB 85 HSWYNDLLVRFDSKOIVDKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHNNRLT 144
 QY 121 EEKKVPINLWIDGKQITVPIDIKVTSKKEVTYQELDLQARHYLHGKFLYNSDFGKQV 180
 DB 145 EEKKVPINLWLDGKQNTVPLETVKTNKNVTYQELDLQARHYLQEKYLYNSDFGKQV 204
 QY 181 RGLIVFHSSEGSVTSVDLFDAGQOYPTLLRIYRDNNTTSSLSLSLYLTT 233
 DB 205 RGLIVFHTSTEPSVNYDLFGAQOQYNTLLRIYRDNKNTINSENHDIYLYTS 257
 RESULT 26
 ABU10081
 ID ABU10081 standard; protein; 257 AA.
 XX
 AC ABU10081;
 XX
 DT 11-AUG-2003 (first entry)
 XX
 DE Staphylococcal enterotoxin A #1.
 XX
 KW Enterotoxin A; superantigen-associated bacterial infection; vaccine;
 KW superantigen toxin.
 XX
 OS Staphylococcus sp.
 XX
 PN US2003009015-A1.

XX 09-JAN-2003.
 PD
 XX 25-JUN-1997; 97US-00882431.
 PF
 XX 25-JUN-1997; 97US-00882431.
 PR
 XX (ULRI/) ULRICH R G.
 XX (OLSO/) OLSON M A.
 PA (BAVA/) BAVARI S.
 PA
 XX Ulrich RG, Olson MA, Bavari S;
 PI
 XX WPI; 2003-401542/38.
 DR N-PSDB; ACA61177.
 DR
 XX New superantigen toxin and/or DNA fragment with an altered binding of the
 PT encoded altered toxin to either MHC class II or T cell antigen receptor,
 PT useful for treating or ameliorating superantigen-associated bacterial
 PT infection.
 XX
 PS Claim 10; Page 18-19; 50pp; English.
 XX
 CC The invention relates to an isolated and purified superantigen toxin
 CC and/or DNA fragment, which has been altered so that the binding of the
 CC encoded toxin to either major histocompatibility complex (MHC) class II
 CC or T cell antigen receptor is altered. The superantigen toxins, DNA
 CC fragments, and vaccines are useful for treating or ameliorating
 CC superantigen-associated bacterial infection. The DNA fragments are
 CC particularly useful for producing vaccine against superantigen toxin
 CC infections. The transformed host cells are useful for analysing the
 CC effectiveness of drugs and agents that affect the binding of
 CC superantigens to MHC class II or T-cell antigen receptors. The present
 CC sequence represents the amino acid sequence of staphylococcal enterotoxin
 CC A #1
 XX
 SQ Sequence 257 AA;
 XX
 Query Match 75.9%; Score 925; DB 6; Length 257;
 Best Local Similarity 75.1%; Pred. No. 4.2e-85;
 Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKQIYYNKAITSSEKSAOQFTNTLLFKGFTTG 60
 DB 25 SEKSEINEKDLRKSELOQTALGNLKQIYYNKAITSSEKSAOQFTNTLLFKGFTTG 84
 QY 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYOCAGGTPNKTACMYGGVTLHNNRLT 120
 DB 85 HSWYNDLLVRFDSKOIVDKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHNNRLT 144
 QY 121 EEKKVPINLWIDGKQITVPIDIKVTSKKEVTYQELDLQARHYLHGKFLYNSDFGKQV 180
 DB 145 EEKKVPINLWLDGKQNTVPLETVKTNKNVTYQELDLQARHYLQEKYLYNSDFGKQV 204
 QY 181 RGLIVFHSSEGSVTSVDLFDAGQOYPTLLRIYRDNNTTSSLSLSLYLTT 233
 DB 205 RGLIVFHTSTEPSVNYDLFGAQOQYNTLLRIYRDNKNTINSENHDIYLYTS 257
 RESULT 27
 ABU62324
 ID ABU62324 standard; protein; 257 AA.
 XX
 AC ABU62324;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE S. aureus periplasmic enterotoxin A mutant #1.
 XX
 KW SEA; staphylococcal enterotoxin A; mutein; mutant; vaccine;
 KW superantigen toxin; MHC; superantigen-associated bacterial infection;
 KW bacterial infection; antibacterial.
 XX

OS Staphylococcus aureus.
OS Synthetic.
XX Key Location/Qualifiers
FH Peptide 1..24
FT /label= Signal_peptide
FT 25..257
FT Protein /label= Mature_SEA_mutant #1
FT Misc-difference 66 /note= "Wild-type Leu substituted by Glu"
FT Misc-difference 72 /note= "Wild-type Leu substituted by Arg"
FT Misc-difference 94 /note= "Wild-type Asp substituted by Arg"
FT Misc-difference 113 /note= "Wild-type Tyr substituted by Gly"
FT Misc-difference 116 /note= "Wild-type Tyr substituted by Ala"
XX US2003036644-A1.
XX 20-FEB-2003.
XX 26-NOV-2001; 2001US-00002784.
XX 25-JUN-1997; 97US-00882431.
XX 01-SEP-1998; 98US-00144776.
XX (ULRI/) ULRICH R G.
XX Ulrich RG;
XX WPI; 2003-492125/46.
XX N-PSDB; ACD28894.
XX New superantigen toxin DNA fragment, useful for preparing a composition
XX for treating or preventing bacterial infection.
XX Disclosure; Page 22-23; 68pp; English.
XX The invention relates to an isolated and purified superantigen toxin DNA
XX fragment is altered so that binding of the encoded altered toxin to
XX either the MHC class II or T cell antigen receptor is altered. Also
XX included are a recombinant DNA construct (comprising a vector and an
XX isolated and purified altered superantigen toxin DNA fragment), a host
XX cell transformed with the recombinant DNA construct, producing altered
XX superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
XX superantigen toxin peptide, diagnosing superantigen-associated bacterial
XX infection, a vaccine (comprising an altered superantigen toxin for
XX producing antigenic and immunogenic response resulting in the protection
XX of a mammal against superantigen-associated bacterial infection),
XX treating/ameliorating a superantigen-associated bacterial infection, an
XX antisera isolated from individuals immunised with one or more altered
XX TSST-1 superantigen toxin and an antibody which recognises altered TSST-
XX 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
XX SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and
XX SPEb). The superantigen toxin DNA fragment is useful for preparing a
XX composition for treating or preventing bacterial infection. The present
XX sequence represents the L42E/L48R/D70R/Y89G/Y92A (with reference to the
XX mature protein sequence) mutant of periplasmic SEA
XX Sequence 257 AA;
XX Query Match 75.9%; Score 925; DB 7; Length 257;
XX Best Local Similarity 75.1%; Pred. No. 4.2e-85;
XX Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
XX 1 SEKSEINEKDLRKSELGQALGNLKOIYYNKAITSSEKSAQDLTNTLLFKGFTG 60
XX 25 SEKSEINEKDLRKSELGQALGNLKOIYYNKAITENKESHDPQRTILFKGFTD 84
XX 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
XX Best Local Similarity 75.1%; Pred. No. 4.2e-85;
XX Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
XX 1 SEKSEINEKDLRKSELGQALGNLKOIYYNKAITSSEKSAQDLTNTLLFKGFTG 60
XX 25 SEKSEINEKDLRKSELGQALGNLKOIYYNKAITENKESHDPQRTILFKGFTD 84
XX 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
XX Best Local Similarity 75.1%; Pred. No. 4.2e-85;
XX Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
XX 1 SEKSEINEKDLRKSELGQALGNLKOIYYNKAITSSEKSAQDLTNTLLFKGFTG 60
XX 25 SEKSEINEKDLRKSELGQALGNLKOIYYNKAITENKESHDPQRTILFKGFTD 84
XX 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120

Db 85 HSWYNDLLVRFDSKDIDVKYKGGKVDLYGAYAGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 BEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 BEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPDTLRIYRDNTTISSTLSISLYLYTT 233
Db 205 RGLIVFHSSEGSTVSVDLFDAGQGYPDTLRIYRDNTTISSTLSISLYLYTT 257
RESULT 28
AAE37676
ID AAE37676 standard; protein; 257 AA.
XX
AC AAE37676;
XX
DT 06-OCT-2003 (first entry)
XX
DE Protein #1 related to the invention.
XX
KW Superantigen toxin; vaccine; infection; gene therapy.
XX
OS Unidentified.
XX
PN WO2003056015-A1.
XX
PD 10-JUL-2003.
XX
PF 26-NOV-2001; 2001WO-05046540.
XX
PR 26-NOV-2001; 2001US-00002784.
XX
PA (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX
PI Ulrich RG;
XX
XX WPI; 2003-492125/46.
XX N-PSDB; AAD56764.
XX
XX New superantigen toxin DNA fragment, useful for preparing a composition
XX for treating or preventing bacterial infection.
XX Disclosure; Page 108-109; 141pp; English.
XX The invention provides a superantigen toxin DNA fragment which has been
XX genetically altered such that binding of the encoded altered toxin to
XX either the MHC class II or T cell antigen receptor is disrupted or
XX altered. DNA fragments of the invention are useful in the production of
XX vaccines against bacterial superantigen toxin infections. They are also
XX useful in gene therapy. The present sequence is a protein related to the
XX CC invention
XX Sequence 257 AA;
XX Query Match 75.9%; Score 925; DB 7; Length 257;
XX Best Local Similarity 75.1%; Pred. No. 4.2e-85;
XX Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
XX 1 SEKSEINEKDLRKSELGQALGNLKOIYYNKAITSSEKSAQDLTNTLLFKGFTG 60
XX 25 SEKSEINEKDLRKSELGQALGNLKOIYYNKAITENKESHDPQRTILFKGFTD 84
XX 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
XX Best Local Similarity 75.1%; Pred. No. 4.2e-85;
XX Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
XX 1 SEKSEINEKDLRKSELGQALGNLKOIYYNKAITSSEKSAQDLTNTLLFKGFTG 60
XX 25 SEKSEINEKDLRKSELGQALGNLKOIYYNKAITENKESHDPQRTILFKGFTD 84
XX 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
XX Best Local Similarity 75.1%; Pred. No. 4.2e-85;
XX Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
XX 1 SEKSEINEKDLRKSELGQALGNLKOIYYNKAITSSEKSAQDLTNTLLFKGFTG 60
XX 25 SEKSEINEKDLRKSELGQALGNLKOIYYNKAITENKESHDPQRTILFKGFTD 84
XX 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120

CC wild-type toxin. Methods of producing and using the altered superantigen
CC toxins as vaccines, and in diagnosis and therapy, are provided. A
CC multivalent vaccine consisting of altered superantigen toxins from SEA,
CC SEB, SEC-1, TSST-1 and streptococcal SpA is predicted to provide
CC protective immunity against the majority of bacterial superantigen toxins
XX
XX Sequence 233 AA;

Query Match 75.6%; Score 921; DB 5; Length 233;
Best Local Similarity 75.0%; Pred. No. 9.2e-85;
Matches 174; Conservative 21; Mismatches 37; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKADQFLTNLLPKGFFTGH 61
Db 2 EKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESHDPQFQHTILFKGFFTDH 61
QY 62 PWYNDLLVDLGSTAATSEYEGSSVDLYCAYGYQCAGTGNKTAACMYGGVTLDHNNRLTE 121
Db 62 SWYNDLLVRPDSKDIDVKYKGGKVDLYGAYGYQCAGTGNKTAACMYGGVTLDHNNRLTE 121
QY 122 EKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQR 181
Db 122 EKKVPINLWLDGKQNTVPLETVTKNKNVTVOELDLQARRYLOEKYNLYNSDVPDGVQR 181
QY 182 GLIVFHSSEGSTVSDYDLFDAQGYPTDLLRIYRDNNTTISSTLSISLYLYTT 233
Db 182 GLIVFHTSTEPSVNDYDLFGAQGYNTLLRIYRDNKNTINSENHMDIYLYTS 233

RESULT 31
ABU10082
ID ABU10082 standard; protein; 233 AA.
XX
AC ABU10082;

DT 11-AUG-2003 (first entry)
XX
XX Staphylococcal enterotoxin A #2.
DE Enterotoxin A; superantigen-associated bacterial infection; vaccine;
KW superantigen toxin.
XX Staphylococcus sp.

Key Location/Qualifiers
FT Misc-difference 1 /note= "Encoded by AT"

XX US2003009015-A1.
XX 09-JAN-2003.
XX 25-JUN-1997; 97US-00882431.
XX 25-JUN-1997; 97US-00882431.
XX (ULRI/) ULRICH R G.
XX (OLSO/) OLSON M A.
XX (BAVA/) BAVARI S.
XX Ulrich RG, Olson MA, Bavari S;
XX WPI; 2003-401542/38.
XX N-PSDB; ACA61178.

XX New superantigen toxin and/or DNA fragment with an altered binding of the
XX encoded altered toxin to either MHC class II or T cell antigen receptor,
XX useful for treating or ameliorating superantigen-associated bacterial
XX infection.

XX Claim 11; Page 20-21; 50pp; English.
XX The invention relates to an isolated and purified superantigen toxin

CC and/or DNA fragment, which has been altered so that the binding of the
CC encoded toxin to either major histocompatibility complex (MHC) class II
CC or T cell antigen receptor is altered. The superantigen toxins, DNA
CC fragments, and vaccines are useful for treating or ameliorating
CC superantigen-associated bacterial infection. The DNA fragments are
CC particularly useful for producing vaccine against superantigen toxin
CC infections. The transformed host cells are useful for analysing the
CC effectiveness of drugs and agents that affect the binding of
CC superantigens to MHC class II or T-cell antigen receptors. The present
CC sequence represents the amino acid sequence of staphylococcal enterotoxin
XX A #2
XX Sequence 233 AA;

Query Match 75.6%; Score 921; DB 6; Length 233;
Best Local Similarity 75.0%; Pred. No. 9.2e-85;
Matches 174; Conservative 21; Mismatches 37; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKADQFLTNLLPKGFFTGH 61
Db 2 EKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESHDPQFQHTILFKGFFTDH 61
QY 62 PWYNDLLVDLGSTAATSEYEGSSVDLYCAYGYQCAGTGNKTAACMYGGVTLDHNNRLTE 121
Db 62 SWYNDLLVRPDSKDIDVKYKGGKVDLYGAYGYQCAGTGNKTAACMYGGVTLDHNNRLTE 121
QY 122 EKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQR 181
Db 122 EKKVPINLWLDGKQNTVPLETVTKNKNVTVOELDLQARRYLOEKYNLYNSDVPDGVQR 181
QY 182 GLIVFHSSEGSTVSDYDLFDAQGYPTDLLRIYRDNNTTISSTLSISLYLYTT 233
Db 182 GLIVFHTSTEPSVNDYDLFGAQGYNTLLRIYRDNKNTINSENHMDIYLYTS 233

RESULT 32
ABU62325
ID ABU62325 standard; protein; 233 AA.
XX
AC ABU62325;
XX 27-AUG-2003 (first entry)
XX S. aureus cytoplasmic enterotoxin A mutant #1.
XX SEA; staphylococcal enterotoxin A; mutein; mutant; vaccine;
KW superantigen toxin; MHC; superantigen-associated bacterial infection;
KW bacterial infection; antibacterial.
XX Staphylococcus aureus.
XX Synthetic.

Key Location/Qualifiers
FT Misc-difference 1.2 /note= "Encoded by ATGAG"
FT Misc-difference 42 /note= "Wild-type Leu substituted by Glu"
FT Misc-difference 48 /note= "Wild-type Leu substituted by Arg"
FT Misc-difference 70 /note= "Wild-type Asp substituted by Arg"
FT Misc-difference 89 /note= "Wild-type Tyr substituted by Gly"
FT Misc-difference 92 /note= "Wild-type Tyr substituted by Ala"

XX US2003036644-A1.
XX 20-FEB-2003.
XX 26-NOV-2001; 2001US-00002784.
XX 25-JUN-1997; 97US-00882431.

PR 01-SEP-1998; 98US-00144776.
 XX (ULRI/) ULRICH R G.
 XX PI Ulrich RG;
 XX WPI: 2003-492125/46.
 XX N-PSDB; AC28895.
 XX
 XX New superantigen toxin DNA fragment, useful for preparing a composition
 XX for treating or preventing bacterial infection.
 XX
 XX Disclosure; Page 24-25; 68pp; English.
 XX
 XX The invention relates to an isolated and purified superantigen toxin DNA
 XX fragment is altered so that binding of the encoded altered toxin to
 XX either the MHC class II or T cell antigen receptor is altered. Also
 XX included are a recombinant DNA construct (comprising a vector and an
 XX isolated and purified altered superantigen toxin DNA fragment), a host
 XX cell transformed with the recombinant DNA construct, producing altered
 XX superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
 XX superantigen toxin peptide, diagnosing superantigen-associated bacterial
 XX infection, a vaccine (comprising an altered superantigen toxin for
 XX producing antigenic and immunogenic response resulting in the protection
 XX of a mammal against superantigen-associated bacterial infection),
 XX treating/ameliorating a superantigen-associated bacterial infection, an
 XX antiserum isolated from individuals immunised with one or more altered
 XX TSST-1 superantigen toxin and an antibody which recognises altered TSST-
 XX 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
 XX SEB, SECI) and streptococcal pyrogenic enterotoxin a and b (SPEa and
 XX SPEb). The superantigen toxin DNA fragment is useful for preparing a
 XX composition for treating or preventing bacterial infection. The present
 XX sequence represents the L42E/L48R/D70R/Y89G/Y92A mutant of cytoplasmic
 XX SEA
 XX SQ Sequence 233 AA;
 Query Match 75.6%; Score 921; DB 7; Length 233;
 Best Local Similarity 75.0%; Pred. No. 9.2e-85;
 Matches 174; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
 QY 2 EKSEENEKDLRKSELOQTALGNLKOIYYVNSKAITSEKSDADQFLNTLLFKGFFTGH 61
 DB 2 EKSEENEKDLRKSELOQTALGNLKOIYYVNEKAKTENKESHDPQROHTILFKGFFTDH 61
 QY 62 PWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
 DB 62 SWYNDLLVRFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
 QY 122 EKVPINLWIDGKQTTVPIDKVTSKKVTVOELDLQARHYLHGKFLYNSDSFGKQVOR 181
 DB 122 EKVPINLWIDGKQNTVPLETVTKNKNVTVOELDLQARRYLQEKYLNYSNDSVDFGKQVOR 181
 QY 182 GLIVFHSSEGSTSVSYDLFDAQGQYPTLLRIYRDNTTISSTLSLSLYLYTT 233
 DB 182 GLIVFHTSTEPSVNYDLFGAGQGYNTLLRIYRDNTKINSENHIDIVLYTS 233
 RESULT 33
 AAE37677
 ID AAE37677 standard; protein; 233 AA.
 XX AC AAE37677;
 XX
 XX 06-OCT-2003 (first entry)
 XX Protein #2 related to the invention.
 XX Superantigen toxin; vaccine; infection; gene therapy.
 XX Unidentified.
 XX Key Location/Qualifiers
 XX FT Misc-difference 14

FT Misc-difference 1 /note= "Encoded by AT"
 XX FT
 XX WO2003056015-A1.
 XX PD 10-JUL-2003.
 XX PF 26-NOV-2001; 2001WO-US046540.
 XX PR 26-NOV-2001; 2001US-00002784.
 XX PA (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
 XX PI Ulrich RG;
 XX WPI: 2003-492125/46.
 XX N-PSDB; AAD56765.
 XX New superantigen toxin DNA fragment, useful for preparing a composition
 XX for treating or preventing bacterial infection.
 XX Disclosure; Page 110-112; 141pp; English.
 XX The invention provides a superantigen toxin DNA fragment which has been
 XX genetically altered such that binding of the encoded altered toxin to
 XX either the MHC class II or T cell antigen receptor is disrupted or
 XX altered. DNA fragments of the invention are useful in the production of
 XX vaccines against bacterial superantigen toxin infections. They are also
 XX useful in gene therapy. The present sequence is a protein related to the
 XX invention
 XX SQ Sequence 233 AA;
 Query Match 75.6%; Score 921; DB 7; Length 233;
 Best Local Similarity 75.0%; Pred. No. 9.2e-85;
 Matches 174; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
 QY 2 EKSEENEKDLRKSELOQTALGNLKOIYYVNSKAITSEKSDADQFLNTLLFKGFFTGH 61
 DB 2 EKSEENEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHDPQROHTILFKGFFTDH 61
 QY 62 PWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
 DB 62 SWYNDLLVRFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
 QY 122 EKVPINLWIDGKQTTVPIDKVTSKKVTVOELDLQARHYLHGKFLYNSDSFGKQVOR 181
 DB 122 EKVPINLWIDGKQNTVPLETVTKNKNVTVOELDLQARRYLQEKYLNYSNDSVDFGKQVOR 181
 QY 182 GLIVFHSSEGSTSVSYDLFDAQGQYPTLLRIYRDNTTISSTLSLSLYLYTT 233
 DB 182 GLIVFHTSTEPSVNYDLFGAGQGYNTLLRIYRDNTKINSENHIDIVLYTS 233
 RESULT 34
 ABU10099
 ID ABU10099 standard; protein; 233 AA.
 XX AC ABU10099;
 XX
 XX 11-AUG-2003 (first entry)
 XX Staphylococcus enterotoxin A K14E substitution mutant.
 XX Enterotoxin A; superantigen-associated bacterial infection; mutant;
 XX superantigen toxin; vaccine; mutein.
 XX Staphylococcus sp.
 XX Synthetic.
 XX Key Location/Qualifiers
 XX FT Misc-difference 14 /note= "Wild-type Lys substituted by Glu"

XX PN US2003009015-A1.
 XX PD 09-JAN-2003.
 XX PF 25-JUN-1997; 97US-00882431.
 XX PR 25-JUN-1997; 97US-00882431.
 XX PA (ULRI/) ULRICH R G.
 XX PA (OLSO/) OLSON M A.
 XX PA (BAVA/) BAVARI S.
 XX PI Ulrich RG, Olson MA, Bavari S;
 XX DR WPI; 2003-401542/38.
 XX XX New superantigen toxin and/or DNA fragment with an altered binding of the
 PT encoded altered toxin to either MHC class II or T cell antigen receptor,
 PT useful for treating or ameliorating superantigen-associated bacterial
 PT infection.
 XX PS Example 7; Page; 50pp; English.
 XX CC The invention relates to an isolated and purified superantigen toxin
 CC and/or DNA fragment, which has been altered so that the binding of the
 CC encoded toxin to either major histocompatibility complex (MHC) class II
 CC or T cell antigen receptor is altered. The superantigen toxins, DNA
 CC fragments, and vaccines are useful for treating or ameliorating
 CC superantigen-associated bacterial infection. The DNA fragments are
 CC particularly useful for producing vaccine against superantigen toxin
 CC infections. The transformed host cells are useful for analyzing the
 CC effectiveness of drugs and agents that affect the binding of
 CC superantigens to MHC class II or T-cell antigen receptors. The present
 CC sequence represents the amino acid sequence of the staphylococcus
 CC enterotoxin A K14E mutant. Note: The present sequence is not present in
 CC the specification but was created by the indexer from the wild-type
 CC staphylococcus enterotoxin A sequence (see ACA61178)
 XX SQ Sequence 233 AA;
 Query Match 75.3%; Score 917; DB 6; Length 233;
 Best Local Similarity 74.6%; Pred. No. 2.3e-84;
 Matches 173; Conservative 22; Mismatches 37; Indels 0; Gaps 0;
 QY 2 EKSEINEKDLRKSELOGTALGNLQIYYNKAITSSEKSAOPLNTLLFKGFTGH 61
 DB 2 EKSEINEKDLRKSELOGTALGNLQIYYNKAITSSEKSHDQFRQHTILFKGFTDH 61
 QY 62 PWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
 DB 62 SWYNDLLVRFDSKDIDVYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
 QY 122 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKQV 181
 DB 122 EKKVPINLWIDGKQNTVPLETVKTKNKNVTVOELDLQARRYLOEKYLNYSNDSVDFGKQV 181
 QY 182 GLIVFHSSEGSTVSVDLPDAQOQYPTDLLRIYRDNNTTSSLSLSLYLTT 233
 DB 182 GLIVFHTSTEPSVNYDLFGAQOQYNTLLRIYRDNKNINSENHMDIYLYTS 233
 RESULT 35
 ID ABU10098
 XX AC ABU10098;
 XX DT 11-AUG-2003 (first entry)
 XX DE Staphylococcus enterotoxin A Y64A substitution mutant.
 XX KW Enterotoxin A; superantigen-associated bacterial infection; mutant;

superantigen toxin; vaccine; mutein.
 OS Staphylococcus sp.
 OS Synthetic.
 XX Key Location/Qualifiers
 FT Misc-difference 64 /note= "Wild-type Tyr substituted by Ala"
 FT US2003009015-A1.
 XX 09-JAN-2003.
 XX 25-JUN-1997; 97US-00882431.
 XX 25-JUN-1997; 97US-00882431.
 XX (ULRI/) ULRICH R G.
 XX (OLSO/) OLSON M A.
 XX (BAVA/) BAVARI S.
 XX Ulrich RG, Olson MA, Bavari S;
 XX WPI; 2003-401542/38.
 XX New superantigen toxin and/or DNA fragment with an altered binding of the
 PT encoded altered toxin to either MHC class II or T cell antigen receptor,
 PT useful for treating or ameliorating superantigen-associated bacterial
 PT infection.
 XX PS Example 7; Page; 50pp; English.
 XX CC The invention relates to an isolated and purified superantigen toxin
 CC and/or DNA fragment, which has been altered so that the binding of the
 CC encoded toxin to either major histocompatibility complex (MHC) class II
 CC or T cell antigen receptor is altered. The superantigen toxins, DNA
 CC fragments, and vaccines are useful for treating or ameliorating
 CC superantigen-associated bacterial infection. The DNA fragments are
 CC particularly useful for producing vaccine against superantigen toxin
 CC infections. The transformed host cells are useful for analysing the
 CC effectiveness of drugs and agents that affect the binding of
 CC superantigens to MHC class II or T-cell antigen receptors. The present
 CC sequence represents the amino acid sequence of the staphylococcus
 CC enterotoxin A Y64A mutant. Note: The present sequence is not present in
 CC the specification but was created by the indexer from the wild-type
 CC staphylococcus enterotoxin A sequence (see ACA61178)
 XX SQ Sequence 233 AA;
 Query Match 74.9%; Score 912; DB 6; Length 233;
 Best Local Similarity 74.6%; Pred. No. 7.5e-84;
 Matches 173; Conservative 21; Mismatches 38; Indels 0; Gaps 0;
 QY 2 EKSEINEKDLRKSELOGTALGNLQIYYNKAITSSEKSAOPLNTLLFKGFTGH 61
 DB 2 EKSEINEKDLRKSELOGTALGNLQIYYNKAITSSEKSHDQFRQHTILFKGFTDH 61
 QY 62 PWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
 DB 62 SWYNDLLVRFDSKDIDVYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
 QY 122 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKQV 181
 DB 122 EKKVPINLWIDGKQNTVPLETVKTKNKNVTVOELDLQARRYLOEKYLNYSNDSVDFGKQV 181
 QY 182 GLIVFHSSEGSTVSVDLPDAQOQYPTDLLRIYRDNNTTSSLSLSLYLTT 233
 DB 182 GLIVFHTSTEPSVNYDLFGAQOQYNTLLRIYRDNKNINSENHMDIYLYTS 233
 RESULT 36
 ID AAY70102
 ID AAY70102 standard; protein; 257 AA.

XX AAY70102;
 AC Superantigen toxin; SAG; Staphylococcal enterotoxin A; SEA; cytostatic;
 XX antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;
 XX antibody; toxoid; staphylococcal/streptococcal toxin; diagnosis;
 XX treatment; superantigen-associated bacterial infection.
 XX Staphylococcus sp.
 XX
 XX Key Location/Qualifiers
 XX Peptide 2..25
 XX /label= Leader peptide
 XX Protein 26..253
 XX /label= Mature Staphylococcal enterotoxin A
 XX /note= "Includes transcription start site residue, Met-"
 XX Misc-difference 42
 XX /note= "Encoded by TTG"
 XX Misc-difference 125
 XX /note= "Encoded by CCA"
 XX
 XX WO200009154-A1.
 XX -24-FEB-2000.
 XX 13-AUG-1998; 98WO-US016766.
 XX 13-AUG-1998; 98WO-US016766.
 XX (REED-) REED ARMY INST RES WALTER.
 XX Ulrich RG, Olson MA, Bavari S;
 XX WPI; 2000-224177/19.
 XX N-PSDB; AA251105.
 XX Nucleic acid encoding superantigen toxin useful as a vaccine and for
 XX diagnosis of superantigen-associated bacterial infections.
 XX Claim 7; Page 72-73; 118pp; English.
 XX
 XX The present amino acid sequence is the Staphylococcal enterotoxin A
 XX (SEA), a bacterial superantigen toxin (SAG). The coding region of the SAG
 XX toxin when altered by site directed mutagenesis, results in disruption of
 XX binding of the toxin to both the MHC class II or T-cell antigen receptor.
 XX SEA has antibacterial and cytostatic activity. This sequence is useful
 XX for the production of SEA vaccines and specific antibodies. This vaccine
 XX overcomes the disadvantages of the chemically inactivated toxins and is
 XX designed to protect individuals against one or several related
 XX staphylococcal and streptococcal toxins. It is used for the diagnosis and
 XX treatment or amelioration of superantigen-associated bacterial
 XX infections
 XX Sequence 257 AA;
 Query Match 74.5%; Score 908; DB 3; Length 257;
 Best Local Similarity 74.2%; Pred. No. 2.2e-83;
 Matches 173; Conservative 21; Mismatches 39; Indels 0; Gaps 0;
 QY 1 SEKSEINKEKLPKKGELGKALGNLQIYYNKAITSSEKSAQFLNTLLPKGFTG 60
 DB 25 SEKSEINKEKLPKKGELGKALGNLQIYYNKAITSSEKSHQFROHTILFKGFTD 84
 QY 61 HPWYNLLVDLGSTAAISYEGSSVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNRILT 120
 DB 85 HSWYNLLVRFDSKDIVDKYGGKVDLYGAYAGYQCAGTGNKTKACMYGGVTLHDNRILT 144
 QY 121 EEKKVPINLWLDGKONTVPLETVKTKKQNVTVQELDLQARRYLQEKYNYNSDVFGRKQV 180

DB 145 EEKKVPINLWLDGKONTVPLETVKTKKQNVTVQELDLQARRYLQEKYNYNSDVFGRKQV 204
 QY 181 RGLIVFHSSEGSVSYDLDPDAQOQYPTLLRIYRDNTTISSTLSISLYLTT 233
 DB 205 RGLIVFHTSTEPSVNYDLFQAQOQYNTLLRIYRDNTKNTINSENWHIDVLYTS 257
 RESULT 37
 AAY70103
 ID AAY70103 standard; protein; 233 AA.
 XX AAY70103;
 AC AAY70103;
 XX
 XX 05-JUN-2000 (first entry)
 XX Mutant Staphylococcal enterotoxin A for vaccine A489270P.
 XX Superantigen toxin; SAG; Staphylococcal enterotoxin A; SEA; cytostatic;
 XX antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;
 XX antibody; toxoid; staphylococcal/streptococcal toxin; diagnosis; mutant;
 XX treatment; superantigen-associated bacterial infection; A489270P.
 XX Staphylococcus sp.
 XX
 XX Key Location/Qualifiers
 XX Protein 1..233
 XX /label= Mature Staphylococcal enterotoxin_A
 XX /note= "Mutant sequence without the leader peptide"
 XX Misc-difference 2
 XX /note= "Encoded by AG"
 XX Misc-difference 18
 XX /note= "Encoded by TTG"
 XX Misc-difference 48
 XX /note= "Wild type Leu substituted with Arg"
 XX Misc-difference 70
 XX /note= "Wild type Asp substituted with Arg"
 XX Misc-difference 92
 XX /note= "Wild type Tyr substituted with Ala"
 XX Misc-difference 157
 XX /note= "Encoded by CTT"
 XX Misc-difference 180
 XX /note= "Encoded by CAG"
 XX
 XX WO200009154-A1.
 XX 24-FEB-2000.
 XX 13-AUG-1998; 98WO-US016766.
 XX 13-AUG-1998; 98WO-US016766.
 XX (REED-) REED ARMY INST RES WALTER.
 XX Ulrich RG, Olson MA, Bavari S;
 XX WPI; 2000-224177/19.
 XX N-PSDB; AA251106.
 XX Nucleic acid encoding superantigen toxin useful as a vaccine and for
 XX diagnosis of superantigen-associated bacterial infections.
 XX Claim 8; Page 74-76; 118pp; English.
 XX
 XX The present amino acid sequence is the mutant Staphylococcal enterotoxin
 XX A (SEA), a bacterial superantigen toxin (SAG), used for the formulation
 XX of SEA vaccine A489270P. The coding region of this SAG toxin is altered
 XX by site directed mutagenesis, that results in disruption of binding of
 XX the toxin to both the MHC class II or T-cell antigen receptor. This
 XX altered SAG toxin has the leader peptide cleaved by native bacterial
 XX enzymatic mechanism and the first residue of the mature protein is
 XX encoded by the transcriptional start site (ATG). SEA has antibacterial
 XX and cytostatic activity. This sequence is useful for the production of
 XX SEA vaccines and specific antibodies. This vaccine overcomes the

disadvantages of the chemically inactivated toxoids and is designed to protect individuals against one or several related staphylococcal and streptococcal toxins. It is used for the diagnosis and treatment or amelioration of superantigen-associated bacterial infections

Query Match 74.1%; Score 903; DB 3; Length 233;
Best Local Similarity 73.7%; Pred. No. 6.1e-83;
Matches 171; Conservative 21; Mismatches 40; Indels 0; Gaps 0;

2 EKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSAQOFLTNLLFKGPTCH 61
2 EKSEINEKDLRKSEKOGTALGNLKOIYYNEKAKTENKESHQOFRQHILFKGPTDH 61
62 PWNDDLVLGSLTAATSEYEGSSVDLYGAYGYOCAGTGNKTCMYGGVTLHDNNELTE 121
62 SWNDDLVRPDSKDINDYKGGKVDLYGAYGYOCAGTGNKTCMYGGVTLHDNNELTE 121
122 EKKVPINLWIDGKOTTPIDKVKTSKEVTVEQLDQARHLYHKGFLYNSDSFGGKQVR 181
122 EKKVPINLWIDGKONTVPLETKNKXNTVQELDKQARRYLOKYNLYNSDVFQGVKVAR 181
182 GLIVFHSSEGTSTVSDYLDFAQOQYPTLLRIYRDNNTTSISLSISLYLVT 233
182 GLIVFHSSTEPSVNYDLFGAGQYNSNLLRIYRDNNTINSNENMHIDILYLS 233

RESULT 38
ABU79071
ID ABU79071 standard; protein; 258 AA.
XX ABU79071;
AC ABU79071;
XX
DT 18-JUN-2003 (first entry)
XX
DE S. aureus SED (staphylococcus enterotoxin D) protein.
XX
KW Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis;
KW gene therapy; mammalian cell receptor; tumour associated lipid; anergy;
KW T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;
KW APC; antitumour.
XX
OS Staphylococcus aureus.
XX
PN US2002177551-A1.
XX
XX 28-NOV-2002.
XX
XX 30-MAY-2001; 2001US-00870759.
XX
XX 31-MAY-2000; 2000US-0208129P.
XX
XX (TERM/) Terman D S.
XX
XX Terman DS;
XX
XX WPI; 2003-361759/34.
XX
XX N-PSDB; ACA64697.
XX
XX A mammalian cell receptor, useful in the treatment of cancer by binding
XX to tumor associated lipids where the binding induces anergy or apoptosis
XX in T cells and antigen presenting cells.
XX
XX Disclosure; Page; 167pp; English.
XX
XX The invention relates to a mammalian cell receptor, useful in the
XX treatment of cancer, which binds to tumour associated lipids and induces
XX anergy or apoptosis in the T cells and antigen presenting cells (APCs).
XX Also included are a mammalian cell useful in the treatment of cancer
XX where the receptor which binds tumour associated lipids and induces
XX cellular inactivation or death is deleted or functionally deactivated,
XX producing (M1) a tumouricidal immunocyte population in vivo in a mammal

(by allowing tumour associated lipids to contact immunocytes in which receptors for immunosuppressive fatty acids, ceramides, glycolipids, sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides, sialylated glycans, lipopeptides and proteoglycolipids are inactivated or deleted), a construct useful in the treatment of cancer comprising a cell superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell useful in the treatment of cancer (where an adaptor protein which inhibits T cell activation by tumour associated antigens is deleted or functionally deactivated), a composition useful in the treatment of cancer (comprising a lipid raft conjugated to a superantigen), producing (M2) a tumouricidal immunocyte population ex vivo in a mammal (by allowing tumour associated lipids to contact immunocytes, in which receptors for the lipids are inactivated or deleted to produce a tumouricidal immunocyte population, and administering the tumouricidal T cell population ex vivo in a mammal) by allowing a tumour associated lipids to contact T cells, in which adaptor proteins, which inhibit T cell activation by tumour associated antigens, are deleted or functionally deactivated to produce a tumouricidal population of T cells, and administering the tumouricidal activated T cells to the host, or allowing a superantigen-lipid raft to contact T cells ex vivo, and administering the tumouricidal activated T cells to the host), treating (M5) cancer in a mammal (by administering a lipid binding molecule which binds immunosuppressive tumour associated lipids in vivo), producing (M6) a tumouricidal T cell population in vivo in a mammal (by allowing a tumour associated antigen to contact immunocytes in which adaptor proteins which inhibit T cell activation by tumour associated antigens are deleted or functionally deactivated) and producing (M7) a tumouricidal T cell population ex vivo in a mammal comprising allowing a superantigen-lipid raft conjugate to contact immunocytes in vivo. The receptors, methods and compositions are useful for treating cancers and tumours. Bacterial superantigens are co-administered or administered as fusion constructs with anti-tumour proteins or motifs. The present sequence represents a bacterial superantigen protein (e.g. a staphylococcal enterotoxin). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from the US patent office website at "seqdata.uspto.gov/sequence.html?docid=20020177551"

XX
XX
XX Sequence 258 AA;

Query Match 50.2%; Score 611; DB 6; Length 258;
Best Local Similarity 51.1%; Pred. No. 2.9e-53;
Matches 118; Conservative 35; Mismatches 78; Indels 0; Gaps 0;

1 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSAQOFLTNLLFKGPTG 60
26 NENIDSVKEKELHKKSELSTALNNKHSYADKNPIIGENKSTGQOFLNTLLYKFFTD 85
61 HPWYNDLLVDLSTATSEYEGSSVDLYGAYGYOCAGTGNKTCMYGGVTLHDNNRLT 120
86 LINFEDLLINFSNKEMACHFKSKNDVYPIRYSINCYGGEIDRTACTYGGVTPHEGNK 145
121 EKKVPINLWIDGKOTTPIDKVKTSKEVTVEQLDQARHLYHKGFLYNSDSFGGKQV 180
146 EKKVPINLWINGVQKESLDKVKQTDKNVTVEQLDQARRYLOKYNLYNSDVFQGVK 205
181 RGLIVFHSSEGTSTVSDYLDFAQOQYPTLLRIYRDNNTTSISLSISLYL 231
206 RGKIEFSDSGSKVSDYLDVKGDFPEKQLRIYSNKNLSTLHLLHIDYLY 256

RESULT 39
AAR45013
ID AAR45013 standard; protein; 228 AA.
XX
XX AAR45013;
XX
XX 25-MAR-2003 (revised)

DT 08-JUN-1994 (first entry)
 XX Staphylococcal enterotoxin SED.
 DE Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
 XX autoimmune disease; toxicity; Protein A; perfusion system.
 KW Staphylococcus aureus.
 XX WO9324136-A1.
 XX 09-DEC-1993.
 PD 01-JUN-1993; 93WO-US005213.
 XX 01-JUN-1992; 92US-00891718.
 XX (TERM/) Terman D S.
 PA (STON/) STONE J L.
 XX Terman DS, Stone JL;
 XX WPI; 1993-405418/50.
 XX Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
 PT in a patient or for the treatment of auto-immune diseases.
 XX Disclosure; Fig 1; 90pp; English.
 PS The sequences given in ARA45011-21 are Staphylococcal enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer in
 CC a patient. These SEs, and homologues of them, can be used as tumouricidal
 CC agents for treating cancers and autoimmune disease. They exhibit
 CC tumouricidal activity and toxicity identical to that observed for the
 CC Protein A perfusion system. They may be administered by i.v. injection.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 228 AA;
 SQ

Query Match 49.7%; Score 605; DB 2; Length 228;
 Best Local Similarity 52.0%; Pred. No. 9.9e-53;
 Matches 117; Conservative 33; Mismatches 75; Indels 0; Gaps 0;

QY 7 INEKDLRKSELOGTALGNLKOIYYNNSKAITSSSEKSDQFLNTLLPKGFTGHPWYND 66
 Db 2 VKEKELHKKSELSSTALNNKHSYADKNPIIGENKSTGQDFLENTLLYKKFFTDLINFED 61

QY 67 LLYDLGSTAATSEYEGSSVDLYGAYYGCAGGTPNKTACMYGVTLHDNNRLTEKKVP 126
 Db 62 LLINFNSEKMAQHFKNKVDVPIRYSINCYGGEIDRTACTYGGVTPHEGNKLERKKIP 121

QY 127 INLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQGLIVF 186
 Db 122 INLWINGVQKEVSLDKVQTDKNVTYQELDAQARYLQKDLKLYNNDTLGGKIQGKIEF 181

QY 187 HSSEGSTSVSDLPDAQQYDPDILLRIYRDNNTTSSLSLSLYLY 231
 Db 182 DSSDGSKVSVDLPDVKGDFPEKQLRIYSDNKTLSLHLDIYLY 226

RESULT 40
 AAB67340
 ID AAB67340 standard; peptide; 228 AA.
 XX AAB67340;
 AC AAB67340;
 XX 23-APR-2001 (first entry)
 DT Staphylococcus aureus enterotoxin D protein.
 DE Tumour; cancer; immune; enterotoxin.
 KW Staphylococcus aureus.
 XX

XX US6180097-B1.
 PN 30-JAN-2001.
 PD 30-OCT-1998; 98US-00183437.
 XX 03-OCT-1989; 89US-00416530.
 PR 17-JAN-1990; 90US-00466577.
 PR 17-JAN-1991; 91WO-USC00342.
 PR 01-JUN-1992; 92US-00891718.
 PR 02-MAR-1993; 93US-00025144.
 PR 31-JAN-1994; 94US-00189424.
 PR 19-JUN-1995; 95US-00491746.
 XX (TERM/) Terman D S.
 XX Terman DS;
 XX WPI; 2001-158657/16.
 DR Tumor cell capable of stimulating antitumor immune reactivity in vitro or
 PT in vivo comprises exogenous nucleic acids encoding a superantigen and a
 PT costimulatory molecule.
 PT Disclosure; Fig 2; 16pp; English.
 XX The present invention relates to a tumour cell capable of stimulating
 CC antitumor immune reactivity in vitro or in vivo contains and expresses an
 CC exogenous nucleic acid molecule encoding a superantigen or its active
 CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
 CC molecule that activates T cells in conjunction with an antigenic
 CC stimulus. The invention may be used for cancer therapy by stimulating an
 CC anticancer immune response in vivo or ex vivo
 XX Sequence 228 AA;
 SQ

Query Match 49.7%; Score 605; DB 4; Length 228;
 Best Local Similarity 52.0%; Pred. No. 9.9e-53;
 Matches 117; Conservative 33; Mismatches 75; Indels 0; Gaps 0;

QY 7 INEKDLRKSELOGTALGNLKOIYYNNSKAITSSSEKSDQFLNTLLPKGFTGHPWYND 66
 Db 2 VKEKELHKKSELSSTALNNKHSYADKNPIIGENKSTGQDFLENTLLYKKFFTDLINFED 61

QY 67 LLYDLGSTAATSEYEGSSVDLYGAYYGCAGGTPNKTACMYGVTLHDNNRLTEKKVP 126
 Db 62 LLINFNSEKMAQHFKNKVDVPIRYSINCYGGEIDRTACTYGGVTPHEGNKLERKKIP 121

QY 127 INLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQGLIVF 186
 Db 122 INLWINGVQKEVSLDKVQTDKNVTYQELDAQARYLQKDLKLYNNDTLGGKIQGKIEF 181

QY 187 HSSEGSTSVSDLPDAQQYDPDILLRIYRDNNTTSSLSLSLYLY 231
 Db 182 DSSDGSKVSVDLPDVKGDFPEKQLRIYSDNKTLSLHLDIYLY 226

RESULT 41
 ABB76236
 ID ABB76236 standard; protein; 228 AA.
 XX ABB76236;
 AC ABB76236;
 XX 09-AUG-2002 (first entry)
 DT Staphylococcus aureus enterotoxin D.
 DE Enterotoxin D; SED; superantigen; antigen; tumour; cancer; antitumour;
 XX therapy.
 KW Staphylococcus aureus.
 XX

RESULT 42
AAR13205
ID AAR1
XX
AC AAR1

PD 09-JAN-2003.
 XX 25-JUN-1997; 97US-00882431.
 XX 25-JUN-1997; 97US-00882431.
 XX (ULRI/) ULRICH R G.
 PA (OLSO/) OLSON M A.
 PA (BAVA/) BAVARI S.
 XX Ulrich RG, Olson MA, Bavari S;
 PI WPI; 2003-401542/38.
 DR New superantigen toxin and/or DNA fragment with an altered binding of the
 XX encoded altered toxin to either MHC class II or T cell antigen receptor,
 PT useful for treating or ameliorating superantigen-associated bacterial
 PT infection.
 XX Example 1; Page 36; 50pp; English.
 PS The invention relates to an isolated and purified superantigen toxin
 CC and/or DNA fragment, which has been altered so that the binding of the
 CC encoded toxin to either major histocompatibility complex (MHC) class II
 CC or T cell antigen receptor is altered. The superantigen toxins, DNA
 CC fragments, and vaccines are useful for treating or ameliorating
 CC superantigen-associated bacterial infection. The DNA fragments are
 CC particularly useful for producing vaccine against superantigen toxin
 CC infections. The transformed host cells are useful for analysing the
 CC effectiveness of drugs and agents that affect the binding of
 CC superantigens to MHC class II or T-cell antigen receptors. The present
 CC sequence represents the amino acid sequence of the bacterial superantigen
 CC toxin SEE
 XX Sequence 82 AA;
 SQ
 Query Match 33.3%; Score 406; DB 6; Length 82;
 Best Local Similarity 89.0%; Pred. No. 3.4e-33;
 Matches 73; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 QY 43 SADQFLNTLLFKGFTGHPWYNDLLVLDLGSSTAATSEYEGSSVDLYGAYGYQCAGGTPN 102
 Db 1 SDDQFLENTLLFKGFTGHPWYNDLLVLDLGSKDATNKYKGVLDLYGAYGYQCAGGTPN 60
 QY 103 KTACMYGGVTLHDNNRLTEKK 124
 Db 61 KTACMYGGVTLHDNNRLTEKK 82
 RESULT 46
 ABU62338
 ID ABU62338 standard; protein; 82 AA.
 XX
 AC ABU62338;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE S. aureus enterotoxin E, SEE, MHC binding region.
 XX
 KW SEE; staphylococcal enterotoxin E; vaccine; superantigen toxin; MHC;
 KW superantigen-associated bacterial infection; bacterial infection;
 KW antibacterial.
 XX
 OS Staphylococcus aureus.
 XX
 FT US2003036644-A1.
 PN
 XX 20-FEB-2003.
 XX
 PD 26-NOV-2001; 2001US-00002784.
 PF
 XX 25-JUN-1997; 97US-00882431.
 PR 01-SEP-1998; 98US-00144776.
 PR

XX (ULRI/) ULRICH R G.
 XX Ulrich RG;
 PI WPI; 2003-492125/46.
 DR New superantigen toxin DNA fragment, useful for preparing a composition
 PT for treating or preventing bacterial infection.
 PT
 XX Disclosure; Fig 3; 68pp; English.
 PS
 XX The invention relates to an isolated and purified superantigen toxin DNA
 CC fragment is altered so that binding of the encoded altered toxin to
 CC either the MHC class II or T cell antigen receptor is altered. Also
 CC included are a recombinant DNA construct (comprising a vector and an
 CC isolated and purified altered superantigen toxin DNA fragment), a host
 CC cell transformed with the recombinant DNA construct, producing altered
 CC superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
 CC superantigen toxin peptide, diagnosing superantigen-associated bacterial
 CC infection, a vaccine (comprising an altered superantigen toxin for
 CC producing antigenic and immunogenic response resulting in the protection
 CC of a mammal against superantigen-associated bacterial infection),
 CC treating/ameliorating a superantigen-associated bacterial infection, an
 CC antiserum isolated from individuals immunised with one or more altered
 CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-
 CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
 CC SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and
 CC SEBb). The superantigen toxin DNA fragment is useful for preparing a
 CC composition for treating or preventing bacterial infection. The present
 CC sequence represents the S. aureus enterotoxin E, SEE, MHC binding region
 XX
 XX Sequence 82 AA;
 SQ
 Query Match 33.3%; Score 406; DB 7; Length 82;
 Best Local Similarity 89.0%; Pred. No. 3.4e-33;
 Matches 73; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
 QY 43 SADQFLNTLLFKGFTGHPWYNDLLVLDLGSSTAATSEYEGSSVDLYGAYGYQCAGGTPN 102
 Db 1 SDDQFLENTLLFKGFTGHPWYNDLLVLDLGSKDATNKYKGVLDLYGAYGYQCAGGTPN 60
 QY 103 KTACMYGGVTLHDNNRLTEKK 124
 Db 61 KTACMYGGVTLHDNNRLTEKK 82
 RESULT 47
 AAW24299
 ID AAW24299 standard; protein; 91 AA.
 XX
 AC AAW24299;
 XX
 DT 14-APR-1998 (first entry)
 XX
 DE Staphylococcus aureus Gene #5 polypeptide sequence 2.
 XX
 KW Staphylococcus aureus WCUH 29; antagonist; antibacterial; immunogen;
 KW vaccine; disease; protection; isolation.
 XX
 OS Staphylococcus aureus.
 XX
 FT Key Location/Qualifiers
 FT Misc-difference 29 /note= "Unspecified amino acid"
 XX
 PN WO9731114-A2.
 XX
 PD 28-AUG-1997.
 XX
 PF 25-FEB-1997; 97WO-GB0000524.
 XX
 PR 26-FEB-1996; 96GB-00004045.
 PR

XX (SMIK) SMITHKLINE BEECHAM PLC.
 PA Burnham MKR, Hodgson JE;
 PI WPI; 1997-435166/40.
 XX N-PSDB; AA01865.
 XX New Staphylococcus aureus polynucleotide and polypeptide(s) - for
 PT isolating antagonist of the polypeptide(s) useful as anti-bacterials.
 XX Claim 11; Page 33; 117pp; English.
 XX The present sequence represents a novel polypeptide, which is optionally
 CC expressed in NCIMB 40771. The polypeptide, and polynucleotide encoding
 CC it, are derived from Staphylococcus aureus. Cells expressing ligands
 CC binding the polypeptide can be used to isolated candidate compounds that
 CC bind and inhibit the activity of the polypeptide. Such compounds can be
 CC used as anti-bacterial compounds. The polypeptide may also be used as an
 CC immunogen to vaccinate an animal for protection against Staphylococcus
 CC aureus caused disease
 XX Sequence 91 AA;
 SQ Query Match 30.4%; Score 370; DB 2; Length 91;
 Best Local Similarity 76.9%; Pred. No. 1.8e-29;
 Matches 70; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
 QY 107 MYGGVTLHDNNRLTEKKVPIINLWIDGKOTTVPIDKVTSKEVTVQELDLQARHYLHGK 166
 DB 1 MYGGVTLHDNNRLTEKKVPIINLWIDGKXNTVPLETVTKNKQNTVQELDLQARRYLOEK 60
 QY 167 FGLYNSDSFGCKVQKORGLIVFHSSEGSTVSVD 197
 DB 61 YNLNSDVFQKQVQKORGLIVFHTSTEPSVNYD 91
 RESULT 48
 ABU10089
 ID ABU10089 standard; protein; 82 AA.
 AC ABU10089;
 XX 11-AUG-2003 (first entry)
 DT Bacterial superantigen toxin SEA.
 DE Superantigen-associated bacterial infection; superantigen toxin; vaccine;
 KW SEA.
 OS Unidentified.
 XX US2003009015-A1.
 PN 09-JAN-2003.
 PD 25-JUN-1997; 97US-00882431.
 PF 25-JUN-1997; 97US-00882431.
 XX (ULRI/) ULRICH R G.
 PA (OLSO/) OLSON M A.
 PA (BAVA/) BAVARI S.
 XX Ulrich RG, Olson MA, Bavari S;
 PI WPI; 2003-401542/38.
 XX New superantigen toxin and/or DNA fragment with an altered binding of the
 PT encoded altered toxin to either MHC class II or T cell antigen receptor,
 PT useful for treating or ameliorating superantigen-associated bacterial
 PT infection.

PS Example 1; Page 35; 50pp; English.
 XX The invention relates to an isolated and purified superantigen toxin
 CC and/or DNA fragment, which has been altered so that the binding of the
 CC encoded toxin to either major histocompatibility complex (MHC) class II
 CC or T cell antigen receptor is altered. The superantigen toxins, DNA
 CC fragments, and vaccines are useful for treating or ameliorating
 CC superantigen-associated bacterial infection. The DNA fragments are
 CC particularly useful for producing vaccine against superantigen toxin
 CC infections. The transformed host cells are useful for analysing the
 CC effectiveness of drugs and agents that affect the binding of
 CC superantigens to MHC class II or T-cell antigen receptors. The present
 CC sequence represents the amino acid sequence of the bacterial superantigen
 CC toxin SEA
 XX Sequence 82 AA;
 SQ Query Match 29.7%; Score 362; DB 6; Length 82;
 Best Local Similarity 79.3%; Pred. No. 9.9e-29;
 Matches 65; Conservative 4; Mismatches 13; Indels 0; Gaps 0;
 QY 43 SAQOFLNTLLFKGFFTGHEWYNDLLVDLGGSTAATSEYEGSSVDLYGAYGYOCAGGTPN 102
 DB 1 SHQOFLQHTILFKGFFFDHSWYNDLLVDFDSKDIDVKYKGVLDLYGAYGYOCAGGTPN 60
 QY 103 KTACMYGGVTLHDNNRLTEKK 124
 DB 61 KTACMYGGVTLHDNNRLTEKK 82
 RESULT 49
 ABU62336
 ID ABU62336 standard; protein; 82 AA.
 AC ABU62336;
 XX 27-AUG-2003 (first entry)
 DT S. aureus enterotoxin A, SEA, MHC binding region.
 DE SEA; staphylococcal enterotoxin A; vaccine; superantigen toxin; MHC;
 KW superantigen-associated bacterial infection; bacterial infection;
 KW antibacterial.
 OS Staphylococcus aureus.
 XX US2003036644-A1.
 PN 20-FEB-2003.
 PD 26-NOV-2001; 2001US-00002784.
 PF 25-JUN-1997; 97US-00882431.
 PR 01-SEP-1998; 98US-00144776.
 XX (ULRI/) ULRICH R G.
 PA Ulrich RG;
 PI WPI; 2003-492125/46.
 DR New superantigen toxin DNA fragment, useful for preparing a composition
 PT for treating or preventing bacterial infection.
 XX Disclosure; Fig 3; 68pp; English.
 PS The invention relates to an isolated and purified superantigen toxin DNA
 CC fragment is altered so that binding of the encoded altered toxin to
 CC either the MHC class II or T cell antigen receptor is altered. Also
 CC included are a recombinant DNA construct (comprising a vector and an
 CC isolated and purified altered superantigen toxin DNA fragment), a host
 CC cell transformed with the recombinant DNA construct, producing altered
 CC superantigen toxin, an altered TSS1-1 (toxic shock syndrome toxin)

CC superantigen toxin peptide, diagnosing superantigen-associated bacterial
 CC infection, a vaccine (comprising an altered superantigen toxin for
 CC producing antigenic and immunogenic response resulting in the protection
 CC of a mammal against superantigen-associated bacterial infection),
 CC treating/ameliorating a superantigen-associated bacterial infection, an
 CC antisera isolated from individuals immunised with one or more altered
 CC TSS-1 superantigen toxin and an antibody which recognises altered TSS-
 CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
 CC SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and
 CC SPEb). The superantigen toxin DNA fragment is useful for preparing a
 CC composition for treating or preventing bacterial infection. The present
 CC sequence represents the *S. aureus* enterotoxin A, SEA, MHC binding region
 XX
 XX Sequence 82 AA;

Query Match 29.7%; Score 362; DB 7; Length 82;
 Best Local Similarity 79.3%; Pred. No. 9.9e-29;
 Matches 65; Conservative 4; Mismatches 13; Indels 0; Gaps 0;
 QY 43 SADQFLNTLFGKFFGTHPWYNDLLVDLGSTAASTSEYEGSSVDLYGAYGYQCAGGTPN 102
 Db 1 SHDQFLQHTILFGKFFGTHPWYNDLLVDLDFDSKDIDVKYKGVYGYQCAGGTPN 60
 QY 103 KTACMYGGVTLHDNNRLTEKK 124
 Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 50
 ABP58460
 ID ABP58460 standard; protein; 217 AA.

XX AC ABP58460;
 XX DT 14-APR-2003 (first entry)
 XX DE Staphylococcal enterotoxin H.
 XX KW Superantigen; staphylococcal enterotoxin H; antibody; cancer; tumour;
 XX KW cytostatic; vaccine.
 XX OS Staphylococcus sp.
 XX DN WO2003002143-A1.
 XX PD 09-JAN-2003.
 XX PF 19-JUN-2002; 2002WO-SE001188.
 XX PR 28-JUN-2001; 2001SE-00002327.
 XX PA (ACTI-) ACTIVE BIOTECH AB.
 XX PI Forsberg G, Erlandsson E, Antonsson P, Walse B;
 XX WPI; 2003-201467/19.

XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
 PT receptor and four regions to determine binding to class II major
 PT histocompatibility complex, antibody to cancer associated cell surface
 PT structure.

XX Example 3; Fig 3; 102pp; English.

XX The present sequence is the protein sequence of staphylococcal
 CC enterotoxin D (SED). The invention provides novel conjugates (see
 CC ABP58454) for human cancer therapy. These comprise an engineered
 CC bacterial superantigen, such as novel SEA/E-120 (see ABP58455), and an
 CC antibody moiety, such as tumour reactive antibody 5T4. Bacterial
 CC enterotoxins such as SEA, SEB, SED and SEH were used in the molecular
 CC modelling of the engineered superantigens. The superantigens were
 CC engineered to reduce seroreactivity whilst maintaining biological
 CC activity and production levels. The novel conjugates were designed to

CC target and destroy cancer cells, including cancer of the lung, breast,
 CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
 XX
 SQ ~Sequence 217 AA;
 Query Match 25.3%; Score 308; DB 6; Length 217;
 Best Local Similarity 33.9%; Pred. No. 1.2e-22;
 Matches 76; Conservative 46; Mismatches 90; Indels 12; Gaps 7;
 QY 10 KDLRKSELOGTALGNLKGIIYNNKATSSSEKSDAQFLNTLLPKGFTGHPWYNDLLV 69
 Db 1 EDLHKSEITDLALAN--AYGQNHFPFKENTKSDSEIGEKDLIFRN--QGDSG-NDLRV 55
 QY 70 DLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINL 129
 Db 56 KATADLAOKFNKQVNDIYGASFYKCEKISENISECIYGGTLL-NSEKLAERVIGANV 114
 QY 130 WIDGKQTTVPIDKVKTSKEVTQBELDLQARHLYHGKFLYNSDSFGGKQVQRLIVFHSS 189
 Db 115 WVDGIQKETEL--IRTNKGNVTQLDIDKIRKILSDKYKIYKDS--EISKGLIEFDWK 169
 QY 190 EGSTVSYDLFDAGQGYPTDLLRIYRDNNTISSTLS-LSLYLYT 232
 Db 170 TPRDYSFDIYDLKGNDEYDIDKIYEDNKTLSDDISHIDVNLTY 213

RESULT 51
 ABP29357
 ID ABP29357 standard; protein; 259 AA.

XX AC ABP29357;
 XX DT 02-JUL-2002 (first entry)
 XX DE Streptococcus polypeptide SEQ ID NO 7890.
 XX KW Streptococcus; GAS; GBS; group B streptococcus; Streptococcus agalactiae;
 XX KW group A streptococcus; Streptococcus pyogenes; antibacterial;
 XX KW antiinflammatory; infection; vaccine; meningitis; gene therapy.
 XX OS Streptococcus pyogenes.
 XX PN WO200234771-A2.
 XX PD 02-MAY-2002.
 XX PF 29-OCT-2001; 2001WO-GB004789.
 XX PR 27-OCT-2000; 2000GB-00026333.
 XX PR 24-NOV-2000; 2000GB-00028727.
 XX PR 07-MAR-2001; 2001GB-00005640.
 XX PA (CHIR-) CHIRON SPA.
 XX PI (GENO-) INST GENOMIC RES.
 XX PI Telford J, Masignani V, Margarit Y RosI, Grandi G, Fraser C;
 XX Tettelin H;
 XX WPI; 2002-352536/38.
 XX DR N-PSDB; ABN69988.
 XX New Streptococcus protein for the treatment or prevention of infection or
 PT disease caused by Streptococcus bacteria, such as meningitis, and for
 PT detecting a compound that binds to the protein.

XX Claim 1; Page 3920; 4525pp; English.

XX The invention relates to a protein (ABP25413-ABP30895) from group B
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5493 sequences (SI), given in
 CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (I), nucleic acids encoding (II), ABN66044-ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for

the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (I) are used to detect Streptococcus in a
 CC biological sample. (I) is used to determine whether a compound binds to
 CC (I). A composition comprising (I) or a nucleic acid encoding (I), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus (I) is prevented or treated may be meningitis. Nucleic
 CC acid encoding (I) may be used to recombinantly produce (I) and may be
 CC used in gene therapy. Antibodies to (I) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins
 XX
 SQ Sequence 259 AA;
 Query Match 23.9%; Score 291.5; DB 5; Length 259;
 Best Local Similarity 31.3%; Pred. No. 7.3e-21;
 Matches 72; Conservative 42; Mismatches 91; Indels 25; Gaps 8;
 QY 17 ELQGTALGNLQIY-YNSKAITSEKSDQTLTLLFKGFTGHPWYN---DLLVDLG 72
 DB 34 EMSVGIVNRLNLYSTYDEYKGNKEGPPF-SGLFYKNI----PYGNSIEKLKVELN 88
 QY 73 STAATSEYEGSSVDLYGAYYQACAGTGNKTCACMYGGVTLHDNNRLTEERKVPINLWID 132
 DB 89 SVEKANFFSGKRVDFITLVEYPPCNSNIKNS---YGGITLSDGNRI-DKKNIPVNIID 144
 QY 133 G---KQTTVPIDKVTSKKEVTVOELDLQARHLYHGKFGFLY-----NSDSFGKVKQ 180
 DB 145 GVQOKYSYTDISTGSTDKKEVTIOELDKVSRYLQKHFNHYGFGVDKFGSRFQSGFE 204
 QY 181 RGLIVFHSSEGSVSDLYDPAQOQYPTLLRIYRDNNTTISSTLSISLYL 230
 DB 205 EGNIIHLNSGERISNLFDTGHDRESMLKXYSNDKNTAYSQDLHIDIVL 254

RESULT 52
 AAY06254
 ID AAY06254 standard; protein; 239 AA.
 XX
 AC AAY06254;
 XX
 DT 23-AUG-1999 (first entry)
 XX
 DE Staphylococcal group C enterotoxin SEC3-FRI909.
 XX
 KW Enterotoxin; SEC3-FRI909; toxin; disulfide loop; protein engineering.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers.
 FT Disulfide-bond 93..110
 XX
 PN WO9927889-A2.
 XX
 PD 10-JUN-1999.
 XX
 PF 01-DEC-1998; 98WO-US025107.
 XX
 PR 02-DEC-1997; 97US-0067357P.
 XX
 PA (IDAH-) IDAHO RES FOUND INC.
 XX
 PI Bohach GI;
 XX
 DR WPI; 1999-358008/30.
 XX
 PT Non-toxic modified staphylococcal enterotoxins.
 XX
 PS Disclosure; Page 17; 25pp; English.
 XX
 CC This protein represents the Staphylococcus aureus type C enterotoxin SEC3
 CC -FRI909. The invention relates to pyrogenic toxins, such as
 CC staphylococcal enterotoxins, modified in the disulfide loop region.
 CC Typically, the modification involves deletions within the disulfide loop
 CC region of SEC (see AAY06261). The modified toxins retain useful
 CC biological properties, such as the ability to induce cytokine production.

CC Typically, the modification involves deletions within the disulfide loop
 CC region of SEC (see AAY06261). The modified toxins retain useful
 CC biological properties, such as the ability to induce cytokine production,
 CC but have substantially reduced toxicity compared to the corresponding
 CC unmodified native toxin. Emetic response inducing activity and fever
 CC inducing activity are typically decreased by at least about 100-fold,
 CC while LD50 (in Dutch Belted rabbits) is at least 100-fold higher than the
 CC native toxin
 XX
 SQ Sequence 239 AA;
 Query Match 23.6%; Score 287.5; DB 2; Length 239;
 Best Local Similarity 31.3%; Pred. No. 1.7e-20;
 Matches 78; Conservative 45; Mismatches 92; Indels 19; Gaps 9;

QY 11 DLKKSELOQTALGNLQIYYNSKAITSE-KSQDQFTNLLFKGFTGHPWYNDLLV 69
 DB 10 DLKHSSEFTGT-MGNMK--YLYDDHYVSATKVKSVDFLAHDLIYNINDKLNNDYDKVKT 66
 QY 70 DLGSTAATSEYEGSSVDLYGAYYQYOC-----AGTGNKTCACMYGGVTLHDNNRLTEE 122
 DB 67 ELLNEDLANIKQBEVDVYGSNYVNCYFSSKDNVGVTSKTCMYGGITKHEGNEFDNG 126
 QY 123 --KKVPINLWIDKQTTVPIDKVTSKKEVTVOELDLQARHLYHGKFGLYNSDSFGKVKQ 180
 DB 127 NLQNLIRVY-ENKRNITISPE-VQTDKSVTAQELDIKARNFLINKNLYEFNS--SPYE 182
 QY 181 RGLIVFHSSEGSVSDLYDPAQOQYPT--TLRIYRDNNTTISSTLSISLYLT 232
 DB 183 TGYIKFIESNGNTFWYDMFPAPGDKFDQSKYLMYKDNKVDKSVKIEVHLTT 236

RESULT 53
 AAY06253
 ID AAY06253 standard; protein; 239 AA.
 XX
 AC AAY06253;
 XX
 DT 23-AUG-1999 (first entry)
 XX
 DE Staphylococcal group C enterotoxin SEC3-FRI913.
 XX
 KW Enterotoxin; SEC3-FRI913; toxin; disulfide loop; protein engineering.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 93..110
 XX
 PN WO9927889-A2.
 XX
 PD 10-JUN-1999.
 XX
 PF 01-DEC-1998; 98WO-US025107.
 XX
 PR 02-DEC-1997; 97US-0067357P.
 XX
 PA (IDAH-) IDAHO RES FOUND INC.
 XX
 PI Bohach GI;
 XX
 DR WPI; 1999-358008/30.
 XX
 PT Non-toxic modified staphylococcal enterotoxins.
 XX
 PS Disclosure; Page 17; 25pp; English.

This protein represents the Staphylococcus aureus type C enterotoxin SEC3
 -FRI913. The invention relates to pyrogenic toxins, such as
 staphylococcal enterotoxins, modified in the disulfide loop region.
 Typically, the modification involves deletions within the disulfide loop
 region of SEC (see AAY06261). The modified toxins retain useful
 biological properties, such as the ability to induce cytokine production,

CC but have substantially reduced toxicity compared to the corresponding
CC unmodified native toxin. Emetic response inducing activity and fever
CC inducing activity are typically decreased by at least about 100-fold,
CC while LD50 (in Dutch Belted rabbits) is at least 100-fold higher than the
CC native toxin
XX
SQ Sequence 239 AA;

Query Match 23.6%; Score 287.5; DB 2; Length 239;
Best Local Similarity 32.5%; Pred. No. 1.7e-20;
Matches 76; Conservative 45; Mismatches 94; Indels 19; Gaps 9;
QY 11 DLKKESELOQTALGNLKIYYNSKAITSS--KSADQFLTNTLLFKGFTGHPWYNDLLV 69
DB 10 DLKSSSEFTGT-MGNWK--LYDDHYVSATKVSVDKFLAHLIYNSDKLKNYDKVKT 66
QY 70 DLGSTAATSEYEGSSVDLYGAYGYQC-----AGGTENKTCACMYGVTLHNNRLTEE 122
DB 67 ELLNEDLAKYKDEVDVYGSNNYVYFSSKDNVGVKGTGTCMYGKITKHEGHNFDNG 126
QY 123 --KKVPINLWDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFLYNSDSFGKVKQ 180
DB 127 NLQNVLVRYV-ENKRNITISFE-VQTDKKSVAQELDIKARNFLINKNLYEFNS--SPYE 182
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPD--TLRLIYRDNTTISSTLSISLYLT 232
DB 183 TGYIKFIENNGTFOYDMMWPAFGDKFDQSKYLMYNDNKTVDKSKVIEVHLTT 236

RESULT 54
ABG71369
ID ABG71369 standard; protein; 240 AA.
XX
AC ABG71369;
XX
DT 29-JAN-2003 (first entry)
XX
DE Staphylococcal enterotoxin SEC3-FRI913.

XX Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
KW emetic response-inducing activity; staphylococcal enterotoxin;
KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
KW SEC3-FRI913.

XX Staphylococcus aureus.
XX Key Location/Qualifiers
FH Misc-difference 240
FT /label= unknown
XX
XX WO200283169-A1.
XX
XX 24-OCT-2002.

XX 11-APR-2002; 2002WO-US011619.
XX
XX 13-APR-2001; 2001US-0283720P.
XX
XX (IDAH-) IDAHO RES FOUND INC.
XX
XX Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
XX WPI; 2003-058608/05.
XX

XX New modified staphylococcal enterotoxin derived from a native disulfide
PT loop-containing pyrogenic toxin, useful for non-specifically enhancing an
PT immune function and as a vaccine against toxic shock syndrome or food
PT poisoning.
XX
XX Disclosure; Fig 15; 67pp; English.

XX The invention relates to a modified pyrogenic toxin derived from a native
CC disulphide loop-containing pyrogenic toxin where the modified toxin

CC comprises a disulphide loop having no more than 10 amino acids. The
CC modified toxin has a fever-inducing activity or an emetic response-
CC inducing activity decreased by about 100-fold in comparison to a native
CC toxin. The modified pyrogenic toxin, that is a staphylococcal
CC enterotoxin, is useful for non-specifically enhancing an immune function
CC and for vaccination against diseases such as toxic shock syndrome and
CC food poisoning. This sequence represents the staphylococcal enterotoxin,
CC SEC3-FRI913
XX
SQ Sequence 240 AA;

Query Match 23.6%; Score 287.5; DB 6; Length 240;
Best Local Similarity 32.5%; Pred. No. 1.7e-20;
Matches 76; Conservative 45; Mismatches 94; Indels 19; Gaps 9;
QY 11 DLKKESELOQTALGNLKIYYNSKAITSS--KSADQFLTNTLLFKGFTGHPWYNDLLV 69
DB 10 DLKSSSEFTGT-MGNWK--LYDDHYVSATKVSVDKFLAHLIYNSDKLKNYDKVKT 66
QY 70 DLGSTAATSEYEGSSVDLYGAYGYQC-----AGGTENKTCACMYGVTLHNNRLTEE 122
DB 67 ELLNEDLAKYKDEVDVYGSNNYVYFSSKDNVGVKGTGTCMYGKITKHEGHNFDNG 126
QY 123 --KKVPINLWDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFLYNSDSFGKVKQ 180
DB 127 NLQNVLVRYV-ENKRNITISFE-VQTDKKSVAQELDIKARNFLINKNLYEFNS--SPYE 182
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPD--TLRLIYRDNTTISSTLSISLYLT 232
DB 183 TGYIKFIENNGTFOYDMMWPAFGDKFDQSKYLMYNDNKTVDKSKVIEVHLTT 236

RESULT 55
ABG71370
ID ABG71370 standard; protein; 240 AA.
XX
AC ABG71370;
XX
DT 29-JAN-2003 (first entry)
XX
DE Staphylococcal enterotoxin SEC3-FRI909.

XX Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
KW emetic response-inducing activity; staphylococcal enterotoxin;
KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
KW SEC3-FRI909.

XX Staphylococcus aureus.
XX Key Location/Qualifiers
FH Misc-difference 240
FT /label= unknown
XX
XX WO200283169-A1.
XX
XX 24-OCT-2002.

XX 11-APR-2002; 2002WO-US011619.
XX
XX 13-APR-2001; 2001US-0283720P.
XX
XX (IDAH-) IDAHO RES FOUND INC.
XX
XX Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
XX WPI; 2003-058608/05.
XX

XX New modified staphylococcal enterotoxin derived from a native disulfide
PT loop-containing pyrogenic toxin, useful for non-specifically enhancing an
PT immune function and as a vaccine against toxic shock syndrome or food
PT poisoning.
XX
XX Disclosure; Fig 15; 67pp; English.

XX The invention relates to a modified pyrogenic toxin derived from a native
 CC disulphide loop-containing pyrogenic toxin where the modified toxin
 CC comprises a disulphide loop having no more than 10 amino acids. The
 CC modified toxin has a fever-inducing activity or an emetic response-
 CC inducing activity decreased by about 100-fold in comparison to a native
 CC toxin. The modified pyrogenic toxin, that is a staphylococcal
 CC enterotoxin, is useful for non-specifically enhancing an immune function
 CC and for vaccination against diseases such as toxic shock syndrome and
 CC food poisoning. This sequence represents the staphylococcal enterotoxin,
 CC SEC3-FR1909
 XX
 SQ Sequence 240 AA;

Query Match 23.6%; Score 287.5; DB 6; Length 240;
 Best Local Similarity 33.3%; Pred. No. 1.7e-20;
 Matches 78; Conservative 45; Mismatches 92; Indels 19; Gaps 9;
 QY 11 DLKXSELOGTALGNLQIYYNSKAITSE--KSADQFLTNLLFKGFTGHPWYNDLLV 69
 DB 10 DLKXSEFTGT-MGNMK--YLYDDHYVSATKVSVDKFLAHLDIYINDKLANNYDKVKT 66
 QY 70 DLGSTAATSEYEGSSVDLYGAYYQOC-----AGGTENKTAACMYGGVTLHNNRLTEE 122
 DB 67 ELLNEDLANKYKDEVDVYGSNYVNCYFSSKDNVKGVTSGKTCMYGGITKEGHNFDNG 126
 QY 123 --KKVPINLWIDKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
 DB 127 NLQNVLIRVY-ENKRNITISFE-VQTDKSVTAQELDIKARNFLINKNLYEFNS--SPYE 182
 QY 181 RGLIVFHSSEGSTVSYDLFDAOGQYD--TLRIYRDNTTISSTLSISLYLT 232
 DB 183 TGYIKFIESNGTFFWYDMPAPGDKFDQSKYLMYKDNKQWDSKVKIEVHLTT 236

RESULT 56
 AAY06256
 ID AAY06256 standard; protein; 239 AA.
 XX
 AC AAY06256;
 XX
 DT 23-AUG-1999 (first entry)
 XX
 DE Staphylococcal group C enterotoxin SEC-4446.
 XX
 KW Enterotoxin; SEC-4446; toxin; disulfide loop; protein engineering.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 93..110
 XX
 PN WO927889-A2.
 XX
 PD 10-JUN-1999.
 XX
 PF 01-DEC-1998; 98WO-US025107.
 XX
 PR 02-DEC-1997; 97US-0067357P.
 XX
 PA (IDAH-) IDAHO RES FOUND INC.
 XX
 PI Bohach GI;
 XX
 DR WPI; 1989-358008/30.
 XX
 XX Non-toxic modified staphylococcal enterotoxins.
 XX
 PS Disclosure; Page 17; 25pp; English.
 XX

XX This protein represents the Staphylococcus aureus type C enterotoxin SEC-
 CC 4446. The invention relates to pyrogenic toxins, such as staphylococcal
 CC enterotoxins, modified in the disulfide loop region. Typically, the

CC modification involves deletions within the disulfide loop region of SEC
 CC (see AAY06256). The modified toxins retain useful biological properties,
 CC such as the ability to induce cytokine production, but have substantially
 CC reduced toxicity compared to the corresponding unmodified native toxin.
 CC Emetic response inducing activity and fever inducing activity are
 CC typically decreased by at least about 100-fold, while ID50 (in Dutch
 CC Belted rabbits) is at least 100-fold higher than the native toxin
 XX
 SQ Sequence 239 AA;

Query Match 23.2%; Score 282.5; DB 2; Length 239;
 Best Local Similarity 32.1%; Pred. No. 5.3e-20;
 Matches 75; Conservative 45; Mismatches 95; Indels 19; Gaps 9;
 QY 11 DLKXSELOGTALGNLQIYYNSKAITSE--KSADQFLTNLLFKGFTGHPWYNDLLV 69
 DB 10 DLKXSEFTGT-MGNMK--YLYDDHYVSATKVSVDKFLAHLDIYINDKLANNYDKVKT 66
 QY 70 DLGSTAATSEYEGSSVDLYGAYYQOC-----AGGTENKTAACMYGGVTLHNNRLTEE 122
 DB 67 ELLNEDLANKYKDEVDVYGSNYVNCYFSSKDNVKGVTSGKTCMYGGITKEGHNFDNG 126
 QY 123 --KKVPINLWIDKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
 DB 127 NLQNVLIRVY-ENKRNITISFE-VQTDKSVTAQELDIKARNFLINKNLYEFNS--SPYE 182
 QY 181 RGLIVFHSSEGSTVSYDLFDAOGQYD--TLRIYRDNTTISSTLSISLYLT 232
 DB 183 TGYIKFIESNGTFFWYDMPAPGDKFDQSKYLMYKDNKQWDSKVKIEVHLTT 236

RESULT 57
 ABG71372
 ID ABG71372 standard; protein; 240 AA.
 XX
 AC ABG71372;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Staphylococcal enterotoxin SEC-4446.
 XX
 KW Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
 KW emetic response-inducing activity; staphylococcal enterotoxin;
 KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
 KW SEC-4446.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 240
 XX /label= unknown
 XX
 PN WO200283169-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 11-APR-2002; 2002WO-US011619.
 XX
 PR 13-APR-2001; 2001US-0283720P.
 XX
 PA (IDAH-) IDAHO RES FOUND INC.
 XX
 PI Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
 XX
 DR WPI; 2003-058608/05.
 XX
 XX New modified staphylococcal enterotoxin derived from a native disulfide
 PT loop-containing pyrogenic toxin, useful for non-specifically enhancing an
 PT immune function and as a vaccine against toxic shock syndrome or food
 PT poisoning.
 XX
 PS Disclosure; Fig 15; 67pp; English.
 XX

CC The invention relates to a modified pyrogenic toxin derived from a native
 CC disulphide loop-containing pyrogenic toxin where the modified toxin
 CC comprises a disulphide loop having no more than 10 amino acids. The
 CC modified toxin has a fever-inducing activity or an emetic response-
 CC inducing activity decreased by about 100-fold in comparison to a native
 CC toxin. The modified pyrogenic toxin, that is a staphylococcal
 CC enterotoxin, is useful for non-specifically enhancing an immune function
 CC and for vaccination against diseases such as toxic shock syndrome and
 CC food poisoning. This sequence represents the staphylococcal enterotoxin,
 CC SEC-4446

XX SQ Sequence 240 AA;

Query Match 23.2%; Score 282.5; DB 6; Length 240;
 Best Local Similarity 32.1%; Pred. No. 5.4e-20;
 Matches 75; Conservative 45; Mismatches 95; Indels 19; Gaps 9;

QY 11 DLKRSKSELGQALGNLQIYYNSKAITSSSE-KSADQFLNTLFLKFGFTGCHPWYNDLLV 69
 Db 10 DLKSSSEFTGT-MGNMK--LYDDHYVSATKVKSVDFLAHDLIYNISDKRLKNYDKVKT 66
 QY 70 DLGTAATSEYEGSSVDLYGAYGYQC-----AGGTPNKTAQMGVTLHNNRLTEE 122
 Db 67 ELLNEDLAKYKDEVDVYGSNYVNCYFSSKDNVGVKVTGKTCMYGGITKHEGNHFDNG 126
 QY 123 --KKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHLYHGKFLYNSDSFGKQV 180
 Db 127 NLQNVLRVY-ENKRNITISFE-VQTDKSVTAQELDIKARNFLINKNLYEFNS--SPYE 182
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYD--TLLRIYRDNTTISSTLSISLYLT 232
 Db 183 TGYIKFIENNNGTFOYDMWPAPGDKFDQSKYLMYNDKNTVDSKRVKIEVHLTT 236

RESULT 58

AAAY06255
 ID AAY06255 standard; protein; 239 AA.

XX AC AAY06255;

DT 23-AUG-1999 (first entry)

XX Staphylococcal group C enterotoxin SEC-MNCopeland.

DE Enterotoxin; SEC-MNCopeland; toxin; disulfide loop; protein engineering.

XX Staphylococcus aureus.

OS Key Location/Qualifiers
 FH Disulfide-bond 93..110

XX WO9927889-A2.

XX 10-JUN-1999.

XX 01-DEC-1998; 98WO-US025107.

XX 02-DEC-1997; 97US-0067357P.

XX (IDAH-) IDAHO RES FOUND INC.

XX Bohach GI;

XX WPI; 1999-358008/30.

XX Non-toxic modified staphylococcal enterotoxins.

XX Disclosure; Page 17; 25pp; English.

CC This protein represents the Staphylococcus aureus type C enterotoxin SEC-MNCopeland. The invention relates to pyrogenic toxins, such as staphylococcal enterotoxins, modified in the disulfide loop region. Typically, the modification involves deletions within the disulfide loop

CC region of SEC (see AAY06261). The modified toxins retain useful
 CC biological properties, such as the ability to induce cytokine production,
 CC but have substantially reduced toxicity compared to the corresponding
 CC unmodified native toxin. Emetic response inducing activity and fever
 CC inducing activity are typically decreased by at least about 100-fold,
 CC while LD50 (in Dutch Belted rabbits) is at least 100-fold higher than the
 CC native toxin

XX Sequence 239 AA;

Query Match 23.0%; Score 280.5; DB 2; Length 239;
 Best Local Similarity 31.3%; Pred. No. 8.5e-20;
 Matches 76; Conservative 46; Mismatches 102; Indels 19; Gaps 9;

QY 2 EKSEENEDLKKSELOGTALGNLQIYYNSKAITSSSE-KSADQFLNTLFLKFGFTG 60
 Db 1 ESQDPTDELKHSSEFTGT-MGNMK--LYDDHYVSATKVKSVDFLAHDLIYNISDKK 57
 QY 61 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQC-----AGGTPNKTAQMGVTL 113
 Db 58 LKNYDKVKTELLNEDLAKYKDEVDVYGSNYVNCYFSSKDNVGVKVTGKTCMYGGITK 117
 QY 114 HNNRLTER--KKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHLYHGKFLYN 171
 Db 118 HEGNHFDNGLQNVLRVY-ENKRNITISFE-VQTDKSVTAQELDIKARNFLINKNLYE 175
 QY 172 SDSFGKQVORGLIVFHSSEGSTVSVDLFDAGQGYD--TLLRIYRDNTTISSTLSISLY 229
 Db 176 FNS--SPYETGYIKFIENNNGTFOYDMWPAPGDKFDQSKYLMYNDKNTVDSKRVKIEVH 233
 QY 230 LYT 232
 Db 234 LTT 236

RESULT 59

ABG71371

ID AEG71371 standard; protein; 240 AA.

XX AC AEG71371;

DT 29-JAN-2003 (first entry)

XX Staphylococcal enterotoxin SEC-MNCopeland.

DE Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
 XX emetic response-inducing activity; staphylococcal enterotoxin;
 KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
 KW SEC-MNCopeland.

XX Staphylococcus aureus.

XX Key Location/Qualifiers
 FH Misc-difference 240
 FT /label= unknown

XX WO200283169-A1.

XX 24-OCT-2002.

XX 11-APR-2002; 2002WO-US011619.

XX 13-APR-2001; 2001US-0283720P.

XX (IDAH-) IDAHO RES FOUND INC.

XX Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;

XX WPI; 2003-058608/05.

XX New modified staphylococcal enterotoxin derived from a native disulfide
 PT loop-containing pyrogenic toxin, useful for non-specifically enhancing an
 PT immune function and as a vaccine against toxic shock syndrome or food

PT poisoning.
 XX Disclosure; Fig 15; 67pp; English.
 XX
 CC The invention relates to a modified pyrogenic toxin derived from a native
 CC disulphide loop-containing pyrogenic toxin where the modified toxin
 CC comprises a disulphide loop having no more than 10 amino acids. The
 CC modified toxin has a fever-inducing activity or an emetic response-
 CC inducing activity decreased by about 100-fold in comparison to a native
 CC toxin. The modified pyrogenic toxin, that is a staphylococcal
 CC enterotoxin, is useful for non-specifically enhancing an immune function
 CC and for vaccination against diseases such as toxic shock syndrome and
 CC food poisoning. This sequence represents the staphylococcal enterotoxin,
 CC SEC-MNCopeland
 XX
 SQ Sequence 240 AA;

Query Match 23.0%; Score 280.5; DB 6; Length 240;
 Best Local Similarity 31.3%; Pred. No. 8.6e-20;
 Matches 76; Conservative 46; Mismatches 102; Indels 19; Gaps 9;

QY 2 EKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSSP-KSADQFLNTLLPKGFFTG 60
 DB 1 ESQDPPTDELHKSSEFTGT-MGNMK--YLYDDHYVSATKMSVDKFLAHDLLIYNISDKK 57
 QY 61 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQC-----AGTPTNKATCMYGGVTL 113
 DB 58 LKNYDKVKTELLNEDLAKKYKDEVDVYGSNNYVNCYFSSKDNVGVKVTGGKTCMYGGITK 117
 QY 114 HDNRLTEP--KKVPINLWIDGQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYN 171
 DB 118 HEGNHFDPNGNLQNLVIRVY-ENKRNITISPE-VQTDKKSVAQELDIKARNFLINKKNLYE 175
 QY 172 SDSFGGKVGORGLIVFHSSEGSTVSYDLFDAQGOYPD--TLLRIYRDNNTTISSTLSISLY 229
 DB 176 FNS--SPYETGYIKFIENNGNTFYQDMPPAPGDKFDQSKYLMYNDNKTVDKRVKIEVH 233
 QY 230 LYT 232
 DB 234 LTT 236

RESULT 60
 AAY06252
 ID AAY06252 standard; protein; 239 AA.
 XX
 AC AAY06252;
 XX
 DT 23-AUG-1999 (first entry)
 XX
 DE Staphylococcal group C enterotoxin SEC2.
 XX
 KW Enterotoxin; SEC2; toxin; disulfide loop; protein engineering.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 93..110
 XX
 PN WO9927889-A2.
 XX
 PD 10-JUN-1999.
 XX
 PF 01-DEC-1998; 98WO-US025107.
 XX
 PR 02-DEC-1997; 97US-0067357P.
 XX
 PA (IDAH-) IDAHO RES FOUND INC.
 XX
 PI Bohach GI;
 XX
 DR WPI; 1999-358008/30.
 XX

PT Non-toxic modified staphylococcal enterotoxins.
 XX Disclosure; Page 17; 25pp; English.
 XX
 CC This protein represents the Staphylococcus aureus type C enterotoxin
 CC SEC2. The invention relates to pyrogenic toxins, such as staphylococcal
 CC enterotoxins, modified in the disulfide loop region. Typically, the
 CC modification involves deletions within the disulfide loop region of SEC
 CC (see AAY06261). The modified toxins retain useful biological properties,
 CC such as the ability to induce cytokine production, but have substantially
 CC reduced toxicity compared to the corresponding unmodified native toxin.
 CC Emetic response inducing activity and fever inducing activity are
 CC typically decreased by at least about 100-fold, while LD50 (in Dutch
 CC Belted rabbits) is at least 100-fold higher than the native toxin
 XX
 SQ Sequence 239 AA;

Query Match 22.9%; Score 279.5; DB 2; Length 239;
 Best Local Similarity 31.3%; Pred. No. 1.1e-19;
 Matches 76; Conservative 46; Mismatches 102; Indels 19; Gaps 9;

QY 2 EKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSSP-KSADQFLNTLLPKGFFTG 60
 DB 1 ESQDPPTDELHKSSEFTGT-MGNMK--YLYDDHYVSATKMSVDKFLAHDLLIYNISDKK 57
 QY 61 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQC-----AGTPTNKATCMYGGVTL 113
 DB 58 LKNYDKVKTELLNEDLAKKYKDEVDVYGSNNYVNCYFSSKDNVGVKVTGGKTCMYGGITK 117
 QY 114 HDNRLTEP--KKVPINLWIDGQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYN 171
 DB 118 HEGNHFDPNGNLQNLVIRVY-ENKRNITISPE-VQTDKKSVAQELDIKARNFLINKKNLYE 175
 QY 172 SDSFGGKVGORGLIVFHSSEGSTVSYDLFDAQGOYPD--TLLRIYRDNNTTISSTLSISLY 229
 DB 176 FNS--SPYETGYIKFIENNGNTFYQDMPPAPGDKFDQSKYLMYNDNKTVDKRVKIEVH 233
 QY 230 LYT 232
 DB 234 LTT 236

RESULT 61
 ABG71368
 ID ABG71368 standard; protein; 240 AA.
 XX
 AC ABG71368;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Staphylococcal enterotoxin SEC2.
 XX
 KW Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
 KW emetic response-inducing activity; staphylococcal enterotoxin; SEC2;
 KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 240
 XX /label= unknown
 FT
 PN WO200283169-A1.
 XX
 PD 24-OCT-2002.
 XX
 PR 11-APR-2002; 2002WO-US011619.
 XX
 PR 13-APR-2001; 2001US-0283720P.
 XX
 PA (IDAH-) IDAHO RES FOUND INC.
 XX
 PI Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
 XX

XX WPI; 2003-058608/05.
XX
XX New modified staphylococcal enterotoxin derived from a native disulfide
PT loop-containing pyrogenic toxin, useful for non-specifically enhancing an
PT immune function and as a vaccine against toxic shock syndrome or food
PT poisoning.
XX
XX Disclosure; Fig 15; 67pp; English.
XX
XX The invention relates to a modified pyrogenic toxin derived from a native
CC disulfide loop-containing pyrogenic toxin where the modified toxin
CC comprises a disulfide loop having no more than 10 amino acids. The
CC modified toxin has a fever-inducing activity or an emetic response-
CC inducing activity decreased by about 100-fold in comparison to a native
CC toxin. The modified pyrogenic toxin, that is a staphylococcal
CC enterotoxin, is useful for non-specifically enhancing an immune function
CC and for vaccination against diseases such as toxic shock syndrome and
CC food poisoning. This sequence represents the staphylococcal enterotoxin,
CC SEC2
XX
XX Sequence 240 AA;
Query Match 22.9%; Score 279.5; DB 6; Length 240;
Best Local Similarity 31.3%; Pred. No. 1.1e-19;
Matches 76; Conservative 46; Mismatches 102; Indels 19; Gaps 9;
QY 2 EKSEINEKDLRKSELOGTALGNLQIYYVNSKAITSSSE-KSADQFLTNTLLFKGFFTG 60
Db 1 ESQDPPTDEHLKSEFTGT-MGNKK--LYDDHVVSATKVMVDKFLAHLDIYNISDKK 57
QY 61 HPWYNDLAVDLSAATSEYEGSSVDLYGAYGYQC-----AGGTPNKTACMYGGVTL 113
Db 58 LKNYDKVKTLLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNVKGVTGGKTCMYGGITK 117
QY 114 HDNNRLTEE--KKYPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYN 171
Db 118 HEGNHFNDNGNLQNVLLIRYV-ENKRNITISFE-VQTDKKSVAQELDIKARNFLINKNLYE 175
QY 172 SDSFGGKQVQGLIVFHSSEGSTSVYDLFDAQGYPD--TLIRIYRDNTTSSSTLSISLY 229
Db 176 FNS--SPYETGVYKFIENNGNTFYDMLPAPGDKFDQSKYLMYNDKNTVDSKSVKIEVH 233
QY 230 LYT 232
Db 234 LTT 236
RESULT 62
AAR45016
ID AAR45016 standard; protein; 238 AA.
XX
XX AAR45016;
XX
XX 25-MAR-2003 (revised)
DT 08-JUN-1994 (first entry)
XX
XX Staphylococcal enterotoxin SEC3.
XX
XX Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
KW autoimmune disease; toxicity; Protein A; perfusion system.
XX
XX Staphylococcus aureus.
OS
XX WO9324136-A1.
XX
XX 09-DEC-1993.
PD
XX 01-JUN-1993; 93WO-US005213.
PF
XX 01-JUN-1992; 92US-00891718.
XX
XX (TERM/) TERMAN D S.
PA

PA (STON/) STONE J L.
XX
XX Terman DS, Stone JL;
PI
XX WPI; 1993-405418/50.
DR
XX Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
PT in a patient or for the treatment of auto-immune diseases.
PT
XX Disclosure; Fig 1; 90pp; English.
XX
XX The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
CC which may be used in the methods of the invention for treating cancer in
CC a patient. These SEs and homologues of them can be used as tumouricidal
CC agents for treating cancers and autoimmune disease. They exhibit
CC tumouricidal activity and toxicity identical to that observed for the
CC Protein A perfusion system. They may be administered by i.v. injection.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 238 AA;
SQ
Query Match 22.8%; Score 277.5; DB 2; Length 238;
Best Local Similarity 32.5%; Pred. No. 1.7e-19;
Matches 76; Conservative 44; Mismatches 95; Indels 19; Gaps 9;
QY 11 DLKKESELOGTALGNLQIYYVNSKAITSSSE-KSADQFLTNTLLFKGFFTGHPWYNDLIV 69
Db 9 ELKKSSEFTGT-MGNKK--LYDDHVVSATKVMVDKFLAHLDIYNISDKKLYDKVKT 65
QY 70 DLGSAATSEYEGSSVDLYGAYGYQC-----AGGTPNKTACMYGGVTLHNNRLTEE 122
Db 66 ELLNEDLAKKYKDEVVDVYGSNYYVNCYFSSKDNVKGVTGGKTCMYGGITKEGNHFDNG 125
QY 123 --KKYPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 126 NQNVLLIRYV-ENKRNITISFE-VQTDKKSVAQELDIKARNFLINKNLYEFNS--SPYE 181
QY 181 RGLIVFHSSEGSTSVYDLFDAQGYPD--TLIRIYRDNTTSSSTLSISLYLT 232
Db 182 TGVYKFIENNGNTFYDMLPAPGDKFDQSKYLMYNDKNTVDSKSVKIEVHLT 235
RESULT 63
AAB67343
ID AAB67343 standard; peptide; 238 AA.
XX
XX AAB67343;
XX
XX 23-APR-2001 (first entry)
DT
XX
XX Staphylococcus aureus enterotoxin C3 protein.
DE
XX Tumour; cancer; immune; enterotoxin.
KW
XX Staphylococcus aureus.
OS
XX US6180097-B1.
XX
XX 30-JAN-2001.
PD
XX 30-OCT-1998; 98US-00183437.
PF
XX 03-OCT-1989; 89US-00416530.
XX 17-JAN-1990; 90US-00466577.
PR 17-JAN-1991; 91WO-US000342.
PR 01-JUN-1992; 92US-00891718.
PR 02-MAR-1993; 93US-00025144.
PR 31-JAN-1994; 94US-00189424.
PR 19-JUN-1995; 95US-00491746.
XX
XX (TERM/) TERMAN D S.
PA
XX Terman DS;
PI

XX WPI; 2001-158657/16.
XX
XX Tumor cell capable of stimulating antitumor immune reactivity in vitro or
XX PT in vivo comprises exogenous nucleic acids encoding a superantigen and a
XX PT costimulatory molecule.
XX
XX PS Disclosure; Fig 2; 16pp; English.
XX
XX The present invention relates to a tumour cell capable of stimulating
XX CC antitumor immune reactivity in vitro or in vivo contains and expresses an
XX CC exogenous nucleic acid molecule encoding a superantigen or its active
XX CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
XX CC molecule that activates T cells in conjunction with an antigenic
XX CC stimulus. The invention may be used for cancer therapy by stimulating an
XX CC anticancer immune response in vivo or ex vivo
XX
XX SQ Sequence 238 AA;

Query Match 22.6%; Score 275.5; DB 4; Length 238;
Best Local Similarity 32.1%; Pred. No. 2.7e-19;
Matches 75; Conservative 45; Mismatches 95; Indels 19; Gaps 9;

QY 11 DLKKSSELOQTALGNLKOIYYNKAITSSE-KSADQFLTNLLFKGFTGHPWYNDLLV 69
DB 9 ELHKSSEFTGT-MGNMK--YLYDDHVVSATKVMVSKFLAHDLIYNSDKKLNVDKVK 65

QY 70 DLGSTAATSEYEGSSVDLYGAYGYQC-----AGTTPNKTAACMYGGVTLHDNNRLTEE 122
DB 66 ELLNEDLAKYKDEVDVYGSNYVNCYFSSKDNVKGVTGGKTCMYGGITKHEGNHFDNG 125

QY 123 --KKVPINLWIDGKQTTVPIDIKVTSKEVTVQELDLQARHYLHGKFLYNSDSFGKVKV 180
DB 126 NLQNVLIRVY-ENKRNITISFE-VQTDKSVTAQELDIKARNFLINKKNLYEFNS--SPYE 181

QY 181 RGLIVFHSSEGSVSYDLFDAQGVDP--TLRIYRDNTTISSTLSISLYVT 232
DB 182 TGYIKFIENNGNTFWYDMNPAQKQKQKYLMMYNDNKTVDSKSVKIEVHLTT 235

RESULT 64
ABB76239
ID ABB76239 standard; protein; 238 AA.
XX
XX ABB76239;
XX
XX 09-AUG-2002 (first entry)
XX
XX Staphylococcus aureus enterotoxin C3.
XX
XX Enterotoxin C3; SEC3; superantigen; antigen; tumour; cancer; antitumour;
XX KW therapy.
XX
XX Staphylococcus aureus.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 208
XX FT /note= "given as 'O' in the specification"
XX
XX US2002051765-A1.
XX
XX 02-MAY-2002.
XX
XX 19-DEC-2000; 2000US-00741503.
XX
XX 03-OCT-1989; 89US-00416530.
XX PR 17-JAN-1990; 90US-00466577.
XX PR 17-JAN-1991; 91WO-US000342.
XX PR 01-JUN-1992; 92US-00891718.
XX PR 02-MAR-1993; 93US-00025144.
XX PR 31-JAN-1994; 94US-00189424.
XX PR 19-JUN-1995; 95US-00491746.
XX

PA (TERM/) Terman D S.
XX
XX Terman DS;
XX
XX WPI; 2002-415198/44.
XX
XX Reagent for treating cancer without the need for e.g. radiotherapy,
XX PT comprises a specific V beta subset of T cells sensitized to a growing
XX PT tumor and stimulated with superantigens.
XX
XX PS Disclosure; Fig 2; 17pp; English.
XX
XX The present sequence is the protein sequence of enterotoxin C3 (SEC3) of
XX CC Staphylococcus aureus. Similarity is shown, in several stretches of
XX CC sequence, between staphylococcal enterotoxins, streptococcal pyrogenic
XX CC exotoxins and staphylococcal exfoliative toxins (see ABB76234-44). In the
XX CC present invention, synthetic polypeptides useful in tumour therapy and in
XX CC blocking or destroying autoreactive T and B lymphocyte populations are
XX CC characterised by substantial structural homology to staphylococcal
XX CC enterotoxin A and enterotoxin B, and to streptococcal pyrogenic
XX CC exotoxins, with statistically significant sequence homology and
XX CC similarity (Z value of Lipman and Pearson algorithm in Monte Carlo
XX CC analysis exceeding 6) to include alignment of cysteine residues and
XX CC similar hydropathy profiles. These superantigens are used to treat solid
XX CC tumours, including their metastases, without radiation, surgery or
XX CC standard chemotherapeutic agents. A claimed method of human cancer
XX CC treatment involves contacting haematopoietic cells from a patient with
XX CC one or more superantigens ex vivo to generate stimulated cells, selecting
XX CC a specific V beta subset of cells, and reintroducing these cells into the
XX CC patient to induce an in vivo therapeutic, tumoricidal reaction
XX
XX SQ Sequence 238 AA;

Query Match 22.6%; Score 275.5; DB 5; Length 238;
Best Local Similarity 32.1%; Pred. No. 2.7e-19;
Matches 75; Conservative 44; Mismatches 96; Indels 19; Gaps 9;

QY 11 DLKKSSELOQTALGNLKOIYYNKAITSSE-KSADQFLTNLLFKGFTGHPWYNDLLV 69
DB 9 ELHKSSEFTGT-MGNMK--YLYDDHVVSATKVMVSKFLAHDLIYNSDKKLNVDKVK 65

QY 70 DLGSTAATSEYEGSSVDLYGAYGYQC-----AGTTPNKTAACMYGGVTLHDNNRLTEE 122
DB 66 ELLNEDLAKYKDEVDVYGSNYVNCYFSSKDNVKGVTGGKTCMYGGITKHEGNHFDNG 125

QY 123 --KKVPINLWIDGKQTTVPIDIKVTSKEVTVQELDLQARHYLHGKFLYNSDSFGKVKV 180
DB 126 NLQNVLIRVY-ENKRNITISFE-VQTDKSVTAQELDIKARNFLINKKNLYEFNS--SPYE 181

QY 181 RGLIVFHSSEGSVSYDLFDAQGVDP--TLRIYRDNTTISSTLSISLYVT 232
DB 182 TGYIKFIENNGNTFWYDMNPAQKQKQKYLMMYNDNKTVDSKSVKIEVHLTT 235

RESULT 65
AAG63856
ID AAG63856 standard; protein; 228 AA.
XX
XX AAG63856;
XX
XX 29-OCT-2001 (first entry)
XX
XX Amino acid sequence of a modified Staphylococcal enterotoxin C1.
XX DE Enterotoxin C1; SEC-SER; infectious disease; mastitis.
XX KW
XX Synthetic.
XX OS Staphylococcus sp.
XX OS
XX WO200160851-A1.
XX PN
XX 23-AUG-2001.
XX PD
XX

PF	31-OCT-2000; 2000WO-KR001241.
XX	
PR	17-FEB-2000; 2000KR-00007612.
XX	
PA	(GLDS) LG CHEM LTD.
PI	Lee H, Park Y, Han K, Chang B, Lee Y;
XX	
DR	WPI; 2001-522585/57.
N-PSDB; AAH74983.	
XX	
PT	Producing stable modified Staphylococcal toxin polypeptide for treating infectious diseases, e.g. mastitis, in animals, involves substituting PT cysteine at specified position of modified Staphylococcal toxin C1 with PT serine.
XX	
PS	Claim 1; Page 59-60; 64pp; English.
XX	
CC	The present sequence represents a modified Staphylococcal enterotoxin C1, designated SEC-SER, the modified toxin is characterised in that the 95th CC amino acid (cysteine) is substituted with serine. This results in a toxin CC that has improved stability. The modified enterotoxin is useful for CC preventing or treating infectious diseases due to microorganisms in CC animals such as cows, pigs, horses, sheep, hens, dogs and cats, e.g. CC mastitis in cows
XX	
SQ	Sequence 228 AA;
Query Match	22.5%; Score 273.5; DB 4; Length 228;
Best Local Similarity	32.1%; Pred.No. 4.1e-19;
Matches	76; Conservative 45; Mismatches 97; Indels 19; Gaps 9;
QY	2 EKSEINEXDLRKSELQGTALGNLKOIY--YNSKAITSEKSAADQFLNTLLFKGFFT 59
Db	2 ESQDPDTPDELHASKFTG-LMENMKVLYDDHYVS---ATKKSVDFKFLAHLINIISDK 57
QY	60 GHFWNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLLHDNNRL 119
Db	58 KLKNYDKVATELINEGLAKKYDEVDVYGSNYYNVCSGKT-----CMYGGITKHGHNHF 112
QY	120 TEE--KKVPINLWDGQTVPIDVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGG 177
Db	113 DNGNLQNVLIRVI--ENKRNITISFE-VQTDKKSVAQAELDIAKRNFLINKXLYEFNS--S 168
QY	178 KVQRGLIVFHSSEGSTVSYDLFDAQGQYPD--TLRIYRDNTTISSTSLSISLYLT 232
Db	169 PYETGVYIKFIENNNGTFWYDMMPAPGDKFQSKYLMMYNDNKTVDKSVKIEVLTT 225
RESULT 66	
AARI3208	
ID	AARI3208 standard; protein; 238 AA.
AC	
AAARI3208;	
DT	15-OCT-1991 (first entry)
DE	
XX	Staphylococcal enterotoxin C3.
XX	
KW	SEC3; cancer treatment; pyrogen; tumouricide.
OS	Staphylococcus aureus.
PN	WO9110680-A.
PD	
PF	25-JUL-1991.
XX	
PR	17-JAN-1990; 90US-00466577.
XX	
PR	17-JAN-1990; 90US-00466577.
XX	
PA	(TERM/) TERMAN D S.
XX	

PI	Terman DS;
XX	
DR	WPI; 1991-237984/32.
XX	
PT	Treating cancer with enterotoxin from Staphylococcus aureus - administered by IV injection, having same tumoricidal activity as PT Staphylococcal protein A without potential toxic reactions.
XX	
PS	Disclosure; Fig 1; 74pp; English.
XX	
CC	SEC3 was isolated and purified from S.aureus. It can be used for treating CC cancer, activating cytokine mediators and procoagulant systems, CC augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be CC administered intravenously, optionally with ibuprofen to attenuate toxic CC reaction to SEC3. Synthetic polypeptides having structural homology to CC Staphylococcal exotoxins are claimed, provided the homology includes CC statistically significant sequence homology, alignment of Cysteine CC residues and similar hydropathy profiles. See AARI3203-R13211
XX	
SQ	Sequence 238 AA;
Query Match	22.4%; Score 272.5; DB 2; Length 238;
Best Local Similarity	31.1%; Pred.No. 5.5e-19;
Matches	76; Conservative 41; Mismatches 88; Indels 39; Gaps 8;
QY	11 DLRRKSELQGTALGNLKGIYYNSKAITSSSE-KSADQFLNTLLFKGFFTHGPWNDDLAV 69
Db	9 ELHKSSFTGT-MGNMK--LYDDHYVSAIKWSVDFKFLAHLIIYNISDKLKNYDKVKT 65
QY	70 DLGSTAATSEYEGSSVDLYGAYGYQC-----AGGTPNKTCMYGGVTLLHDNN---- 117
Db	66 ELLNEDLAKKYDEVDVYGSNYYNVCVFSSKDNVGKVTGGKTCMYGGITKHGHNHDNG 125
QY	118 -----PLTEKKVPINLWDGQTVPIDVKTSKKEVTVOELDLQARHYLHGKFGLY 170
Db	126 NLQNCLIRIYVENKRNITISF-----EVQTDKKSVAQAELDIAKARNFLINKQLY 173
QY	171 NSDSFGGRVORGLIVFHSSEGSTVSYDLFDAQGQYPD--TLRIYRDNTTISSTSLSISL 228
Db	174 EFNS--SPYETGVYIKFIENNNGTFWYDLMPAPGDKFQSKYLMMYNDNKTVDKSVKIEV 231
QY	229 VLYT 232
Db	232 HLTT 235
RESULT 67	
AAWI2153	
ID	AAWI2153 standard; protein; 251 AA.
AC	
AAWI2153;	
DT	04-NOV-1997 (first entry)
XX	
DE	Streptococcus pyogenes Streptococcal toxin A mutant Cys90Ser.
XX	
KW	Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine; protection; treatment; cancer; neutralising antibody;
KW	streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
KW	hypotension; group A streptococcal infection; myositis; fasciitis;
XX	liver damage; T cell; lymphoma; ovarian; uterine.
OS	Streptococcus pyogenes.
OS	Synthetic.
XX	
FH	Key Location/Qualifiers
FT	Peptide 1..30
FT	/label= sig_peptide
FT	Peptide 31..251
FT	/label= mat_peptide
FT	Misc-difference 120
XX	/note= "wild type Cys replaced by Ser"
XX	

PN WO9640930-A1.
 XX 19-DEC-1996.
 PD 07-JUN-1996; 96WO-US010252.
 XX 07-JUN-1995; 95US-00480261.
 PR (MINU) UNIV MINNESOTA.
 XX
 PA Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;
 XX WPI; 1997-089936/09.
 DR
 XX
 XX Mutant SPE-A toxin with at least one amino acid change is substantially
 PT non-lethal - used in vaccine composition for treatment of cancer and
 PT streptococcal toxic shock syndrome etc.
 XX
 XX Example 4; Page; 102pp; English.
 PS
 XX The present sequence is a non-lethal Streptococcus pyogenes Streptococcal
 CC toxin A (SPE-A) mutant, which can be used to produce vaccines to protect
 CC animals against wild type SPE-A and to treat cancer and streptococcal
 CC toxic shock syndrome (STSS). The mutant SPE-A causes neutralising
 CC antibodies (Ab) to be produced, which may be used to ameliorate STSS
 CC symptoms, e.g. fever, hypotension, group A streptococcal infection,
 CC myositis, fascitis and liver damage. The neutralising Ab is preferably
 CC administered in conjunction with antibiotic therapy. The mutant SPE-A is
 CC especially useful for treating T cell lymphomas, and ovarian and uterine
 CC cancer. It is thought that mutant SPE-A can be selectively toxic to T
 CC cell lymphoma cells. N.B. Sequence not given in the specification, but
 CC constructed using the wild type SPE-A sequence given on pages 77-79
 XX
 XX Sequence 251 AA;
 SQ
 Query Match 22.3%; Score 271.5; DB 2; Length 251;
 Best Local Similarity 32.5%; Pred. No. 7.5e-19;
 Matches 77; Conservative 45; Mismatches 96; Indels 19; Gaps 10;
 QY 4 SBEINFKLRKSELOGTAL-GNLKQIYY-YNSKAIT-SSEKSAQDQFLTNTLLPKGFTG 60
 DB 25 SGEVFAQQDPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLSHLLIYN---VS 81
 QY 61 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYOC-AGGTPNKTCMYGGVTLHDNNRL 119
 DB 82 GPNYDKLTKELKNQEMATLFKDKNVDIYGVEYHLCYLSENAERSACIYGGVTNHEGNHL 141
 QY 120 TEEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKV 179
 DB 142 ETPKKIVKVSIDGIQ-SLSFD-IETNKKWVTAQELDYKVRKYLTDNKQLYTNGP--SKY 197
 QY 180 QRGGLIVFHSSEGSTVSVDLFD---AQQYPTLLRIYRDNTTISSTLSISLYLT 232
 DB 198 ETGYIKFIPKNKESFWDFPPEFTQSKY----LMIYKDNETLDSNTSQIEVYLTT 250
 RESULT 68
 AAR13209
 ID AAR13209 standard; protein; 221 AA.
 AC
 XX AAR13209;
 XX
 DT 27-AUG-2003 (revised)
 DT 15-OCT-1991 (first entry)
 XX Streptococcal pyrogenic enterotoxin A.
 XX SPE A; cancer treatment; pyrogen; tumouricide; scarlet fever.
 XX Streptococcus sp.
 OS
 XX WO9110680-A.
 PN
 XX

PD 25-JUL-1991.
 XX 17-JAN-1990; 90US-00466577.
 XX 17-JAN-1990; 90US-00466577.
 PR (TERM/) TERMAN D S.
 PA Terman DS;
 XX WPI; 1991-237984/32.
 XX
 XX Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumoricidal activity as
 PT Staphylococcal protein A without potential toxic reactions.
 XX
 PS Disclosure; Fig 1; 74pp; English.
 XX
 CC SPE A can be used for tumoricidal treatment, esp. with a haemolysin.
 CC Synthetic polypeptides having structural homology to Streptococcal
 CC pyrogenic exotoxins are claimed, provided the homology includes
 CC statistically significant sequence homology, alignment of Cysteine
 CC residues and similar hydrophathy profiles. See AAR13203-R13211. (Updated
 CC on 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 221 AA;
 Query Match 22.2%; Score 270.5; DB 2; Length 221;
 Best Local Similarity 33.8%; Pred. No. 7.9e-19;
 Matches 76; Conservative 42; Mismatches 88; Indels 19; Gaps 10;
 QY 16 SELQGTAL-GNLKQIYY-YNSKAIT-SSEKSAQDQFLTNTLLPKGFTGHPWYNDLLVDLG 72
 DB 7 SQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLSHLLIYN---VSGPNYDKLTKELK 63
 QY 73 STAATSEYEGSSVDLYGAYGYOC-AGGTPNKTCMYGGVTLHDNNRLTEEEKKVPINLWI 131
 DB 64 NQEMATLFKDKNVDIYGVEYHLCYLCENAERSACIYGGVTNHEGNHLIPKIVVKVSI 123
 QY 132 DGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQRGGLIVFHSSE 191
 DB 124 DGIQ-SLSFD-IETNKKWVTAQELDYKVRKYLTDNKQLYTNGP--SKYETGYIKFIPKNK 179
 QY 192 STVSVDLFD---AQQYPTLLRIYRDNTTISSTLSISLYLT 232
 DB 180 ESFWDLPPEFTQSKY----LMIYKDNETLDSNTSQIEVYLTT 220
 RESULT 69
 AAR45017
 ID AAR45017 standard; protein; 221 AA.
 AC
 XX AAR45017;
 XX
 DT 25-MAR-2003 (revised)
 DT 08-JUN-1994 (first entry)
 XX Staphylococcal enterotoxin SPE A.
 XX Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
 XX autoimmune disease; toxicity; Protein A; perfusion system.
 OS
 XX Staphylococcus aureus.
 XX WO9324136-A1.
 PN
 XX 09-DEC-1993.
 PD
 XX 01-JUN-1993; 93WO-US005213.
 PF
 XX 01-JUN-1992; 92US-00891718.
 PR
 XX (TERM/) TERMAN D S.
 PA


```
AAW12154
ID AAW12154 standard; protein; 251 AA.
XX
AC AAW12154;
XX
DT 04-NOV-1997 (first entry)
XX
DE Streptococcus pyogenes Streptococcal toxin A mutant Ser195Ala.
XX
KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
protection; treatment; cancer; neutralising antibody;
XX
KW streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
XX
KW hypotension; group A streptococcal infection; myositis; fasciitis;
XX
KW liver damage; T cell; lymphoma; ovarian; uterine.
XX
OS Streptococcus pyogenes.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT /label= sig_peptide
FT Peptide 31..251
FT /label= mat_peptide
FT Misc-difference 225
FT /note= "wild type Ser replaced by Ala"
XX
PN WO9640930-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US010252.
XX
PR 07-JUN-1995; 95US-00480261.
XX
PA (MINU ) UNIV MINNESOTA.
XX
PI Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;
XX
DR WPI; 1997-099936/09.
XX
XX
XX Mutant SPE-A toxin with at least one amino acid change is substantially
non-lethal - used in vaccine composition for treatment of cancer and
streptococcal toxic shock syndrome etc.
XX
XX Example 4; Page; 102pp; English.
XX
XX The present sequence is a non-lethal Streptococcus pyogenes Streptococcal
toxin A (SPE-A) mutant, which can be used to produce vaccines to protect
animals against wild type SPE-A and to treat cancer and streptococcal
toxic shock syndrome (STSS). The mutant SPE-A causes neutralising
antibodies (Ab) to be produced, which may be used to ameliorate STSS
symptoms, e.g. fever, hypotension, group A streptococcal infection,
myositis, fasciitis and liver damage. The neutralising Ab is preferably
administered in conjunction with antibiotic therapy. The mutant SPE-A is
especially useful for treating T cell lymphomas, and ovarian and uterine
cancer. It is thought that mutant SPE-A can be selectively toxic to T
cell lymphoma cells. N.B. Sequence not given in the specification, but
constructed using the wild type SPE-A sequence given on pages 77-79
XX
XX Sequence 251 AA;
XX
Query Match 22.0%; Score 268.5; DB 2; Length 251;
Best Local Similarity 32.5%; Pred. No. 1.5e-18;
Matches 77; Conservative 45; Mismatches 96; Indels 19; Gaps 10;
QY 4 SEEINEKDLRKKSLEQGTAL-GNLKQIYY-YNSKAIT-SSEKSAQDLTNTLLFKGFTTG 60
DB 25 SQEYFAQQDPDPQSOLHRSLLVKNLQNIYFLYEGDPVTHENVKSVDDLHLLIYN--VS 81
QY 61 HPWYNDLLVDLGSTAARSEYEGSSVDLYGAYYQC-AGGTPNKTAGYGVTLHNNRL 119
DB 82 GPNYDKLTKELKNOEMATLFKDKNVDYGVVEYHLCYLCENAKRSACIYGGVTNHEGNHL 141
```


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OM protein - protein search, using sw model

Run on: August 12, 2004, 13:32:36 / Search time 24.7742 Seconds
(without alignments)
2952.472 Million cell updates/sec

Title: US-09-900-766-2
Perfect score: 1218
Sequence: 1 SEKSEINEKDLKKSELOG.....RDNTTISSTLSISLYLYTT 233

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1292805 seqs, 313927144 residues

Total number of hits satisfying chosen parameters: 1292805

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1218	100.0	233	10	US-09-900-766-2
2	1218	100.0	672	10	US-09-900-766-1
3	1130	92.8	233	10	US-09-900-766-3
4	1107	90.9	233	10	US-09-900-766-7
5	1107	90.9	233	14	US-10-283-838-8
6	1107	90.9	257	12	US-10-267-682-112
7	1107	90.9	257	12	US-10-267-748-111
8	1072	88.0	248	9	US-09-870-759-16
9	1072	88.0	248	10	US-09-751-708A-16
10	948	77.8	233	10	US-09-900-766-4
11	948	77.8	233	14	US-10-283-838-7
12	948	77.8	257	12	US-10-267-682-113
13	948	77.8	257	12	US-10-267-748-111
14	944	77.5	233	12	US-10-354-948-4
15	935	76.8	257	9	US-09-870-759-8
16	935	76.8	257	9	US-09-870-759-10
17	935	76.8	257	10	US-09-751-708A-8
18	935	76.8	257	14	US-10-002-784A-2
19	908	74.5	233	14	US-10-002-784A-4
20	903	74.1	233	8	US-08-882-431-2
21	611	50.2	258	9	US-08-882-431-4
22	611	50.2	258	10	US-09-870-759-14
23	611	50.2	258	10	US-09-751-708A-14
24	486	39.8	203	10	US-09-900-766-5
25	362	29.7	82	14	US-10-002-784A-34
26	308	25.3	217	10	US-09-900-766-6
27	268.5	22.0	251	8	US-08-973-391A-13
28	268.5	22.0	251	12	US-09-308-830-13
29	268.5	22.0	266	9	US-09-870-759-10
30	268.5	22.0	266	10	US-09-751-708A-10
31	267.5	22.0	239	9	US-09-150-947B-12
32	267.5	22.0	239	14	US-10-172-425B-12
33	267.5	22.0	255	12	US-10-354-948-2
34	263.5	21.6	251	8	US-08-882-431-16
35	263.5	21.6	251	14	US-10-002-784A-16
36	263.5	21.6	266	9	US-09-870-759-12
37	263.5	21.6	266	10	US-09-751-708A-12
38	260.5	21.4	266	14	US-10-002-784A-6
39	260.5	21.4	266	14	US-10-151-336-8
40	255.5	21.0	239	14	US-10-002-784A-10
41	255.5	21.0	266	8	US-08-882-431-14
42	255.5	21.0	266	14	US-10-002-784A-14
43	254.5	20.9	239	8	US-08-882-431-10
44	250.5	20.6	266	14	US-10-002-784A-8
45	247	20.3	265	8	US-08-882-431-6
46	244	20.0	265	8	US-08-882-431-8
47	225.5	18.5	220	14	US-10-002-784A-26
48	225.5	18.5	468	14	US-10-002-784A-27
49	220	18.1	250	9	US-09-870-759-20
50	220	18.1	250	10	US-09-751-708A-20
51	194	15.9	82	14	US-10-002-784A-33
52	155.5	12.8	235	12	US-09-308-829-2
53	155.5	12.8	235	12	US-09-336-036-2
54	112	9.2	79	14	US-10-002-784A-39
55	111.5	9.2	89	14	US-10-002-784A-35
56	103.5	8.5	621	12	US-10-424-599-264720
57	103.5	8.5	528	12	US-10-425-114-57792
58	102.5	8.4	233	8	US-08-882-431-12
59	100	8.2	234	9	US-09-870-759-18
60	100	8.2	234	10	US-09-751-708A-18
61	100	8.2	234	12	US-10-267-682-111
62	100	8.2	234	12	US-10-267-748-111
63	100	8.2	234	14	US-10-002-784A-12
64	99.5	8.2	89	14	US-10-002-784A-36
65	98	8.0	194	10	US-09-465-714-3
66	98	8.0	194	12	US-10-465-714-3
67	98	8.0	227	12	US-10-354-948-6
68	98	8.0	234	12	US-10-282-122A-70390
69	98	8.0	238	10	US-09-465-714-1
70	97.5	8.0	89	14	US-10-002-784A-37
71	97.5	8.0	89	14	US-10-002-784A-38
72	94	7.7	231	12	US-10-282-122A-70240
73	93	7.6	16	14	US-10-283-838-20
74	92	7.6	600	16	US-10-437-963-191455
75	91	7.5	1634	15	US-10-435-766-23
76	88.5	7.3	402	14	US-10-284-400-6
77	88.5	7.3	403	14	US-10-284-400-14
78	88	7.2	1351	16	US-10-437-963-154108
79	88	7.2	1500	16	US-10-437-963-154440
80	87.5	7.2	1361	12	US-10-282-122A-48282
81	87	7.1	226	9	US-09-815-242-5900
82	87	7.1	226	9	US-09-815-242-13156
83	87	7.1	1152	12	US-10-424-599-239246
84	86	7.1	1847	12	US-10-282-122A-59134
85	86	7.1	1017	15	US-10-369-493-20166
86	86	7.1	1497	15	US-10-369-493-2310
87	85.5	7.0	394	15	US-10-371-264-71
88	85.5	7.0	394	15	US-10-371-099-367

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Sequence 367, App
Sequence 71, Appl
Sequence 367, App
Sequence 78278, A
Sequence 32, Appl
Sequence 115, App
Sequence 70242, A
Sequence 1671, Ap
Sequence 1645, Ap
Sequence 162337,
Sequence 43929, A
Sequence 43957, A

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ALIGNMENTS

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RESULT 1
US-09-900-766-2
; Sequence 2, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(233)
; OTHER INFORMATION: Chimeric Protein
US-09-900-766-2

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Query Match 100.0%; Score 1218; DB 10; Length: 233;
Best Local Similarity 100.0%; Pred. No. 3.4e-116;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKQIYYNSKAITSEKSADQFLNTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKSELOQTALGNLKQIYYNSKAITSEKSADQFLNTLLFKGFFTG 60

QY 61 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
Db 61 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120

QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180

QY 181 RGLIVFHSSEGSTVSVDLFDQAQGYPTLLRIYRDNTTISSTLSISLYLYTT 233
Db 181 RGLIVFHSSEGSTVSVDLFDQAQGYPTLLRIYRDNTTISSTLSISLYLYTT 233

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RESULT 2
US-09-900-766-1
; Sequence 1, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY

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; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 672
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(672)
; OTHER INFORMATION: Conjugate protein
US-09-900-766-1

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Query Match 100.0%; Score 1218; DB 10; Length 672;
Best Local Similarity 100.0%; Pred. No. 1.1e-115;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKQIYYNSKAITSEKSADQFLNTLLFKGFFTG 60
Db 226 SEKSEINEKDLRKSELOQTALGNLKQIYYNSKAITSEKSADQFLNTLLFKGFFTG 285

QY 61 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
Db 286 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 345

QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 346 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405

QY 181 RGLIVFHSSEGSTVSVDLFDQAQGYPTLLRIYRDNTTISSTLSISLYLYTT 233
Db 406 RGLIVFHSSEGSTVSVDLFDQAQGYPTLLRIYRDNTTISSTLSISLYLYTT 458

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RESULT 3
US-09-900-766-3
; Sequence 3, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: peptide
; LOCATION: (1)..(233)
; OTHER INFORMATION: Chimeric Protein
US-09-900-766-3

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Query Match 92.8%; Score 1130; DB 10; Length 233;
Best Local Similarity 91.4%; Pred. No. 3.5e-107;
Matches 213; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKQIYYNSKAITSEKSADQFLNTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKSELOQTALGNLKQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60

QY 61 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
Db 61 HPWYNDLLVDLGSKDAINKTKGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120

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QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
QY 181 RGLVFSHSGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYLYTT 233
Db 181 RGLVFSHSGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYLYTT 233

RESULT 4

US-09-900-766-7
; Sequence 7, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPRANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P0218USO:10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-900-766-7

Query Match 90.9%; Score 1107; DB 10; Length 233;
Best Local Similarity 89.7%; Pred. No. 7.9e-105;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLQIYYYNKAITSEKSDAQPLTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKSELOQTALGNLQIYYYNKAITSEKSDAQPLTLLFKGFFTG 60
QY 61 HPWYNDLLVLDGSAATSEYEGSSVDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 61 HPWYNDLLVLDGSAATSEYEGSSVDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNRLT 120
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
QY 181 RGLVFSHSGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYLYTT 233
Db 181 RGLVFSHSGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYLYTT 233

RESULT 5

US-10-283-838-8
; Sequence 8, Application US/10283838
; Publication No. US20030092894A1
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
; Johan Hansson, Terje Kalland, Lars
; Abrahamson and Goran Foraberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,838
FILING DATE: 30-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/695,692
FILING DATE: August 12, 1996
APPLICATION NUMBER: 9601245-5
FILING DATE: March 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Krieger, Paul E.
REGISTRATION NUMBER: 25,986
REFERENCE/DOCKET NUMBER: 41986/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-283-838-8

Query Match 90.9%; Score 1107; DB 14; Length 233;
Best Local Similarity 89.7%; Pred. No. 7.9e-105;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLQIYYYNKAITSEKSDAQPLTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKSELOQTALGNLQIYYYNKAITSEKSDAQPLTLLFKGFFTG 60
QY 61 HPWYNDLLVLDGSAATSEYEGSSVDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 61 HPWYNDLLVLDGSAATSEYEGSSVDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNRLT 120
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
QY 181 RGLVFSHSGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYLYTT 233
Db 181 RGLVFSHSGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYLYTT 233

RESULT 6

US-10-267-682-112
; Sequence 112, Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Belognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: US/10/267,682
 APPLICATION NUMBER: US/10/267,682
 FILING DATE: 08-Oct-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,223A
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7872-029
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 112:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 257 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 112:

US-10-267-682-112

Query Match 90.9%; Score 1107; DB 12; Length 257;
 Best Local Similarity 89.7%; Pred. No. 9.1e-105;
 Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELQGTALGNLQIYYYNKAITSEKSDQFLNTLLFKGFTG 60
 DB 25 SEKSEINEKDLRKSELQGNLQIYYYNKAITSEKSDQFLNTLLFKGFTG 84
 QY 61 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHNNRLT 120
 DB 85 HPWYNDLLVLDGSKATNKYKGGKVDLYGAYGYQCAGTGNKTCMYGGVTLHNNRLT 144
 QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
 DB 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204
 QY 181 RGLIVHSSSEGSTVSDLPDAQQYPTLLRIYRDNNTTSSLSISLYLTT 233
 DB 205 RGLIVHSSSEGSTVSDLPDAQQYPTLLRIYRDNNTTSSLSISLYLTT 257

RESULT 7
 US-10-267-748-112
 Sequence 112, Application US/10267748
 Publication No. US20040052820A1
 GENERAL INFORMATION:
 APPLICANT: Bolognesi, Dani P.
 Matthews, Thomas J.
 Wild, Carl T.
 Barney, Shawn O.
 Lambert, Dennis M.
 Petteway, Stephen R.
 Langlois, Alphonse J.
 TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
 MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
 TRANSMISSION
 NUMBER OF SEQUENCES: 239
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036-2711
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: US/10/267,748
 APPLICATION NUMBER: US/10/267,748
 FILING DATE: 08-Oct-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,223A
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7872-029
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE
 INFORMATION FOR SEQ ID NO: 112:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 257 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 112:

US-10-267-748-112

Query Match 90.9%; Score 1107; DB 12; Length 257;
 Best Local Similarity 89.7%; Pred. No. 9.1e-105;
 Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELQGTALGNLQIYYYNKAITSEKSDQFLNTLLFKGFTG 60
 DB 25 SEKSEINEKDLRKSELQGNLQIYYYNKAITSEKSDQFLNTLLFKGFTG 84
 QY 61 HPWYNDLLVLDGSTAATSEYEGSSVDLYGAYGYQCAGTGNKTCMYGGVTLHNNRLT 120
 DB 85 HPWYNDLLVLDGSKATNKYKGGKVDLYGAYGYQCAGTGNKTCMYGGVTLHNNRLT 144
 QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
 DB 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204
 QY 181 RGLIVHSSSEGSTVSDLPDAQQYPTLLRIYRDNNTTSSLSISLYLTT 233
 DB 205 RGLIVHSSSEGSTVSDLPDAQQYPTLLRIYRDNNTTSSLSISLYLTT 257

RESULT 8
 US-09-870-759-16
 Sequence 16, Application US/09870759
 Patent No. US20020177551A1
 GENERAL INFORMATION:
 APPLICANT: TERMAN, David S
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 FILE REFERENCE: 870759
 CURRENT APPLICATION NUMBER: US/09/870,759
 CURRENT FILING DATE: 2002-01-14
 PRIOR APPLICATION NUMBER: US 60/208,128
 PRIOR FILING DATE: 2000-05-30
 NUMBER OF SEQ ID NOS: 166
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 15
 LENGTH: 248
 TYPE: PRT
 ORGANISM: Staphylococcus aureus
 US-09-870-759-16

Query Match 88.0%; Score 1072; DB 9; Length 248;
 Best Local Similarity 90.2%; Pred. No. 3.3e-101;
 Matches 202; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

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QY 1 SEKSEINEKDLRKSELQGTALGNLKOIYYYNKAITSEKSDAQFLNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELQGTALGNLKOIYYYNKAITSEKSDAQFLNTLLFKGFFTG 84
QY 61 HPWNDDLVLGSLTAATSEYEGSSVDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HPWNDDLVLGSLTAATSEYEGSSVDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 BEKKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDQARHYLHGKFGLYNSDSFGKVKQ 180
Db 145 BEKKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDQARHYLHGKFGLYNSDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNNTTISSTSL 224
Db 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNNTTISSTSL 248

RESULT 9
US-09-751-708A-16
; Sequence 16, Application US/09751.708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751.708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 16
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-16

Query Match 88.0%; Score 1072; DB 10; Length 248;
Best Local Similarity 90.2%; Pred. No. 3.3e-101;
Matches 202; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELQGTALGNLKOIYYYNKAITSEKSDAQFLNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELQGTALGNLKOIYYYNKAITSEKSDAQFLNTLLFKGFFTG 84
QY 61 HPWNDDLVLGSLTAATSEYEGSSVDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HPWNDDLVLGSLTAATSEYEGSSVDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 BEKKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDQARHYLHGKFGLYNSDSFGKVKQ 180
Db 145 BEKKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDQARHYLHGKFGLYNSDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNNTTISSTSL 224
Db 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNNTTISSTSL 248

RESULT 10
US-09-900-766-4
; Sequence 4, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US010104199
; CURRENT APPLICATION NUMBER: US/09/900.766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: Patent in version 3.0
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; SEQ ID NO 4
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-900-766-4

Query Match 77.8%; Score 948; DB 10; Length 233;
Best Local Similarity 76.4%; Pred. No. 1.5e-88;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELQGTALGNLKOIYYYNKAITSEKSDAQFLNTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKSELQGTALGNLKOIYYYNKAITSEKSDAQFLNTLLFKGFFTG 60
QY 61 HPWNDDLVLGSLTAATSEYEGSSVDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 61 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNRLT 120
QY 121 BEKKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDQARHYLHGKFGLYNSDSFGKVKQ 180
Db 121 BEKKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDQARHYLHGKFGLYNSDSFGKVKQ 180
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNNTTISSTSLISLYLYTT 233
Db 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNNTTISSTSLISLYLYTT 233

RESULT 11
US-10-283-838-7
; Sequence 7, Application US/10283838
; Publication No. US20030092894A1
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
; Johan Haasson, Terje Kalland, Lars
; Abrahamson and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,838
; FILING DATE: 30-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,692
; FILING DATE: August 12, 1996
; APPLICATION NUMBER: 9601245-5
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 41996/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
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US-10-283-838-7

Query Match 77.8%; Score 948; DB 14; Length 233;
 Best Local Similarity 76.4%; Pred. No. 1.5e-88;
 Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDKRKSELOGTALGNLKOIYYNKAITSSEKSDAOFLLNTLLFKGFFTG 60
 DB 1 SEKSEINEKDKRKSELOGTALGNLKOIYYNKAITSSEKSDAOFLLNTLLFKGFFTG 60
 QY 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYYGQCAGGTPNKATCMYGGVTLHDNNRLT 120
 DB 61 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYYGQCAGGTPNKATCMYGGVTLHDNNRLT 120
 QY 121 BEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
 DB 121 BEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
 QY 181 RGLIVFHSSEGSVSYDLFDAQOQYPTLLRIYRDNNTTSSLSISLYLYTT 233
 DB 181 RGLIVFHTSTEPSVNYDLFGAQOQYNTLLRIYRDNKNTINSENHIDIYLYTS 233

RESULT 12

US-10-267-682-113
 ; Sequence 113, Application US/10267682
 ; Publication No. US2004003235A1
 ; GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
 Matthews, Thomas J.
 Wild, Carl T.
 Barney, Shawn O.
 Lambert, Dennis M.
 Petteway, Stephen R.
 Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
 MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
 TRANSMISSION

NUMBER OF SEQUENCES: 239
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036-2711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/267,682
 FILING DATE: 08-Oct-2002
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,223A
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7872-029
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 113:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 257 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: unknown
 MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 113:
 US-10-267-682-113

Query Match 77.8%; Score 948; DB 12; Length 257;
 Best Local Similarity 76.4%; Pred. No. 1.7e-88;
 Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDKRKSELOGTALGNLKOIYYNKAITSSEKSDAOFLLNTLLFKGFFTG 60
 DB 25 SEKSEINEKDKRKSELOGTALGNLKOIYYNKAITSSEKSDAOFLLNTLLFKGFFTG 84
 QY 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYYGQCAGGTPNKATCMYGGVTLHDNNRLT 120
 DB 61 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYYGQCAGGTPNKATCMYGGVTLHDNNRLT 144
 QY 121 BEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
 DB 145 BEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204
 QY 181 RGLIVFHSSEGSVSYDLFDAQOQYPTLLRIYRDNNTTSSLSISLYLYTT 233
 DB 205 RGLIVFHTSTEPSVNYDLFGAQOQYNTLLRIYRDNKNTINSENHIDIYLYTS 257

RESULT 13

US-10-267-748-113
 ; Sequence 113, Application US/10267748
 ; Publication No. US20040052820A1
 ; GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
 Matthews, Thomas J.
 Wild, Carl T.
 Barney, Shawn O.
 Lambert, Dennis M.
 Petteway, Stephen R.
 Langlois, Alphonse J.

TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
 MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
 TRANSMISSION

NUMBER OF SEQUENCES: 239
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10036-2711

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/267,748
 FILING DATE: 08-Oct-2002
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/08/484,223A
 FILING DATE: 07-JUN-1995
 ATTORNEY/AGENT INFORMATION:

NAME: Coruzzi, Laura A.
 REGISTRATION NUMBER: 30,742
 REFERENCE/DOCKET NUMBER: 7872-029
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 790-9090
 TELEFAX: (212) 869-9741/8864
 TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 113:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 257 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: unknown


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; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-267-748-113

Query Match      77.8%; Score 948; DB 12; Length 257;
Best Local Similarity 76.4%; Pred. No. 1.7e-88;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSEKSAQOFLNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESHQFLOHTILFKGFFTD 84

QY 61 HPWYNDLLVDLSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVQ 180
Db 145 EEKVPINLWLDGKQNTVPLETVTKNKQNTVOELDLQARRYLQEKYKLYNSDVDFGKVQ 204

QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQGYSNLTLRIYRDNKNTINSENHMDIYLYTS 257

RESULT 14
US-10-354-948-4
; Sequence 4, Application US/10354948
; Publication No. US20030202962A1
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; Elmslie, Robyn E.
; Potter, Terence A.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/354,948
; FILING DATE: 29-Jan-2003
; CLASSIFICATION DATA:
; APPLICATION NUMBER: US/08/580,806
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-29-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-354-948-4

Query Match      77.5%; Score 944; DB 12; Length 233;
Best Local Similarity 76.3%; Pred. No. 3.9e-88;
Matches 177; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-267-748-113

Query Match      77.8%; Score 948; DB 12; Length 257;
Best Local Similarity 76.4%; Pred. No. 1.7e-88;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSEKSAQOFLNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESHQFLOHTILFKGFFTD 84

QY 61 HPWYNDLLVDLSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVQ 180
Db 145 EEKVPINLWLDGKQNTVPLETVTKNKQNTVOELDLQARRYLQEKYKLYNSDVDFGKVQ 204

QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQGYSNLTLRIYRDNKNTINSENHMDIYLYTS 257

RESULT 15
US-09-870-759-8
; Sequence 8, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-8

Query Match      76.8%; Score 935; DB 9; Length 257;
Best Local Similarity 75.5%; Pred. No. 3.7e-87;
Matches 176; Conservative 21; Mismatches 36; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSEKSAQOFLNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESHQFLOHTILFKGFFTN 84

QY 61 HPWYNDLLVDLSTAAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVQ 180
Db 145 EEKVPINLWLDGKQNTVPLETVTKNKQNTVOELDLQARRYLQEKYKLYNSDVDFGKVQ 204

QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQGYSNLTLRIYRDNKNTINSENHMDIYLYTS 257

RESULT 16
US-09-751-708A-8
; Sequence 8, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patent in version 3.1
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```

; SEQ ID NO 8
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-8

Query Match          76.8%; Score 935; DB 10; Length 257;
Best Local Similarity 75.5%; Pred. No. 3.7e-87;
Matches 176; Conservative 21; Mismatches 36; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKSADQFLNTLLFKGFTG 60
Db 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHDFLOHTILFKGFTN 84

QY 61 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 120
Db 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 144

QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFLGYNDSFGGKVQ 180
Db 145 EEKKVPINLWLDGKQNTVPLETVTNKNVTVQELDQARRYLOEKYNLYNSDVDFGKVQ 204

QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYLTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQGQSNLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 17
US-10-002-784A-2
; Sequence 2, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 2
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin A periplasmic
US-10-002-784A-2

Query Match          75.9%; Score 925; DB 14; Length 257;
Best Local Similarity 75.1%; Pred. No. 4e-86;
Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKSADQFLNTLLFKGFTG 60
Db 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHDFLOHTILFKGFTD 84

QY 61 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 120
Db 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLT 144

QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFLGYNDSFGGKVQ 180
Db 145 EEKKVPINLWLDGKQNTVPLETVTNKNVTVQELDQARRYLOEKYNLYNSDVDFGKVQ 204

QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYLTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQGQSNLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 18
US-10-002-784A-4

```

```

; Sequence 4, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 4
; LENGTH: 233
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin A cytoplasmic
US-10-002-784A-4

Query Match          75.6%; Score 921; DB 14; Length 233;
Best Local Similarity 75.0%; Pred. No. 8.8e-86;
Matches 174; Conservative 21; Mismatches 37; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKSADQFLNTLLFKGFTGH 61
Db 2 EKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHDFLOHTILFKGFTDH 61

QY 62 PWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLTE 121
Db 62 SWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHNNRLTE 121

QY 122 EKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFLGYNDSFGGKVQ 181
Db 122 EKVPINLWLDGKQNTVPLETVTNKNVTVQELDQARRYLOEKYNLYNSDVDFGKVQ 181

QY 182 GLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNTTISSTLSISLYLTT 233
Db 182 GLIVFHTSTEPSVNYDLFGAQGQSNLLRIYRDNKTINSENHIDIYLYTS 233

RESULT 19
US-08-882-431-2
; Sequence 2, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRCM -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

```

```

; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-2

Query Match 74.5%; Score 908; DB 8; Length 257;
Best Local Similarity 74.2%; Pred. No. 2.2e-84;
Matches 173; Conservative 21; Mismatches 39; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSEKQGTALGNLKOIYYNSKAITSEKSDAQFLTNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSEKQGTALGNLKOIYYNEKAKTENKESHDPQROHTLLFKGFFTD 84
QY 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVRFDSKDIVDKYKKGKVDLYGAYGYQCAGGTFNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 145 EEKVPINLWDGKQNTVPIDKVTSKKNTVQELDLQARHYLHGKFGLYNSDSVDFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQGYSTNLLRIYRDNNTINSENHIDIYLYTS 257

RESULT 20
US-08-882-431-4
; Sequence 4, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Ulrich
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRCM -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-4

Query Match 74.1%; Score 903; DB 8; Length 233;
Best Local Similarity 73.7%; Pred. No. 6.1e-84;
Matches 171; Conservative 21; Mismatches 40; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSEKQGTALGNLKOIYYNSKAITSEKSDAQFLTNTLLFKGFFTG 61
Db 2 EKSEINEKDLRKSEKQGTALGNLKOIYYNEKAKTENKESHDPQROHTLLFKGFFTDH 61
QY 62 PWYNDLLVLDGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
Db 62 SWYNDLLVRFDSKDIVDKYKKGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
QY 122 EEKVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 181
Db 122 EEKVPINLWDGKQNTVPIDKVTSKKNTVQELDLQARHYLHGKFGLYNSDSVDFGKVAR 181
QY 182 GLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYLYTT 233
Db 182 GLIVFHTSTEPSVNYDLFGAQGYSTNLLRIYRDNNTINSENHIDIYLYTS 233

RESULT 21
US-09-870-759-14
; Sequence 14, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 14
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-14

Query Match 50.2%; Score 611; DB 9; Length 258;
Best Local Similarity 51.1%; Pred. No. 5.7e-54;
Matches 118; Conservative 35; Mismatches 78; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSEKQGTALGNLKOIYYNSKAITSEKSDAQFLTNTLLFKGFFTG 60
Db 26 NENIDSVKEKELHKSEKSSALNNMKHSYADKNPIIGENKSTGQDFLENTLLYKFFTD 85
QY 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 86 LNFEDLLINFNSKEMAOHFKSKNVDPYPIRINCYGGEIDRTACTYGGVTPHGNK 145
QY 121 EEKVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 146 ERKTFPINLWINGVQKESVLDKVTDKKNTVQELDLQARHYLHGKFGLYNSDNLGG 205
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISSTLSISLYLY 231
Db 206 RGLIEFSDSDGSKVSYDLFDVKGDFPEKQLRIYSDNKTILSTEHLHIDIYLY 256

RESULT 22
US-09-751-708A-14
```


Matches 77; Conservative 45; Mismatches 96; Indels 19; Gaps 10;
 QY 4 SBEINEKDLRKSELOGTALGNLKOIYY-YNSKAIT-SSEKSAQOFTNTLLFKGFTTG 60
 DB 25 SQEFAQQDPDPSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHLIYN--VS 81
 QY 61 HPWYNDLLVDLGSTAATSSEYSGSSVDLYGAYGYOC-AGGTENKTACMYGGVTLHDNNRL 119
 DB 82 GPNYDKLKTTELKNQENWATLFDKQNDIYGVETIYHLCYLCENABRSACIYGGVTHNEGHL 141
 QY 120 TBEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKV 179
 DB 142 EIPKKIWKVSDIGIQ-SLSFD-IETNKQWTAQELDKVKRYLTDNKQLYNGP--SKY 197
 QY 180 QRLIVFHSSEGSTVSIDLFD-----AQGYPTTLRIYRDNTTISSTLSLSLYLT 232
 DB 198 ETGYIKFIPKNKESFWDFPEFETQSKY----LMIYKONETLDSNTSQIEVLYLT 250
 RESULT 29
 US-09-870-759-10
 ; Sequence 10, Application US/09870759
 ; Patent No. US20020177551A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TERMAN, David S
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 ; FILE REFERENCE: 870759
 ; CURRENT APPLICATION NUMBER: US/09/870,759
 ; CURRENT FILING DATE: 2002-01-14
 ; PRIOR APPLICATION NUMBER: US 60/208,128
 ; PRIOR FILING DATE: 2000-05-30
 ; NUMBER OF SEQ ID NOS: 166
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 266
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-870-759-10

Query Match 22.0%; Score 268.5; DB 9; Length 266;
 Best Local Similarity 31.6%; Pred. No. 7e-19;
 Matches 77; Conservative 44; Mismatches 104; Indels 19; Gaps 8;
 QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSAQOFTNTLLFKGFTTG 60
 DB 27 AESQDPKPEDELHKSFKFTG-LMENMK-VLYDDNHVSAINVKSIDQFLYFLDIYSIKDTK 84
 QY 61 HPWYNDLLVDLGSTAATSSEYSGSSVDLYGAYGYOC-----AGGTENKTACMYGG 110
 DB 85 LGYNDVNRVEFKNLDADKYKVDVFGANYYYQCYFSKKTNDINSHQTDKKTCTMYGG 144
 QY 111 VTLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLY 170
 DB 145 VTEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAEQLDYLTRHYLVKNKKLY 202
 QY 171 NSDSFGGKVQRLIVFHSSEGSTVSIDLFDQAQGYPD--TLRIYRDNTTISSTLSLSL 228
 DB 203 EFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFDQSKYLMYNDNKNVDSKDVKIEV 259
 QY 229 YLYT 232
 DB 260 YLYT 263
 ; LENGTH: 266
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-870-759-10
 Query Match 22.0%; Score 268.5; DB 9; Length 266;
 Best Local Similarity 31.6%; Pred. No. 7e-19;
 Matches 77; Conservative 44; Mismatches 104; Indels 19; Gaps 8;
 QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSAQOFTNTLLFKGFTTG 60
 DB 27 AESQDPKPEDELHKSFKFTG-LMENMK-VLYDDNHVSAINVKSIDQFLYFLDIYSIKDTK 84
 QY 61 HPWYNDLLVDLGSTAATSSEYSGSSVDLYGAYGYOC-----AGGTENKTACMYGG 110
 DB 85 LGYNDVNRVEFKNLDADKYKVDVFGANYYYQCYFSKKTNDINSHQTDKKTCTMYGG 144
 QY 111 VTLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLY 170
 DB 145 VTEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAEQLDYLTRHYLVKNKKLY 202
 QY 171 NSDSFGGKVQRLIVFHSSEGSTVSIDLFDQAQGYPD--TLRIYRDNTTISSTLSLSL 228
 DB 203 EFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFDQSKYLMYNDNKNVDSKDVKIEV 259
 QY 229 YLYT 232
 DB 260 YLYT 263
 ; LENGTH: 266
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-870-759-10

CURRENT FILING DATE: 2002-10-15
 PRIOR APPLICATION NUMBER: US 60/173,371
 PRIOR FILING DATE: 1999-12-28
 NUMBER OF SEQ ID NOS: 166
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 10
 LENGTH: 266
 TYPE: PRT
 ORGANISM: Staphylococcus aureus
 US-09-751-708A-10
 Query Match 22.0%; Score 268.5; DB 10; Length 266;
 Best Local Similarity 31.6%; Pred. No. 7e-19;
 Matches 77; Conservative 44; Mismatches 104; Indels 19; Gaps 8;
 QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSAQOFTNTLLFKGFTTG 60
 DB 27 AESQDPKPEDELHKSFKFTG-LMENMK-VLYDDNHVSAINVKSIDQFLYFLDIYSIKDTK 84
 QY 61 HPWYNDLLVDLGSTAATSSEYSGSSVDLYGAYGYOC-----AGGTENKTACMYGG 110
 DB 85 LGYNDVNRVEFKNLDADKYKVDVFGANYYYQCYFSKKTNDINSHQTDKKTCTMYGG 144
 QY 111 VTLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLY 170
 DB 145 VTEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAEQLDYLTRHYLVKNKKLY 202
 QY 171 NSDSFGGKVQRLIVFHSSEGSTVSIDLFDQAQGYPD--TLRIYRDNTTISSTLSLSL 228
 DB 203 EFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFDQSKYLMYNDNKNVDSKDVKIEV 259
 QY 229 YLYT 232
 DB 260 YLYT 263
 ; LENGTH: 266
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-751-708A-10

RESULT 31
 US-09-150-947B-12
 ; Sequence 12, Application US/09150947B
 ; Patent No. US20020028211A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaempfer, Raymond
 ; APPLICANT: Arad, Gila
 ; TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
 ; TITLE OF INVENTION: ANTAGONISTS AND VACCINES
 ; FILE REFERENCE: A31967-PCT-USA-A
 ; CURRENT APPLICATION NUMBER: US/09/150,947B
 ; CURRENT FILING DATE: 1998-09-10
 ; PRIOR APPLICATION NUMBER: PCT/IL97/00438
 ; PRIOR FILING DATE: 1997-12-30
 ; PRIOR APPLICATION NUMBER: ISRAEL 119938
 ; PRIOR FILING DATE: 1996-12-30
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 12
 ; LENGTH: 239
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-150-947B-12
 Query Match 22.0%; Score 267.5; DB 9; Length 239;
 Best Local Similarity 31.7%; Pred. No. 7.6e-19;
 Matches 77; Conservative 43; Mismatches 104; Indels 19; Gaps 8;
 QY 2 EKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSAQOFTNTLLFKGFTTG 61
 DB 1 ESQDPKPEDELHKSFKFTG-LMENMK-VLYDDNHVSAINVKSIDQFLYFLDIYSIKDTK 58
 QY 62 PWYNDLLVDLGSTAATSSEYSGSSVDLYGAYGYOC-----AGGTENKTACMYGG 111
 DB 59 GYNDVNRVEFKNLDADKYKVDVFGANYYYQCYFSKKTNDINSHQTDKKTCTMYGG 118
 QY 112 TLDHNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLY 171

Db 119 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAAQELDYLTRHYLVNKKLYE 176
Qy 172 SDSFGGKVQRLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNNTTISSTLSISLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMMAPGDKFDQSKYLMYNDNKWVDSKDVKIEVY 233
Qy 230 LYT 232
Db 234 LTT 236

RESULT 32
US-10-172-425B-12
; Sequence 12, Application US/10172425B
; Publication No. US20030147908A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Atad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
; TITLE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
; FILE REFERENCE: A31967-PCT-USA-A-A 066031.0164
; CURRENT APPLICATION NUMBER: US/10/172,425B
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 09/150,947
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-172-425B-12

Query Match 22.0%; Score 267.5; DB 14; Length 239;
Best Local Similarity 31.7%; Pred. No. 7.6e-19;
Matches 77; Conservative 43; Mismatches 104; Indels 19; Gaps 8;
Qy 2 EKSEINEKDLRKSELOQTALGNLKIYYNKAITSSEKSADQFLNTLLFKGFFTGH 61
Db 1 ESQDPKPDDELHKSSKFTG-LMENMK-VLYDDNHVSAINVKSIDQFLYDLIYSIKDTKL 58
Qy 62 PWYNDLLVDLGS"AAATSEYEGSSVDLYGAYGYQC-----AGGTENKTACMYGV 111
Db 59 GNYDNRVVEFNKDLADKYDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTMYGV 118
Qy 112 TLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLOARHYLHGKFLYN 171
Db 119 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAAQELDYLTRHYLVNKKLYE 176
Qy 172 SDSFGGKVQRLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNNTTISSTLSISLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMMAPGDKFDQSKYLMYNDNKWVDSKDVKIEVY 233
Qy 230 LYT 232
Db 234 LTT 236

RESULT 33
US-10-354-948-2
; Sequence 2, Application US/10354948
; Publication No. US20030202962A1
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; Elmslie, Robyn E.
; Potter, Terence A.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/354,948
FILING DATE: 29-Jan-2003
CLASSIFICATION: 424
PRIOR APPLICATION NUMBER:
APPLICATION NUMBER: US/08/580,806
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-29-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-354-948-2

Query Match 22.0%; Score 267.5; DB 12; Length 255;
Best Local Similarity 31.7%; Pred. No. 8.3e-19;
Matches 77; Conservative 43; Mismatches 104; Indels 19; Gaps 8;
Qy 2 EKSEINEKDLRKSELOQTALGNLKIYYNKAITSSEKSADQFLNTLLFKGFFTGH 61
Db 17 ESQDPKPDDELHKSSKFTG-LMENMK-VLYDNRVVEFNKDLADKYDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTMYGV 134
Qy 62 PWYNDLLVDLGS"AAATSEYEGSSVDLYGAYGYQC-----AGGTENKTACMYGV 111
Db 75 GNYDNRVVEFNKDLADKYDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTMYGV 134
Qy 112 TLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLOARHYLHGKFLYN 171
Db 135 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAAQELDYLTRHYLVNKKLYE 192
Qy 172 SDSFGGKVQRLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNNTTISSTLSISLY 229
Db 193 FNN--SPYETGYIKFIENENS-FWYDMMAPGDKFDQSKYLMYNDNKWVDSKDVKIEVY 249
Qy 230 LYT 232
Db 250 LTT 252

RESULT 34
US-08-892-431-16
; Sequence 16, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran

```
STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 251
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431-16

Query Match 21.6%; Score 263.5; DB 8; Length 251;
Best Local Similarity 32.1%; Pred. No. 2.1e-18;
Matches 76; Conservative 45; Mismatches 97; Indels 19; Gaps 10;

QY 4 SBEINEKDLRKSELGQTAL-GNLKQIYY-YNSKAIT-SSEKSAQDFLTNTLLFKGFFTG 60
Db 25 SQEVAQQDPDPQSRLHRSLSVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYN--VS 81

QY 61 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQC-AGGTPNKTCMYGGVTLHDNNRL 119
Db 82 GPNYDKLTTELKNOEMATLFDKKNVDIYGVEYVHLCYLCEAERSACIYGGVTNHEGNHL 141

QY 120 TEEKKVPINLWDGKQTTVPIDKVTSKKEVTQVQELDQARHYLHGKFLGYNDSFGGKV 179
Db 142 EIPKKIIVKVSIDGIQ-SLSFD-IETNKQWTAQELDYKVRKYLTDNKQLYTNGP--SKY 197

QY 180 QRGLIVFHSSEGSTVSVDLFD----AQGOYPTLLRIYRDNTTISSTLSISLYLT 232
Db 198 ETGYIKFIPKNKESFWDFPEPEFTQSKY----LMIYKDNETLDSNTSQIEVILTT 250

RESULT 35
US-10-002-784A-16
; Sequence 16, Application US/10002784A
; Publication No. US2003036644A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 16
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Artificial sequence

STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/870,759
FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: Patent in version 3.1
SEQ ID NO 12
LENGTH: 266
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-870-759-12

Query Match 21.6%; Score 263.5; DB 9; Length 266;
Best Local Similarity 30.6%; Pred. No. 2.3e-18;
Matches 75; Conservative 45; Mismatches 104; Indels 21; Gaps 9;

QY 1 SEKSEINEKDLRKSELGQTALGNLQIYY--YNSKAITSSSEKSAQDFLTNTLLFKGFF 58
Db 27 AESQDPPTPDELHAKSKFTG-LMENMKVLYDDHYVS---ATKVKSVDFKLAHDLITNISD 82

QY 59 TGHFWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQC-----AGGTPNKTCMYGGV 111
Db 83 KKLKNYDKVTTELNEGLAKYKDEVDVYVYNSYVYVYVYVYVYVYVYVYVYVYVYVYVYV 142

QY 112 TLHDNNRLTEE--KKVPINLWDGKQTTVPIDKVTSKKEVTQVQELDQARHYLHGKFLG 169
Db 143 TRHEGNHFDNGNLQNYLIRY-ENKENT-SFE-VQTDKSVTAQELDIKARPLINKKWL 200

QY 170 YNSDSFGGKVQRGLIVFHSSEGSTVSVDLFDQAQGYPD--TLRIYRDNTTISSTLSIS 227
Db 201 YFNPS--SPYETGYIKFIEENNGTTFWDMWMPAGDFKQSKILMYNDNKTVDSKSVKIE 258

QY 228 LYLYT 232
Db 259 VHLTT 263

RESULT 37
US-09-751-708A-12
; Sequence 12, Application US/09751708A
```



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; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 10
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Mutant staphylococcal enterotoxin B cytoplasmic
; US-10-002-784A-10.

Query Match      21.0%; Score 255.5; DB 14; Length 239;
Best Local Similarity 32.1%; Pred. No. 1.3e-17;
Matches 75; Conservative 41; Mismatches 99; Indels 19; Gaps 8;

QY 11 DLRKSELOGTALGNLQKQIYYNNKAITSSSEKSDAQFLTNLLFKGFTGHPWINDLLVD 70
DB 10 ELHKSFKFTG-LMENMK-VLYDDNHVSAINVKSIDQFRYFDLIYSIKDTKLGNVDNRVE 67
QY 71 LGSTAATSEYEGSSVDLYGAYGYOCAGG-----TNNKTACMYGGVTLHDNNRLT 120
DB 68 FKXKLADIKYKVDVFGANNAYQCARSKTNDINSHQTKRKTCKMYGGVTEHNGQLD 127
QY 121 BEKKVPINLWIDGKQTPIDPKVTSKKEVTVQELDLQARHYLHGKFGLYNSDGGKQV 180
DB 128 KYRSITRVFEDGK-NLLSFD-VQTNKKKVTQAQLDYLTRHYLVKNKKLYEFNN--SPYE 183
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNTTISSTLSLSLYLT 232
DB 184 TGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNRWVDSDKDVKIEVYLT 236

RESULT 41
US-08-882-431-14
; Sequence 14, Application US/08882431
; Publication No. US2003009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065

```

```

; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431-14

Query Match      21.0%; Score 255.5; DB 8; Length 266;
Best Local Similarity 30.2%; Pred. No. 1.5e-17;
Matches 74; Conservative 45; Mismatches 105; Indels 21; Gaps 9;

QY 1 SEKSEINEKDLRKSELOGTALGNLQKQIYYNNKAITSSSEKSDAQFLTNLLFKGFF 58
DB 27 AESQDPPTDELHKASKFTG-LMENMKVLYDDHYVS---ATKVKSVDKFRAHDLIYNISD 82
QY 59 TGHFWYNDLLDLGSTAATSEYEGSSVDLYGAYGYQC-----AGTPTNKTCMYGGV 111
DB 83 KKLKNYDKVKTTELLNEGLAKYKDEVDVYGSYYNVCYFSSKDNVKGVTGGTCMYGGI 142
QY 112 TLHDNNRLTEE--KKVPINLWIDGKQTPIDPKVTSKKEVTVQELDLQARHYLHGKFG 169
DB 143 TKHEGNHFDNGNLQNLVIRVY-ENKENTISFE-VQTDKKSVTQAQLDIKARNFINKKNL 200
QY 170 YNSDSFGGKVGQRLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNTTISSTLS 227
DB 201 YEFNS--SFYETGYIKFIENNGNTFWYDMPAPGDKFDQSKYLMYNDNRWVDSDK 258
QY 228 LYLTY 232
DB 259 VHLTT 263

RESULT 42
US-10-002-784A-14
; Sequence 14, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 14
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: staphylococcal enterotoxin C-1 mutant
; US-10-002-784A-14

Query Match      21.0%; Score 255.5; DB 14; Length 266;
Best Local Similarity 30.2%; Pred. No. 1.5e-17;
Matches 74; Conservative 45; Mismatches 105; Indels 21; Gaps 9;

QY 1 SEKSEINEKDLRKSELOGTALGNLQKQIYYNNKAITSSSEKSDAQFLTNLLFKGFF 58
DB 27 AESQDPPTDELHKASKFTG-LMENMKVLYDDHYVS---ATKVKSVDKFRAHDLIYNISD 82
QY 59 TGHFWYNDLLDLGSTAATSEYEGSSVDLYGAYGYQC-----AGTPTNKTCMYGGV 111
DB 83 KKLKNYDKVKTTELLNEGLAKYKDEVDVYGSYYNVCYFSSKDNVKGVTGGTCMYGGI 142
QY 112 TLHDNNRLTEE--KKVPINLWIDGKQTPIDPKVTSKKEVTVQELDLQARHYLHGKFG 169
DB 143 TKHEGNHFDNGNLQNLVIRVY-ENKENTISFE-VQTDKKSVTQAQLDIKARNFINKKNL 200

```

QY 170 YNSDFGKVGORGLIVFHSSEGSTVSVDLFDAGQGYD--TLRIYRDNTTISTSLIS 227
DB 201 YEFNS--SFYETGYIKFIENNGNTFWYDMPAPGDKFDQSKYLMYVNDNKTVDKSKVIE 258
QY 228 YLYT 232
DB 259 VHLT 263

RESULT 43
US-08-882-431-10
; Sequence 10, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-10

Query Match 20.9%; Score 254.5; DB 8; Length 239;
Best Local Similarity 32.1%; Pred. No. 1.6e-17;
Matches 75; Conservative 41; Mismatches 99; Indels 19; Gaps 8;

QY 11 DLKRSSELOGTALGNLKOIYYNSKAITSSSEKSDQFLNTLLPKGFTTGHPPVNDLLVD 70
DB 10 ELHSSKFTG-KMENMK-VLYDDNHVSAINVKSIDQFYFDLIYSIKDTKLGNVNVNVE 67
QY 71 LGSTAATSEYEGSSVDLYGAYGYCCAGG-----TPNKTCMYGGVTLHDNNRLT 120
DB 68 FKNKDLADKYDKYVDFGANAYYQCAFSSKKTNDINSHQTDKRTCMYGVTEHNGNOLD 127
QY 121 EEKVPINLWDGQTTVPIDKVTSKKEVTVOELDLQARHYLHGKGLYNSDSFGKQV 180
DB 128 KYRSITVRVFDGK-NLISFD-VQNKXKVTQAQELDYLRHYLVKDKLYEFNN--SPYE 183
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYD--TLRIYRDNTTISTSLISLYLT 232

DB 184 TGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYVNDNKNQVDSKQVIEVILTT 236

RESULT 44
US-10-002-784A-8
; Sequence 8, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 8
; LENGTH: 266
; TYPE: PRI
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin B periplasmic
US-10-002-784A-8

Query Match 20.6%; Score 250.5; DB 14; Length 266;
Best Local Similarity 30.7%; Pred. No. 4.9e-17;
Matches 75; Conservative 43; Mismatches 107; Indels 19; Gaps 8;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSDQFLNTLLPKGFTT 60
DB 27 AESQDPKPEDELHKSSKFTG-LMENMK-VLYDDNHVSAINVKSIDQFYFDLIYSIKDTK 84
QY 61 HPWYNDLLVDLSTAAATSEYEGSSVDLYGAYGYCCAGG-----TPNKTCMYGG 110
DB 85 LGNYDNVRVEFFNKDLADKYDKYVDFGANAYYQCAFSSKKTNDINSHQTDKRTCMYGG 144
QY 111 VTLHDNNRLTEEEKVPINLWDGQTTVPIDKVTSKKEVTVOELDLQARHYLHGKGLY 170
DB 145 VTEHNGNQLDKYRSITVRVFDGK-NLISFD-VQNKXKVTQAQELDYLRHYLVKNKKLY 202
QY 171 NSDSFGKVGORGLIVFHSSEGSTVSVDLFDAGQGYD--TLRIYRDNTTISTSLISL 228
DB 203 EFNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYVNDNKNQVDSKQVIEV 259
QY 229 YLYT 232
DB 260 YLT 263

RESULT 45
US-08-882-431-6
; Sequence 6, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 265
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431-6

Query Match 20.3%; Score 247; DB 8; Length 265;
Best Local Similarity 29.5%; Pred. No. 1.1e-16;
Matches 72; Conservative 43; Mismatches 109; Indels 20; Gaps 7;
QY 1 SEKSEINBKDLRKSELOQTALGNLKOIYYNKAITSSEKSAOQFLNTLLFKGFTG 60
Db 27 AESQDPKPELHKSKFTG--TGLMEDMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTK 84
QY 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYOC-----AGTPTNKTCMYGG 110
Db 85 LGDYDNVRVFEKNLADKYKIVDFGANYVQCAFSSKKTNDINSHQTDKRTCMYGG 144
QY 111 VTLDHNNRLTEKKVPINLWIDGKQTPIDKVKTSKKEVTVOELDQARHYLHGKFGLY 170
Db 145 VTEHNGNQLDKYRSITVRVFEDEK-NLLSFD-VQYNNKKVTAQELDYLTRHYLVKNKKLY 202
QY 171 NSDSFGKVGQRLIVHSSSEGSTVSVDLEDAOQ--YPTLLRIYRDNTTISSTLSISL 228
Db 203 EFNN--SPYETGYIKF--TENQNFYDMMFAPGDKFAOSKLYLMYNDNMVDSKDVKLEV 258
QY 229 YLYT 232
Db 259 YLTT 262

RESULT 46
US-08-882-431-8
Sequence 8, Application US/08882431
Publication No. US20030009015A1
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
NUMBER OF INVENTIONS: Vaccines
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: John Moran
STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 265
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431-8

Query Match 20.0%; Score 244; DB 8; Length 265;
Best Local Similarity 29.9%; Pred. No. 2.2e-16;
Matches 73; Conservative 43; Mismatches 108; Indels 20; Gaps 8;
QY 1 SEKSEINBKDLRKSELOQTALGNLKOIYYNKAITSSEKSAOQFLNTLLFKGFTG 60
Db 27 AESQDPKPELHKSKFTG-LMENKK-VLYDDNHVSAINVKSIDQFRYFDLIYSIKDTK 84
QY 61 HPWYNDLLVLDGTAATSEYEGSSVDLYGAYGYOCAGG-----TPNKTACMYGG 110
Db 85 LGDYDNVRVFEKNLADKYKIVDFGANYVQCAFSSKKTNDINSHQTDKRTCMYGG 144
QY 111 VTLDHNNRLTEKKVPINLWIDGKQTPIDKVKTSKKEVTVOELDQARHYLHGKFGLY 170
Db 145 VTEHNGNQLDKYRSITVRVFEDEK-NLLSFD-VQYNNKKVTAQELDYLTRHYLVKNKKLY 202
QY 171 NSDSFGKVGQRLIVHSSSEGSTVSVDLEDAOQYDP--TLRIYRDNTTISSTLSISL 228
Db 203 EFNN--SPYETGYIKF--TENQNFYDMMFAPGDKFDQSKYLMYNDNMVDSKDVKLEV 258
QY 229 YLYT 232
Db 259 YLTT 262

RESULT 47
US-10-002-784A-26
Sequence 26, Application US/10002784A
Publication No. US20030036644A1
GENERAL INFORMATION:
/33
APPLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 26
LENGTH: 220
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: mutant streptococcal pyrogenic exotoxin-A
US-10-002-784A-26

Query Match 18.5%; Score 225.5; DB 14; Length 220;
Best Local Similarity 31.6%; Pred. No. 1.3e-14;

Matches 71; Conservative 43; Mismatches 90; Indels 21; Gaps 12;
Qy 16 SELOGTAL-GNLKQIYY-YNSKAIT-SSEKSAQDLNTLLFKGFFTGHPWYNDLLVDLG 72
Db 8 SOLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYN---VSGPNYDKLKTLEK 64
Qy 73 STAATSEYEGSSVDLYGAYGYQC-AGTPTNKTCACMYGGVTLHDNNRLTEBEKVPINLWI 131
Db 65 NQEMATLFPKDNIDYGVVEYHLCYLCEAERSACI-GGVNREGNHLIPEPKIIVKVS 123
Qy 132 DGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQGLIVFHSSEG 191
Db 124 DGIO-SLSFD-IETNKKWMTAQELDYKVRKYLTDNKLQYINGP--SKYETGYIKFIPKNK 179
Qy 192 STVSVDLFD----AQGYPDTLRLIYRDNTTISSTLSISLYLT 232
Db 180 ESFWDFPFPEFTQSKY----LMIYKDNETLDSNT-QIEVLYLT 219

RESULT 48
US-10-002-784A-27
; Sequence 27, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
/33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002.784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 27
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant SpeA-mutant SpeB fusion
US-10-002-784A-27

Query Match 18.5%; Score 225.5; DB 14; Length 468;
Best Local Similarity 31.6%; Pred. No. 4e-14;
Matches 71; Conservative 43; Mismatches 90; Indels 21; Gaps 12;
Qy 16 SELOGTAL-GNLKQIYY-YNSKAIT-SSEKSAQDLNTLLFKGFFTGHPWYNDLLVDLG 72
Db 8 SOLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLRSHDLIYN---VSGPNYDKLKTLEK 64
Qy 73 STAATSEYEGSSVDLYGAYGYQC-AGTPTNKTCACMYGGVTLHDNNRLTEBEKVPINLWI 131
Db 65 NQEMATLFPKDNIDYGVVEYHLCYLCEAERSACI-GGVNREGNHLIPEPKIIVKVS 123
Qy 132 DGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQGLIVFHSSEG 191
Db 124 DGIO-SLSFD-IETNKKWMTAQELDYKVRKYLTDNKLQYINGP--SKYETGYIKFIPKNK 179
Qy 192 STVSVDLFD----AQGYPDTLRLIYRDNTTISSTLSISLYLT 232
Db 180 ESFWDFPFPEFTQSKY----LMIYKDNETLDSNT-QIEVLYLT 219

RESULT 49
US-09-870-759-20
; Sequence 20, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14

; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-870-759-20
Query Match 18.1%; Score 220; DB 9; Length 250;
Best Local Similarity 28.9%; Pred. No. 5.9e-14;
Matches 66; Conservative 42; Mismatches 98; Indels 22; Gaps 9;
Qy 14 KXSELQGTALGNLKQIYY-YNSKAITTSSE--KSAQDLNTLLFKGFFTGHPWYNDLLVD 70
Db 35 KPSQLQRSNLVKTFKIYFFMRVTLVTHENVKSDQLLSHDLIYN---VSGPNYDKLKT 91
Qy 71 LGSTAATSEYEGSSVDLYGAYGYQC-AGTPTNKTCACMYGGVTLHDNNRLTEBEKVPINL 129
Db 92 LKQEMATLFPKDNIDYGVVEYHLCYLCEAERSACIYGGVTHNEGNHLEIPKKIIVKV 151
Qy 130 WIDGKQT-TVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQGLIVFHS 188
Db 152 SIDGIQSLSFIDIEQIKNG---NCSRIISYTVRKYLTDNKLQYINGP--SKYETGYIKFIP 205
Qy 189 SEGSTVSVDLFD----AQGYPDTLRLIYRDNTTISSTLSISLYLT 232
Db 206 KKNESFWDFPFPEFTQSKY----LMIYKDNETLDSNTSQIEVLYLT 249

RESULT 50
US-09-751-708A-20
; Sequence 20, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-751-708A-20

Query Match 18.1%; Score 220; DB 10; Length 250;
Best Local Similarity 28.9%; Pred. No. 5.9e-14;
Matches 66; Conservative 42; Mismatches 98; Indels 22; Gaps 9;
Qy 14 KXSELQGTALGNLKQIYY-YNSKAITTSSE--KSAQDLNTLLFKGFFTGHPWYNDLLVD 70
Db 35 KPSQLQRSNLVKTFKIYFFMRVTLVTHENVKSDQLLSHDLIYN---VSGPNYDKLKT 91
Qy 71 LGSTAATSEYEGSSVDLYGAYGYQC-AGTPTNKTCACMYGGVTLHDNNRLTEBEKVPINL 129
Db 92 LKQEMATLFPKDNIDYGVVEYHLCYLCEAERSACIYGGVTHNEGNHLEIPKKIIVKV 151
Qy 130 WIDGKQT-TVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQGLIVFHS 188
Db 152 SIDGIQSLSFIDIEQIKNG---NCSRIISYTVRKYLTDNKLQYINGP--SKYETGYIKFIP 205
Qy 189 SEGSTVSVDLFD----AQGYPDTLRLIYRDNTTISSTLSISLYLT 232
Db 206 KKNESFWDFPFPEFTQSKY----LMIYKDNETLDSNTSQIEVLYLT 249

RESULT 51

```

US-10-002-784A-33
; Sequence 33, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 33
; LENGTH: 82
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin D
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-33

Query Match      15.9%; Score 194; DB 14; Length 82;
Best Local Similarity 45.1%; Pred. No. 5.5e-12;
Matches 37; Conservative 13; Mismatches 32; Indels 0; Gaps 0;

QY 43 SADOFLNTLLFKGFTGHPWYNDLLVLDLSTAATSEYEGSSVDLYGAYGYQCAGGTGN 102
Db      1 TGDQFLENTLLYKFTDILNFDLLNENSKMAQHFKSKNDVYPIRYSINCYGGID 60

QY 103 KTACMTGGVTLHDNNRLTEKK 124
Db      61 RTACTYGGVTPHEGNLKERKK 82

RESULT 52
US-09-308-829-2
; Sequence 2, Application US/09308829
; Publication No. US20020039585A1
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Ohlendorf, Douglas
; APPLICANT: Mitchell, David T.
; APPLICANT: Gahr, Pamela J.
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN C AND METHODS OF USE
; FILE REFERENCE: 600.347USW0
; CURRENT APPLICATION NUMBER: US/09/308,829
; CURRENT FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: PCT/US97/22125
; PRIOR FILING DATE: 1997-12-05
; PRIOR APPLICATION NUMBER: US 60/033,251
; PRIOR FILING DATE: 1996-12-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-308-829-2

Query Match      12.8%; Score 155.5; DB 12; Length 235;
Best Local Similarity 24.2%; Pred. No. 2.2e-07;
Matches 57; Conservative 37; Mismatches 77; Indels 65; Gaps 11;

QY 47 FLNTLLFKGFTGH-----PW-YNDLLVDLGSTAA-----TSE 79
Db 11 FITVILISTYFTYHQSDSKDISNVKSDLLYATITPYDKDCRVNFSTHTLNIDTQK 70

QY 80 YEGSS-----VDLYGAYGYQCAGGTGNKTACMYGGVTLHDNNRL 119
Db 71 YRGKDYIISSEMSYEASQKFKRDDHVDVFLGFLYILNSHTG-----EYIYGGITPAQNNKV 125

QY 120 TEEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFLYNSDS--FGG 177
Db 126 NH--KLGNLFISSGSOQNLNNKILLEKDIIVTQEDIFKIRKYLMDNYKIYDATSPVSG 183

QY 178 KVQKGLIVFHSSEGSTVSYDLFDA--QGQYPTDLLRIYRDNNTTISSTLS--ISLYL 230
Db 184 RIEIG-----TKDGKHEQIDLFDSPEGTRSDIFAK-YKDNRIINMKNFHFHDYIL 233

RESULT 54
US-10-002-784A-39
; Sequence 39, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
US-10-002-784A-39

Query Match      12.8%; Score 155.5; DB 12; Length 235;
Best Local Similarity 24.2%; Pred. No. 2.2e-07;
Matches 57; Conservative 37; Mismatches 77; Indels 65; Gaps 11;

QY 47 FLNTLLFKGFTGH-----PW-YNDLLVDLGSTAA-----TSE 79
Db 11 FITVILISTYFTYHQSDSKDISNVKSDLLYATITPYDKDCRVNFSTHTLNIDTQK 70

QY 80 YEGSS-----VDLYGAYGYQCAGGTGNKTACMYGGVTLHDNNRL 119
Db 71 YRGKDYIISSEMSYEASQKFKRDDHVDVFLGFLYILNSHTG-----EYIYGGITPAQNNKV 125

QY 120 TEEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFLYNSDS--FGG 177
Db 126 NH--KLGNLFISSGSOQNLNNKILLEKDIIVTQEDIFKIRKYLMDNYKIYDATSPVSG 183

QY 178 KVQKGLIVFHSSEGSTVSYDLFDA--QGQYPTDLLRIYRDNNTTISSTLS--ISLYL 230
Db 184 RIEIG-----TKDGKHEQIDLFDSPEGTRSDIFAK-YKDNRIINMKNFHFHDYIL 233

```

```
; SEQ ID NO 39
; LENGTH: 79
; TYPE: PRT
; ORGANISM: streptococcal pyrogenic enterotoxin a
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-39

Query Match          9.2%; Score 112; DB 14; Length 79;
Best Local Similarity 32.1%; Pred. No. 0.0013;
Matches 25; Conservative 17; Mismatches 32; Indels 4; Gaps 2;

QY 43 SADQFLNTLTKGFTGHPWYNDLLVDLGSTAAATSEYSSVDLYGAYGYQC-AGGTP 101
Db 1 SVDQLLSHDLVY--VSGPNYDKLTKELKQEMATLFDKKNVDIYGVVEYVHLVCYLCNA 57

QY 102 NKTACMYGGVTLHDNNRL 119
Db 58 ERSACIYGGVTNHEGNHL 75

RESULT 55
US-10-002-784A-35
; Sequence 35, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 35
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin B
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-35

Query Match          9.2%; Score 111.5; DB 14; Length 89;
Best Local Similarity 33.3%; Pred. No. 0.0017;
Matches 29; Conservative 15; Mismatches 32; Indels 11; Gaps 2;

QY 43 SADQFLNTLTKGFTGHPWYNDLLVDLGSTAAATSEYSSVDLYGAYGYQC----- 96
Db 1 SIDQLFLDLIYSKDTKLGNVDNVRFEKFKDLADKFKKYVDVFGANY-YQCYFSKKT 59

QY 97 ----AGGTPNKTACMYGGVTLHDNNRL 119
Db 60 NDINSHQTDKRKTCMYGGVTEHNGNQL 86

RESULT 56
US-10-424-599-264720
; Sequence 264720, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 264720
```

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; LENGTH: 621
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_81062C.1.pap
US-10-424-599-264720

Query Match          8.5%; Score 103.5; DB 12; Length 621;
Best Local Similarity 23.0%; Pred. No. 0.18;
Matches 51; Conservative 39; Mismatches 83; Indels 49; Gaps 11;

QY 24 GNLKQIYYN---SKAITSEKSADQFLNTLLFKGFTGHPWYNDLLVDLGSTAAATSEY 80
Db 155 GNGTDVYQDGDESLTDSSEEDSSVNN--YSGFSRNGS-----DLGINRRIMEL 205

QY 81 EGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPI 140
Db 206 ETELREVKELWQE-----BEHA---DGSTRGRNENTEDLYTKINAY---EQELMTV 253

QY 141 -DKVTSKKEVTVQELDLQARHYLHGKFLGYNDSFGGKVQGLIVFHSSEGST----- 193
Db 254 NEKLRLSEEEITKQIELQ-----KYRLFNTENLEAGFESSLTKKHINEGGEAHKMIE 306

QY 194 -----VSVDLFDAGQGYPTL-----LRIYRDNNTTISSTLS 225
Db 307 VEGSIDGVDKELFDQNGEI-ETLARELRITKENLKASEMQIT 347

RESULT 57
US-10-425-114-57792
; Sequence 57792, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 57792
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-GMROPIC107B05_FLI.pap
US-10-425-114-57792

Query Match          8.5%; Score 103.5; DB 12; Length 628;
Best Local Similarity 23.0%; Pred. No. 0.19;
Matches 51; Conservative 39; Mismatches 83; Indels 49; Gaps 11;

QY 24 GNLKQIYYN---SKAITSEKSADQFLNTLLFKGFTGHPWYNDLLVDLGSTAAATSEY 80
Db 162 GNGTDVYQDGDESLTDSSEEDSSVNN--YSGFSRNGS-----DLGINRRIMEL 212

QY 81 EGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPI 140
Db 213 ETELREVKELWQE-----BEHA---DGSTRGRNENTEDLYTKINAY---EQELMTV 260

QY 141 -DKVTSKKEVTVQELDLQARHYLHGKFLGYNDSFGGKVQGLIVFHSSEGST----- 193
Db 261 NEKLRLSEEEITKQIELQ-----KYRLFNTENLEAGFESSLTKKHINEGGEAHKMIE 313

QY 194 -----VSVDLFDAGQGYPTL-----LRIYRDNNTTISSTLS 225
Db 314 VEGSIDGVDKELFDQNGEI-ETLARELRITKENLKASEMQIT 354
```

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RESULT 58
US-08-882-431-12
; Sequence 12, Application US/08882431
; Publication No. US2003009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-12

Query Match      8.4%; Score 102.5; DB 8; Length 233;
Best Local Similarity 24.5%; Pred. No. 0.058;
Matches 48; Conservative 33; Mismatches 60; Indels 55; Gaps 12;

QY 25 NLKQI---YYNSKAITSS-----KSADQFLNTLLFKGFFTGHPWYNDLL-- 68
D5 45 NIKDLLWYSSGSDTFTNSEVLDNSGSMRIKNTDGSISK-IIFPS-----PYYSFAFTK 98
QY 69 ---VDLGSTAATSEYEGSSVDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLTEKKV 125
D5 99 GEKVDL-NTRKTKKSQHTS---GTIHFQISGVT-----NTEKLPTPIEL 139
QY 126 PINLWIDGKQTTVPIDKVKTSKEVTQELDLQARHVLHGKFGLY-NSDSFGG--KVQRG 182
D5 140 PLKVKVHGKDSPLKYG-PKDKKQLAISTLDFFIRHQLTQIHGLYRSDTKGYWKIT-- 196
QY 183 LIVFHSSEGSTVSVDL 198
D5 197 -----MNDGSTYQSDL 207

RESULT 59
US-09-870-759-18
; Sequence 18, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:

```

```

; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-18

Query Match      8.2%; Score 100; DB 9; Length 234;
Best Local Similarity 24.5%; Pred. No. 0.1;
Matches 48; Conservative 33; Mismatches 61; Indels 54; Gaps 12;

QY 25 NLKQI---YYNSKAITSS-----KSADQFLNTLLFKGFFTGHPWYNDLL-- 68
D5 45 NIKDLLWYSSGSDTFTNSEVLDNSGSMRIKNTDGSISK-IIFPS-----PYYSFAFTK 98
QY 69 ---VDLGSTAATSEYEGSSVDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLTEKKV 125
D5 99 GEKVDL-NTRKTKKSQHTS---EGTVHFQISGVT-----NTEKLPTPIEL 140
QY 126 PINLWIDGKQTTVPIDKVKTSKEVTQELDLQARHVLHGKFGLY-NSDSFGG--KVQRG 182
D5 141 PLKVKVHGKDSPLKYG-PKDKKQLAISTLDFFIRHQLTQIHGLYRSDTKGYWKIT-- 197
QY 183 LIVFHSSEGSTVSVDL 198
D5 198 -----MNDGSTYQSDL 208

RESULT 60
US-09-751-708A-18
; Sequence 18, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 18
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-18

Query Match      8.2%; Score 100; DB 10; Length 234;
Best Local Similarity 24.5%; Pred. No. 0.1;
Matches 48; Conservative 33; Mismatches 61; Indels 54; Gaps 12;

QY 25 NLKQI---YYNSKAITSS-----KSADQFLNTLLFKGFFTGHPWYNDLL-- 68
D5 45 NIKDLLWYSSGSDTFTNSEVLDNSGSMRIKNTDGSISK-IIFPS-----PYYSFAFTK 98
QY 69 ---VDLGSTAATSEYEGSSVDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLTEKKV 125
D5 99 GEKVDL-NTRKTKKSQHTS---EGTVHFQISGVT-----NTEKLPTPIEL 140
QY 126 PINLWIDGKQTTVPIDKVKTSKEVTQELDLQARHVLHGKFGLY-NSDSFGG--KVQRG 182
D5 141 PLKVKVHGKDSPLKYG-PKDKKQLAISTLDFFIRHQLTQIHGLYRSDTKGYWKIT-- 197
QY 183 LIVFHSSEGSTVSVDL 198

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Db 198 -----MNDGSTYQSDL 208
:::|:|:| |
RESULT 61
US-10-267-682-111
; Sequence 111, Application US/10267682
; Publication No. US2004003235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,682
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 111:
US-10-267-682-111
Query Match 8.2%; Score 100; DB 12; Length 234;
Best Local Similarity 24.5%; Pred. No. 0.1;
Matches 48; Conservative 33; Mismatches 61; Indels 54; Gaps 12;
Qy 25 NLKQI---YYNSKAITSE-----KSAQDLTNTLLFKGFTGHPYNDLL-- 68
Db 45 NIKOLLWYSGSDFTNSEVLDNSLGSRMRIKNTDGSI-SLIIFPS-----PYSPAFK 98
Qy 69 ---VDLGSTATSEYEGSSVDLYGAYGYOCAGGTPNKTCMYGGVTLHDNNRLTEKKV 125
Db 99 GEKVDL-NTRKTKSQHTS---EGYIHFIQISGVT-----NTEKLPPIEL 140
Qy 126 PINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLY-NSDSFGG--KVQRG 182
Db 141 PLKVKVHGKDSPLKYG-KFDKKQLAISTLDLDFEIRHQLTQIHGLYRSSDKTGGYWKIT-- 197
Qy 183 LIVFHSSEGSTVSYDL 198
Db 198 -----MNDGSTYQSDL 208
:::|:|:| |
RESULT 62
US-10-267-748-111
; Sequence 111, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,748
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 111:
US-10-267-748-111
Query Match 8.2%; Score 100; DB 12; Length 234;
Best Local Similarity 24.5%; Pred. No. 0.1;
Matches 48; Conservative 33; Mismatches 61; Indels 54; Gaps 12;
Qy 25 NLKQI---YYNSKAITSE-----KSAQDLTNTLLFKGFTGHPYNDLL-- 68
Db 45 NIKOLLWYSGSDFTNSEVLDNSLGSRMRIKNTDGSI-SLIIFPS-----PYSPAFK 98
Qy 69 ---VDLGSTATSEYEGSSVDLYGAYGYOCAGGTPNKTCMYGGVTLHDNNRLTEKKV 125
Db 99 GEKVDL-NTRKTKSQHTS---EGYIHFIQISGVT-----NTEKLPPIEL 140
Qy 126 PINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLY-NSDSFGG--KVQRG 182
Db 141 PLKVKVHGKDSPLKYG-KFDKKQLAISTLDLDFEIRHQLTQIHGLYRSSDKTGGYWKIT-- 197

```
QY 183 LIVFHSSEGSTVSVDL 198
Db 198 -----MNDGSTYQSDL 208

RESULT 63
US-10-002-784A-12
; Sequence 12, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 12
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: toxin shock syndrom toxin-1 mutant
US-10-002-784A-12

Query Match      8.2%; Score 100; DB 14; Length 234;
Best Local Similarity 24.5%; Pred. No. 0.1;
Matches 48; Conservative 33; Mismatches 61; Indels 54; Gaps 12;

QY 25 NLKQI---YYNSKAITSS-----KSADQFLTNTLLFKGFFTHGHPWYNDLL-- 68
Db 45 NIKDLWDYSSGSDFTNSEVLDSNGSMRIKNTDGS-SLIIFPS-?-PYSPATK 98

QY 69 ---VLGSTAATSEYSGSVVDLYGAYGYQCAGTGNKTACMGVGTLDHNNRLTEKKV 125
Db 99 GEKVDL-NTRTKKSQHTS---EGTVHFQISGVT-----NTEKLPPIEL 140

QY 126 PINLWIDGKQTTV---PIDKVTSKKEVTVOELDLQARHYLHGKFGLY-NSDSFG--KVQ 182
Db 141 PLKVKGKDSPLKYGP-KFDKQLAISTLDLFEIRHQLTQIHGLYRSSDKTGGYWKI-- 197

QY 183 LIVFHSSEGSTVSVDL 198
Db 198 -----MNDGSTYQSDL 208

RESULT 64
US-10-002-784A-36
; Sequence 36, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 36
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C1
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-36

Query Match      8.2%; Score 99.5; DB 14; Length 89;
Best Local Similarity 28.0%; Pred. No. 0.03;
Matches 23; Conservative 14; Mismatches 38; Indels 7; Gaps 1;

QY 43 SADQFLTNTLLFKGFFTHGHPWYNDLLVLGSTAATSEYSGSVVDLYGAYGYQC----- 96
Db 1 SVDFLAHLDIYNISDKLKNYDKVKTLELNEGLAKKYKDEVDVYGSNYNYNCYFSSKD 60

QY 97 -AGGTPNKTACMGVGTLDHNN 117
Db 61 NVGKVTGGTCMYGGITKEGN 82

RESULT 65
US-09-465-714-3
; Sequence 3, Application US/09465714
; Publication No. US20030032582A1
; GENERAL INFORMATION:
; APPLICANT: Wahlsten, Jennifer L.
; APPLICANT: Ramakrishnan, S.
; APPLICANT: Schlievert, Patrick M.
; TITLE OF INVENTION: SPONTANEOUS MEMBRANE INSERTION
; FILE REFERENCE: 09531/003001
; CURRENT APPLICATION NUMBER: US/09/465,714
; CURRENT FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/001,593
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 194
; TYPE: PRT
; ORGANISM: Bacterial Sequence
US-09-465-714-3

Query Match      8.0%; Score 98; DB 10; Length 194;
Best Local Similarity 24.6%; Pred. No. 0.13;
Matches 49; Conservative 33; Mismatches 57; Indels 60; Gaps 13;

QY 25 NLKQI---YYNSKAITSS-----KSADQFLTNTLLFKGFFTHGHPWYNDLL-- 68
Db 5 NIKDLWDYSSGSDFTNSEVLDSNGSMRIKNTDGS-SLIIFPS-----PYSPATK 58

QY 69 ---VLGSTAATSEYSGSVVDLYGAYGYQCAGTGNKTACMGVGTLDHNNRLTEKKV 125
Db 59 GEKVDL-NTRTKKSQHTS---EGTVHFQISGVT-----NTEKLPPIEL 100

QY 126 PINLWIDGKQTTV---PIDKVTSKKEVTVOELDLQARHYLHGKFGLY-NSDSFG--KV 179
Db 101 PLKVKGKDSPLKYWP---KFDKQLAISTLDLFEIRHQLTQIHGLYRSSDKTGGYWKI 156

QY 180 QRLIVFHSSEGSTVSVDL 198
Db 157 T-----MNDGSTYQSDL 168

RESULT 66
US-10-354-948-6
; Sequence 6, Application US/10354948
; Publication No. US20030202962A1
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmslie, Robyn E.
; APPLICANT: Potter, Terence A.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
```

[illegible]

Query Match. 8.0%; Score 98; DB 10; Length 238;
Best Local Similarity 24.6%; Pred. No. 0.17;
Matches 49; Conservative 33; Mismatches 57; Indels 60; Gaps 13;

RESULT 71
US-10-002-784A-38
Sequence 38, Application US/10002784A
Publication No. US20030036644A1
GENERAL INFORMATION:
/33
APPLICANT: Ulrich, Robert G.
TITLE OF INVENTION: Bacterial Superantigen Vaccines
FILE REFERENCE: 003/233/SAP
CURRENT APPLICATION NUMBER: US/10/002,784A
CURRENT FILING DATE: 2001-11-26
PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
PRIOR FILING DATE: 97-06-25; 98-09-01
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 38
LENGTH: 89
TYPE: PRT
ORGANISM: staphylococcal enterotoxin C3
FEATURE:

OTHER INFORMATION: partial sequence as shown in Figure 3

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US-10-002-784A-38
Query Match      8.0%; Score 97.5; DB 14; Length 89;
Best Local Similarity 28.0%; Pred. No. 0.047;
Matches 23; Conservative 14; Mismatches 38; Indels 7; Gaps 1;

QY 43 SADQFLTNLTFKGFTHPWNLDLVLGSGTAATSEYEGSSVDLYGAYGYQC-----96
Db 1 SVDKFLAHDLYNISDKLKNYDKVKTLLNEDLAKKYKDEVDVYGSNYVYVCFSSKD 60

QY 97 -AGTPNKTACMYGVTLLHNN 117
Db 61 NVGKVTGGKTCMYGKITKEGN 82

RESULT 72
US-10-282-122A-70240
; Sequence 70240, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282.122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70240
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-282-122A-70240
Query Match      7.7%; Score 94; DB 12; Length 231;
Best Local Similarity 23.6%; Pred. No. 0.42;
Matches 43; Conservative 27; Mismatches 84; Indels 28; Gaps 6;

QY 2 EKSEINEKDLRKSELOGLTALGNKQIY-YNYSKAITSE---KSAQFLTNLTFKGF 57
Db 32 EKOERVOH-----LYDKOLRYYSSESFEFSNISKVNGSNVWFNQE 78

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QY 58 FTGHPWYNLDLVLGSGTAATSEYEGSSVDLYGAYGYQCAGTTPNKTACMYGVTLLHNN 117
Db 79 KQNHQLF---LLGKDXDKYKKGLEGQNVFVVKELI-----DPNGRLSTVGVTKKNNK 128
QY 118 RLTEEEKVPINLWIDGKQITVPIDKVKTSKKEVTVOELDQARHYLHGKFLGYNSSFG 177
Db 129 SSETNHLFVNK-VYGNLNDASIDSLINKKEVSLKELDFKIRKQLVKEYLYKGTTKYG 187
QY 178 KV 179
Db 188 KI 189

RESULT 73
US-10-283-838-20
; Sequence 20, Application US/10283838
; Publication No. US20030092894A1
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
; Johan Hansson, Terje Kalland, Lars
; Abrahamson and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,838
; FILING DATE: 30-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,692
; FILING DATE: August 12, 1996
; APPLICATION NUMBER: 9601245-5
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 41986/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-283-838-20
Query Match      7.6%; Score 93; DB 14; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 161 HYLHGKFGLYNSDSPG 176
Db 1 HYLHGKFGLYNSDSPG 16

RESULT 74
US-10-437-963-191455

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; Sequence 191455, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 191455
; LENGTH: 600
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_87772C.1.pep
US-10-437-963-191455

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Query Match      7.6%; Score 92; DB 16; Length 600;
Best Local Similarity 20.5%; Pred. No. 2.6; Indels 76; Gaps 8;
Matches 45; Conservative 30; Mismatches 68;

QY 24 GNLKQIYYNSKAITSSSEKSDQFLNTLLFKGFFTGHPWYNDLVLGSLTAATSEYEGS 83
Db 79 GNI-PIYACSGTAISQEGSGIFLTSASLVAFAFYDTEIYDNLKIEV-----RHEGN 130

QY 84 SVDLGAYGYOCAGTGNKTAACMGVTLHNNRLTEKKVPINLWIDGKQTVPIDKV 143
Db 131 EV-----YKGLAKYDLDLKNFAVY----- 150

QY 144 KTSKKEVTVOELDLQ---ARH-----YLHGKFGLYNSDSFGGKVVQRLIV--FHSSEGSTV 194
Db 151 -----TWESLDVHVVLSEHLKDRYAKKLVASRNKYGGILITKSVVVGSHHNSRSEV 203

QY 195 SYD-----LFDAGQGYPTLLRIYRDNNTISS 221
Db 204 CHDISVWAEDWEGGPLDFDGRFVGMKNKFLAMDITFILS 242

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RESULT 75
US-10-435-766-23
; Sequence 23, Application US/10435766
; Publication No. US20030228616A1
; GENERAL INFORMATION:
; APPLICANT: Strategene
; APPLICANT: Sorge, Joseph A
; APPLICANT: Arezi, Bahram
; APPLICANT: Hogrefe, Holly
; APPLICANT: Hansen, Connie J
; TITLE OF INVENTION: DNA Polymerase Mutants with Reverse Transcriptase Activity
; FILE REFERENCE: 25436/1565C
; CURRENT APPLICATION NUMBER: US/10/435,766
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: US 10/223,650
; PRIOR FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 09/896,923
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 09/698,341
; PRIOR FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: US 60/162,600
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: PCT/US00/29706
; PRIOR FILING DATE: 2000-10-27
; NUMBER OF SEQ ID NOS: 104
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 23

```

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; LENGTH: 1634
; TYPE: PRT
; ORGANISM: Methanococcus jannaschii
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (382)..(382)
; OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-10-435-766-23

Query Match      7.5%; Score 91; DB 15; Length 1634;
Best Local Similarity 21.6%; Pred. No. 14;
Matches 50; Conservative 36; Mismatches 79; Indels 66; Gaps 10;

QY 12 LRKSELOGTALGNLQIYYNSKAITSSSEKSDQFLNTLLFKGFFTGHPWYNDLVL 71
Db 614 VRRKGTGKAITGCAKADYLLKIEEL---KNKEKYLPAAIL-RGFFEGDGYVNTVRAV 669

QY 72 GSTAATSEYE-----GSSVDLYGAYGYOCAGTGNKTAACMGVTLHNNRLTEKKVP 126
Db 670 VVNOGTNNYDKIKFIASLLDLRLGKIYF-----YTYSYEERKKLRYV 713

QY 127 INLWIDGKQTVPIDKVTS-----KKEVTVOELDLQARHLYHGKFGLYNSD----- 173
Db 714 IEIFSKG-----DLIKFSILISFISRRNNLLNLEIRQKLYKIGDYGFDLDDVCVS 766

QY 174 --SFGGKV-----QRGLIVFHSSEGS-TVSYDLFDAQGYPTLL 209
Db 767 LESYKGEVVDLTLEGRPYFANGILTHNSLYPSIIISYNI-----SPDTL 811

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Search completed: August 12, 2004, 13:46:20
Job time : 26.7742 secs

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OM protein - protein search, using sw model

Run on: August 12, 2004, 13:27:15 ; Search time 9.21353 Seconds
(without alignments)
1305.563 Million cell updates/sec

Title: US-09-900-766-2

Perfect score: 1218

Sequence: 1 SEKSEINEXDLKXKSELOG.....RDNTTISSTLSISLXLYTT 233

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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1: /cgn2_6/ptodata/2/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/2/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/2/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/2/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pep.*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1107	90.9	233	4	US-08-695-692B-8
2	1107	90.9	257	3	US-08-486-099-112
3	1107	90.9	257	3	US-08-360-107A-122
4	1107	90.9	257	3	US-08-484-233B-112
5	1107	90.9	257	3	US-08-919-597-112
6	1107	90.9	257	3	US-08-475-668A-112
7	1107	90.9	257	3	US-08-485-551A-112
8	1107	90.9	257	3	US-08-471-913A-112
9	1107	90.9	257	4	US-08-485-264A-112
10	1107	90.9	257	4	US-08-474-349A-112
11	1107	90.9	257	4	US-08-470-896-112
12	1107	90.9	257	3	US-08-485-546A-112
13	1040	85.4	226	3	US-08-896-933-24
14	1040	85.4	226	4	US-09-314-235-24
15	948	77.8	233	4	US-08-695-692B-7
16	948	77.8	257	3	US-08-486-099-113
17	948	77.8	257	3	US-08-360-107A-123
18	948	77.8	257	3	US-08-484-233B-113
19	948	77.8	257	3	US-08-919-597-113
20	948	77.8	257	3	US-08-475-668A-113
21	948	77.8	257	3	US-08-485-551A-113
22	948	77.8	257	3	US-08-471-913A-113
23	948	77.8	257	4	US-08-485-264A-113
24	948	77.8	257	4	US-08-474-349A-113
25	948	77.8	257	4	US-08-470-896-113
26	948	77.8	257	4	US-08-485-546A-113
27	944	77.5	233	1	US-08-446-918A-4

28	944	77.5	233	2	US-08-580-806-4	Sequence 4, Appli
29	931.5	76.5	232	3	US-08-896-933-23	Sequence 23, Appl
30	931.5	76.5	232	4	US-09-314-235-23	Sequence 23, Appl
31	925	75.9	257	4	US-09-144-776B-2	Sequence 2, Appli
32	921	75.6	233	4	US-09-144-776B-4	Sequence 4, Appli
33	605	49.7	228	3	US-08-896-933-25	Sequence 25, Appl
34	605	49.7	228	4	US-09-314-235-25	Sequence 25, Appl
35	406	33.3	82	4	US-09-144-776B-19	Sequence 19, Appl
36	362	29.7	82	4	US-09-144-776B-17	Sequence 17, Appl
37	277.5	22.8	238	3	US-08-896-933-28	Sequence 28, Appl
38	277.5	22.8	238	4	US-09-314-235-28	Sequence 28, Appl
39	270.5	22.2	221	3	US-08-896-933-29	Sequence 29, Appl
40	270.5	22.2	221	4	US-09-314-235-29	Sequence 29, Appl
41	268.5	22.0	251	4	US-08-973-391C-13	Sequence 13, Appl
42	267.5	22.0	255	1	US-08-446-918A-2	Sequence 2, Appli
43	267.5	22.0	255	2	US-08-580-806-2	Sequence 2, Appli
44	265.5	21.8	221	4	US-08-973-391C-14	Sequence 14, Appl
45	264.5	21.7	239	3	US-08-896-933-27	Sequence 27, Appl
46	264.5	21.7	239	4	US-09-314-235-27	Sequence 27, Appl
47	263.5	21.6	251	4	US-09-144-776B-16	Sequence 16, Appl
48	260.5	21.4	239	3	US-08-896-933-26	Sequence 26, Appl
49	260.5	21.4	239	4	US-09-314-235-26	Sequence 26, Appl
50	260.5	21.4	266	4	US-09-414-276-8	Sequence 8, Appli
51	260.5	21.4	266	4	US-09-144-776B-6	Sequence 6, Appli
52	255.5	21.0	239	4	US-09-144-776B-10	Sequence 10, Appl
53	255.5	21.0	266	4	US-09-144-776B-14	Sequence 14, Appl
54	250.5	20.6	266	4	US-09-144-776B-8	Sequence 8, Appli
55	225.5	18.5	239	3	US-08-896-933-21	Sequence 21, Appl
56	225.5	18.5	239	4	US-09-314-235-21	Sequence 21, Appl
57	220	18.1	220	3	US-08-896-933-20	Sequence 20, Appl
58	220	18.1	220	4	US-09-314-235-20	Sequence 20, Appl
59	194	15.9	82	4	US-09-144-776B-18	Sequence 18, Appl
60	189	15.5	45	1	US-08-220-378-1	Sequence 1, Appli
61	189	15.5	45	2	US-08-696-012-1	Sequence 1, Appli
62	150	12.3	208	3	US-08-896-933-30	Sequence 30, Appl
63	150	12.3	208	4	US-09-314-235-30	Sequence 30, Appl
64	131	10.8	27	3	US-08-896-933-34	Sequence 34, Appl
65	131	10.8	27	4	US-09-314-235-34	Sequence 34, Appl
66	127	10.4	24	3	US-08-838-413A-22	Sequence 22, Appl
67	126	10.3	23	1	US-08-220-378-5	Sequence 5, Appli
68	126	10.3	23	2	US-08-696-012-5	Sequence 5, Appli
69	124	10.2	29	1	US-08-220-378-6	Sequence 6, Appli
70	124	10.2	29	2	US-08-696-012-6	Sequence 6, Appli
71	112	9.2	79	4	US-09-144-776B-24	Sequence 24, Appl
72	111.5	9.2	89	4	US-09-144-776B-20	Sequence 20, Appl
73	110	9.0	22	1	US-08-220-378-4	Sequence 4, Appli
74	110	9.0	22	2	US-08-696-012-4	Sequence 4, Appli
75	107	8.8	28	1	US-08-220-378-2	Sequence 2, Appli
76	107	8.8	28	2	US-08-696-012-2	Sequence 2, Appli
77	106	8.7	28	1	US-08-220-378-7	Sequence 7, Appli
78	106	8.7	28	2	US-08-696-012-7	Sequence 7, Appli
79	101.5	8.3	29	1	US-08-220-378-9	Sequence 9, Appli
80	101.5	8.3	29	2	US-08-696-012-9	Sequence 9, Appli
81	100	8.2	28	1	US-08-220-378-8	Sequence 8, Appli
82	100	8.2	28	2	US-08-696-012-8	Sequence 8, Appli
83	100	8.2	234	3	US-08-486-099-111	Sequence 111, App
84	100	8.2	234	3	US-08-360-107A-121	Sequence 121, App
85	100	8.2	234	3	US-08-484-233B-111	Sequence 111, App
86	100	8.2	234	3	US-08-919-597-111	Sequence 111, App
87	100	8.2	234	3	US-08-475-668A-111	Sequence 111, App
88	100	8.2	234	3	US-08-485-551A-111	Sequence 111, App
89	100	8.2	234	3	US-08-471-913A-111	Sequence 111, App
90	100	8.2	234	4	US-08-485-264A-111	Sequence 111, App
91	100	8.2	234	4	US-08-474-349A-111	Sequence 111, App
92	100	8.2	234	4	US-08-470-896-112	Sequence 12, Appl
93	100	8.2	234	4	US-08-470-896-111	Sequence 11, App
94	100	8.2	234	4	US-08-485-546A-111	Sequence 11, App
95	99.5	8.2	89	4	US-09-144-776B-21	Sequence 21, Appl
96	99.5	8.2	193	3	US-08-896-933-31	Sequence 31, Appl
97	99.5	8.2	193	4	US-09-314-235-31	Sequence 31, Appl
98	98	8.0	194	1	US-08-446-918A-6	Sequence 6, Appli
99	98	8.0	194	2	US-08-580-806-6	Sequence 6, Appli
100	97.5	8.0	89	4	US-09-144-776B-22	Sequence 22, Appl

ALIGNMENTS

RESULT 1
 US-08-695-692B-8
 ; Sequence 8, Application US/08695692B
 ; Patent No. 6514498
 ; GENERAL INFORMATION:
 ; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
 ; APPLICANT: Johan Hansson, Terje Kalland, Lars
 ; APPLICANT: Abrahamson and Goran Forsberg
 ; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
 ; TITLE OF INVENTION: AND THEIR USE
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
 ; STREET: 1177 West Loop South, 10th Floor
 ; CITY: Houston
 ; STATE: TX
 ; COUNTRY: USA
 ; ZIP: 77027-9095
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/695,692B
 ; FILING DATE: August 12, 1996
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 9601245-5
 ; FILING DATE: March 29, 1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Krieger, Paul E.
 ; REGISTRATION NUMBER: 25,886
 ; REFERENCE/DOCKET NUMBER: 41986/1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 713-850-0909
 ; TELEFAX: 713-850-0165
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 233 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-695-692B-8

Query Match 90.9%; Score 1107; DB 4; Length 233;
 Best Local Similarity 89.7%; Pred. No. 2.5e-110; Indels 0; Gaps 0;
 Matches 209; Conservative 9; Mismatches 15;
 QY 1 SEKSEINEKDLRKKSELOQTALGNLQIYYNKAITSSEKSAQDLNTLLFKGFTG 60
 DB 1 SEKSEINEKDLRKKSELOQTALGNLQIYYNKAITSSEKSAQDLNTLLFKGFTG 60
 QY 61 HPWYNDLLVDLGSTATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
 DB 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
 QY 121 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 DB 121 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 QY 181 RGLIVFHSSEGSTVSVDLFDQAQGYPTLLRIYRDNTTISSTLSISLYTT 233
 DB 181 RGLIVFHSSEGSTVSVDLFDQAQGYPTLLRIYRDNTTISSTLSISLYTT 233

RESULT 2
 US-08-486-099-112

; Sequence 112, Application US/08486099
 ; Patent No. 6013263
 ; GENERAL INFORMATION:
 ; APPLICANT: Bolognesi, Dani P.
 ; APPLICANT: Matthews, Thomas J.
 ; APPLICANT: Wild, Carl T.
 ; APPLICANT: Barney, Shawn O.
 ; APPLICANT: Lambert, Dennis M.
 ; APPLICANT: Petteway, Stephen R.
 ; APPLICANT: Langlois, Alphonse J.
 ; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
 ; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
 ; TITLE OF INVENTION: B VIRUS TRANSMISSION
 ; NUMBER OF SEQUENCES: 209
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/486,099
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Cortuzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7872-031
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 112:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 257 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-08-486-099-112

Query Match 90.9%; Score 1107; DB 3; Length 257;
 Best Local Similarity 89.7%; Pred. No. 2.9e-110; Indels 0; Gaps 0;
 Matches 209; Conservative 9; Mismatches 15;
 QY 1 SEKSEINEKDLRKKSELOQTALGNLQIYYNKAITSSEKSAQDLNTLLFKGFTG 60
 DB 25 SEKSEINEKDLRKKSELOQTALGNLQIYYNKAITSSEKSAQDLNTLLFKGFTG 84
 QY 61 HPWYNDLLVDLGSTATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
 DB 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
 QY 121 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 DB 145 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
 QY 181 RGLIVFHSSEGSTVSVDLFDQAQGYPTLLRIYRDNTTISSTLSISLYTT 233
 DB 205 RGLIVFHSSEGSTVSVDLFDQAQGYPTLLRIYRDNTTISSTLSISLYTT 257

RESULT 3
 US-08-360-107A-122
 ; Sequence 122, Application US/08360107A
 ; Patent No. 6017536
 ; GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-360-107A-122

Query Match 90.9%; Score 1107; DB 3; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.9e-110;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSDQFLNTLLFKGFTG 60
DB 25 SEKSEINEKDLRKSELQNALSLRQIYYNEKAITENKESDDQFLENTLLFKGFTG 84
QY 61 HPWYNDLLVDLGSATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 144
QY 121 BEKKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
DB 145 BEKKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNNTTISSTLSISLYLYTT 233
DB 205 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNNTTINSENHLIDLYLYTT 257

RESULT 4
US-08-484-223B-112
Sequence 112, Application US/08484223B
Patent No. 6020459
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.

APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 245
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-223B-112

Query Match 90.9%; Score 1107; DB 3; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.9e-110;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSDQFLNTLLFKGFTG 60
DB 25 SEKSEINEKDLRKSELQNALSLRQIYYNEKAITENKESDDQFLENTLLFKGFTG 84
QY 61 HPWYNDLLVDLGSATSEYEGSSVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 144
QY 121 BEKKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
DB 145 BEKKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNNTTISSTLSISLYLYTT 233
DB 205 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNNTTINSENHLIDLYLYTT 257

RESULT 5
US-08-919-597-112
Sequence 112, Application US/08919597
Patent No. 6054265
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.

```

; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/919,597
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,896
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-919-597-112

Query Match 90.9%; Score 1107; DB 3; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.9e-110;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSKELQGTALGNLKOIYYNKAITSSEKSADOFNTLLFKGFTG 60
DB 25 SEKSEINEKDLRKSKELQGTALGNLKOIYYNKAITSSEKSADOFNTLLFKGFTG 84
QY 61 HPWYNDLLVLDGSKATNKKYKGVLDYGYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVLDGSKATNKKYKGVLDYGYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTQVELDQARHYLHGKFGLYNSDSFGKVQ 180
DB 145 EEKVPINLWIDGKQTTPIDKVKTSKEVTQVELDQARHYLHGKFGLYNSDSFGKVQ 204
QY 181 RGLVFSHSGSVSYDLFDAQOQYPTLLRIYRDNNTTSSISLSLYLYTT 233
DB 205 RGLVFSHSGSVSYDLFDAQOQYPTLLRIYRDNNTTSSISLSLYLYTT 257

RESULT 6
US-08-475-668A-112
; Sequence 112, Application US/08475668A
; Patent No. 6060065
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP

```

```

; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,668A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-475-668A-112

Query Match 90.9%; Score 1107; DB 3; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.9e-110;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSKELQGTALGNLKOIYYNKAITSSEKSADOFNTLLFKGFTG 60
DB 25 SEKSEINEKDLRKSKELQGTALGNLKOIYYNKAITSSEKSADOFNTLLFKGFTG 84
QY 61 HPWYNDLLVLDGSKATNKKYKGVLDYGYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVLDGSKATNKKYKGVLDYGYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTQVELDQARHYLHGKFGLYNSDSFGKVQ 180
DB 145 EEKVPINLWIDGKQTTPIDKVKTSKEVTQVELDQARHYLHGKFGLYNSDSFGKVQ 204
QY 181 RGLVFSHSGSVSYDLFDAQOQYPTLLRIYRDNNTTSSISLSLYLYTT 233
DB 205 RGLVFSHSGSVSYDLFDAQOQYPTLLRIYRDNNTTSSISLSLYLYTT 257

RESULT 7
US-08-485-551A-112
; Sequence 112, Application US/08485551A
; Patent No. 6069973
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP

```

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-551A-112

Query Match 90.9%; Score 1107; DB 3; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.9e-110;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYYNKAITSEKSDAQFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYYNKAITSEKSDAQFLNTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSTAAATSEYSGSSVDLYGAYGYCCAGGTENKACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYCCAGGTENKACMYGGVTLHDNNRLT 144
QY 121 EKKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EKKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGQYPTLLRIYRDNKTINSNLHIDLTYTT 233
DB 205 RGLIVFHSSEGSTVSYDLFDAQGQYPTLLRIYRDNKTINSNLHIDLTYTT 257

RESULT 8
US-08-471-913A-112
Sequence 112, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York

COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-471-913A-112

Query Match 90.9%; Score 1107; DB 3; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.9e-110;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYYNKAITSEKSDAQFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYYNKAITSEKSDAQFLNTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSTAAATSEYSGSSVDLYGAYGYCCAGGTENKACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYCCAGGTENKACMYGGVTLHDNNRLT 144
QY 121 EKKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EKKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGQYPTLLRIYRDNKTINSNLHIDLTYTT 233
DB 205 RGLIVFHSSEGSTVSYDLFDAQGQYPTLLRIYRDNKTINSNLHIDLTYTT 257

RESULT 9
US-08-485-264A-112
Sequence 112, Application US/08485264A
Patent No. 6228983
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,264A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-021
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-485-264A-112

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Query Match          90.9%; Score 1107; DB 3; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.9e-110;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSADQPLNTLLPKGFTG 60
   |||||
Db 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITENKESDDQFLENTLLFKGFTG 84
   |||||

QY 61 HPWYNDLLVLDGKATNKYKGGVDLYGAYGYQCAGGTPNKTACWYGGVTLHDNNELT 120
   |||||
Db 85 HPWYNDLLVLDGKATNKYKGGVDLYGAYGYQCAGGTPNKTACWYGGVTLHDNNELT 144
   |||||

QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
   |||||
Db 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 204
   |||||

QY 181 RGLIVFHSSEGSVSYDLFDAQGYPTLLRIYRDNTTISSTLSLSLYTT 233
   |||||
Db 205 RGLIVFHSSEGSVSYDLFDAQGYPTLLRIYRDNTTISSTLSLSLYTT 257
   |||||

```

```

RESULT 10
US-08-474-349A-112
; Sequence 112, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
; TITLE OF INVENTION: VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,264A

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; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-474-349A-112

```

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Query Match          90.9%; Score 1107; DB 4; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.9e-110;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSADQPLNTLLPKGFTG 60
   |||||
Db 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITENKESDDQFLENTLLFKGFTG 84
   |||||

QY 61 HPWYNDLLVLDGKATNKYKGGVDLYGAYGYQCAGGTPNKTACWYGGVTLHDNNELT 120
   |||||
Db 85 HPWYNDLLVLDGKATNKYKGGVDLYGAYGYQCAGGTPNKTACWYGGVTLHDNNELT 144
   |||||

QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
   |||||
Db 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 204
   |||||

QY 181 RGLIVFHSSEGSVSYDLFDAQGYPTLLRIYRDNTTISSTLSLSLYTT 233
   |||||
Db 205 RGLIVFHSSEGSVSYDLFDAQGYPTLLRIYRDNTTISSTLSLSLYTT 257
   |||||

```

```

RESULT 11
US-08-470-896-112
; Sequence 112, Application US/08470896
; Patent No. 6479055
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,896

```

; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-470-896-112

Query Match 90.9%; Score 1107; DB 4; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.9e-110;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSAQDLTNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYCCAGGTPNKTCACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVDLGSKDATNKYKGGVDLYGAYGYCCAGGTPNKTCACMYGGVTLHDNNRLT 144
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISLSISLYLYTT 233
DB 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTINSENHLIDLYLYTT 257

RESULT 12
US-08-485-546A-112
; Sequence 112, Application US/08485546A
; Patent No. 6518013
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/485,546A
; APPLICATION NUMBER: US/08/485,546A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-485-546A-112

Query Match 90.9%; Score 1107; DB 4; Length 257;
Best Local Similarity 89.7%; Pred. No. 2.9e-110;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSAQDLTNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYCCAGGTPNKTCACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVDLGSKDATNKYKGGVDLYGAYGYCCAGGTPNKTCACMYGGVTLHDNNRLT 144
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISLSISLYLYTT 233
DB 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTINSENHLIDLYLYTT 257

RESULT 13
US-08-896-933-24
; Sequence 24, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-896-933-24

Query Match 85.4%; Score 1040; DB 3; Length 226;
Best Local Similarity 85.2%; Pred. No. 3.6e-103;
Matches 196; Conservative 13; Mismatches 17; Indels 4; Gaps 1;

QY 4 SEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSAQDLTNTLLFKGFFTGHPW 63
DB 1 SEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 60
QY 64 YNDLLVDLGSTAAATSEYEGSSVDLYGAYGYCCAGGTPNKTCACMYGGVTLHDNNRLTEEK 123
DB 61 YNDLLVDGSKDATNKYKGGVDLYGAYGYCCAGGTPNKTCACMYGGVTLHDNNRLTEB- 119
QY 124 KVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQVRL 183
DB 120 ---VBKWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQVRL 176

QY 184 IVFHSSEGSTVSYDLFDAQGYPTDILLRIYRNTTISSTLSISLYLYTT 233
 Db 177 IVFHSSEGSTVSYDLFDAQGYPTDILLRIYRNTTISSTLSISLYLYTT 226

RESULT 14

US-09-314-235-24
 ; Sequence 24, Application US/09314235
 ; Patent No. 6338845
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 ; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
 ; FILE REFERENCE: 09629/005004
 ; CURRENT APPLICATION NUMBER: US/09/314,235
 ; CURRENT FILING DATE: 1999-05-18
 ; EARLIER APPLICATION NUMBER: 08/896,933
 ; EARLIER FILING DATE: 1997-07-18
 ; EARLIER APPLICATION NUMBER: 08/252,978
 ; EARLIER FILING DATE: 1994-06-02
 ; EARLIER APPLICATION NUMBER: 07/891,718
 ; EARLIER FILING DATE: 1992-06-01
 ; EARLIER APPLICATION NUMBER: US91/00342
 ; EARLIER FILING DATE: 1991-01-17
 ; EARLIER APPLICATION NUMBER: 07/466,577
 ; EARLIER FILING DATE: 1990-01-17
 ; EARLIER APPLICATION NUMBER: 07/416,530
 ; EARLIER FILING DATE: 1989-10-03
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 24
 ; LENGTH: 226
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus

US-09-314-235-24

Query Match 85.4%; Score 1040; DB 4; Length 226;
 Best Local Similarity 85.2%; Pred. No. 3.6e-103;
 Matches 196; Conservative 13; Mismatches 17; Indels 4; Gaps 1;
 QY 4 SEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSADQFLNTLLFKGFFTHPW 63
 Db 1 SEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSADQFLNTLLFKGFFTHPW 60
 QY 64 YNDLLVLDGSTAATSEYEGSSVDLYGAYGYCAGGTPNKTCMYGGVTLHDNNRLTEK 123
 Db 61 YNDLLVLDGSTAATSEYEGSSVDLYGAYGYCAGGTPNKTCMYGGVTLHDNNRLTEK 119
 QY 124 KVPINWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVGRL 183
 Db 120 ---VBKWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVGRL 176
 QY 184 IVFHSSEGSTVSYDLFDAQGYPTDILLRIYRNTTISSTLSISLYLYTT 233
 Db 177 IVFHSSEGSTVSYDLFDAQGYPTDILLRIYRNTTISSTLSISLYLYTT 226

RESULT 15

US-08-695-692B-7
 ; Sequence 7, Application US/08695692B
 ; Patent No. 6514498
 ; GENERAL INFORMATION:
 ; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
 ; APPLICANT: Johan Hansson, Terje Kalland, Lars
 ; APPLICANT: Abrahamsen and Goran Forsberg
 ; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
 ; FILE OF INVENTION: AND THEIR USE
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
 ; STREET: 1177 West Loop South, 10th Floor
 ; CITY: Houston

STATE: TX
 COUNTRY: USA
 ZIP: 77027-9095
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/695,692B
 FILING DATE: August 12, 1996
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 9601245-5
 FILING DATE: March 29, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Krieger, Paul E.
 REGISTRATION NUMBER: 25,886
 REFERENCE/DOCKET NUMBER: 41986/1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 713-850-0909
 TELEFAX: 713-850-0165
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 233 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-695-692B-7

Query Match 77.8%; Score 948; DB 4; Length 233;
 Best Local Similarity 76.4%; Pred. No. 2.6e-93;
 Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
 QY 1 SESEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSADQFLNTLLFKGFFTG 60
 Db 1 SESEINEKDLRKSELOGTALGNLKOIYYNSKAITSSSEKSADQFLNTLLFKGFFTG 60
 QY 61 HPWYNDLLVDLSTAAATSEYEGSSVDLYGAYGYCAGGTPNKTCMYGGVTLHDNNRLT 120
 Db 61 HSWYNDLLVDLSTAAATSEYEGSSVDLYGAYGYCAGGTPNKTCMYGGVTLHDNNRLT 120
 QY 121 BEKVPINWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVG 180
 Db 121 BEKVPINWIDGKQTTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVG 180
 QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTDILLRIYRNTTISSTLSISLYLYTT 233
 Db 181 RGLIVFHSSEGSTVSYDLFDAQGYPTDILLRIYRNTTISSTLSISLYLYTT 233

RESULT 16

US-08-486-099-113
 ; Sequence 113, Application US/08486099
 ; Patent No. 6013263
 ; GENERAL INFORMATION:
 ; APPLICANT: Bolognesi, Dani P.
 ; APPLICANT: Matthews, Thomas J.
 ; APPLICANT: Wild, Carl T.
 ; APPLICANT: Barney, Shawn O.
 ; APPLICANT: Lambert, Dennis M.
 ; APPLICANT: Petteway, Stephen R.
 ; APPLICANT: Langleis, Alphonse J.
 ; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
 ; FILE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
 ; TITLE OF INVENTION: B VIRUS TRANSMISSION
 ; NUMBER OF SEQUENCES: 209
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA

```

; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,099
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-486-099-113

Query Match 77.8%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.1e-93;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps- 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSADOFLTNTLLFKGFTTG 60
Db 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSADOFLTNTLLFKGFTTG 84
QY 61 HPWYNDLLVDLSTAAATSEYEGSSVDLYGAYGYQCAGGTENKTAACMYGGVTLHNNRLT 120
Db 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTENKTAACMYGGVTLHNNRLT 144
QY 121 EEKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGCKVQ 180
Db 145 EEKVPINLWDGKQTTVPLETVTNKKNVTVPQELDLQARHYLQEKYKLYNSDVFDCVKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISLSISLYLYTT 233
Db 205 RGLIVFHTSTSPSVNYDLFGAGQGYNTLLRIYRDNKNTINSENMHIDIYLYTS 257

RESULT 17
US-08-360-107A-123
; Sequence 123 Application US/08360107A
; Patent No. 6017336
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; NUMBER OF SEQUENCES: 149
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30

; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,099
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-486-099-113

Query Match 77.8%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.1e-93;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps- 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSADOFLTNTLLFKGFTTG 60
Db 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITSSEKSADOFLTNTLLFKGFTTG 84
QY 61 HPWYNDLLVDLSTAAATSEYEGSSVDLYGAYGYQCAGGTENKTAACMYGGVTLHNNRLT 120
Db 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTENKTAACMYGGVTLHNNRLT 144
QY 121 EEKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGCKVQ 180
Db 145 EEKVPINLWDGKQTTVPLETVTNKKNVTVPQELDLQARHYLQEKYKLYNSDVFDCVKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNNTTISLSISLYLYTT 233
Db 205 RGLIVFHTSTSPSVNYDLFGAGQGYNTLLRIYRDNKNTINSENMHIDIYLYTS 257

RESULT 18
US-08-484-223B-113
; Sequence 113 Application US/08484223B
; Patent No. 6020459
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; NUMBER OF SEQUENCES: 245
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30

```

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-223B-113

Query Match 77.8%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.1e-93;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSSSEKSAOFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHQFLQHTILFKGFFTD 84
QY 61 HPWYNLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVDFDSKDIVDKYKGVLDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EEKVPINLWIDGKQNTVPLETVKTKKNVTVOELDLQARRYLQEKYLYNSDVFDFGKVQ 204
QY 181 RGLIVFHSSEGSVSYDLFDAQOQYPTDTLRIYRDNTTISSTLSLSLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFCAQOQYNSNTLLRIYRDNKTINSENHDIYLYTS 257

RESULT 19
US-08-919-597-113
Sequence 113, Application US/08919597
Patent No. 6054265
GENERAL INFORMATION:
APPLICANT: Boicognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langleis, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/919,597
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/470,896
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-919-597-113

Query Match 77.8%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.1e-93;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSSSEKSAOFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHQFLQHTILFKGFFTD 84
QY 61 HPWYNLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVDFDSKDIVDKYKGVLDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EEKVPINLWIDGKQNTVPLETVKTKKNVTVOELDLQARRYLQEKYLYNSDVFDFGKVQ 204
QY 181 RGLIVFHSSEGSVSYDLFDAQOQYPTDTLRIYRDNTTISSTLSLSLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFCAQOQYNSNTLLRIYRDNKTINSENHDIYLYTS 257

RESULT 20
US-08-475-668A-113
Sequence 113, Application US/08475668A
Patent No. 6060065
GENERAL INFORMATION:
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,668A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742

REFERENCE/DOCKET NUMBER: 7872-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-475-668A-113

Query Match 77.8%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.1e-93;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKLSELOQTALGNLKOIYYNKAITSSEKSAQDFLNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKLSELOQTALGNLKOIYYNKAITSSEKSHDQFLOHTILFKGFFTD 84
QY 61 HPWYNDLLVDLGSTAAATSEYSSVDLYGAYGYCCAGGTENKTACMYGGVTLHNNRLT 120
Db 85 HSWYNDLLVDFDSKDIDVKYKGVKVDLYGAYGYCCAGGTENKTACMYGGVTLHNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVQ 180
Db 145 EEKVPINLWLDGKQNTVPLETVTNKKNVTVOELDQARHYLQEKYLYNSDVFDDGVQ 204
QY 181 RGLIVFHSSEGSTSVSYDLFDAQQGQYPTDILLRIYRDNNTTISLSISLYLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQQGQYNTLLRIYRDNKNTINSENMHIDIYLYTS 257

RESULT 21
US-08-485-551A-113
Sequence 113, Application US/08485551A
Patent No. 6068973
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485.551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-551A-113

Query Match 77.8%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.1e-93;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKLSELOQTALGNLKOIYYNKAITSSEKSAQDFLNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKLSELOQTALGNLKOIYYNKAITSSEKSHDQFLOHTILFKGFFTD 84
QY 61 HPWYNDLLVDLGSTAAATSEYSSVDLYGAYGYCCAGGTENKTACMYGGVTLHNNRLT 120
Db 85 HSWYNDLLVDFDSKDIDVKYKGVKVDLYGAYGYCCAGGTENKTACMYGGVTLHNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVQ 180
Db 145 EEKVPINLWLDGKQNTVPLETVTNKKNVTVOELDQARHYLQEKYLYNSDVFDDGVQ 204
QY 181 RGLIVFHSSEGSTSVSYDLFDAQQGQYPTDILLRIYRDNNTTISLSISLYLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQQGQYNTLLRIYRDNKNTINSENMHIDIYLYTS 257

RESULT 22
US-08-471-913A-113
Sequence 113, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471.913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:

SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-471-913A-113

Query Match 77.8%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.1e-93;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSAOQFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSHDQFLQHTILFKGFFTD 84
QY 61 HPWYNDLLVDFDSDKIDVVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSDKIDVVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKVKQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKVKQ 204
QY 181 RGLIVHSSGTSVSYDLFDAQOQYPTLLRIYRDNTTSSLSLSLYTT 233
DB 205 RGLIVHSTEPSVNYDLFDAQOQYNTLLRIYRDNKTINSENNHIDIYLYTS 257

RESULT 23
US-08-485-264A-113
Sequence 113, Application US/08485264A
Patent No. 628983
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 232
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-021
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 113:
LENGTH: 257 amino acids
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-264A-113

Query Match 77.8%; Score 948; DB 3; Length 257;
Best Local Similarity 76.4%; Pred. No. 3.1e-93;
Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSAOQFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSHDQFLQHTILFKGFFTD 84
QY 61 HPWYNDLLVDFDSDKIDVVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSDKIDVVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKVKQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKVKQ 204
QY 181 RGLIVHSSGTSVSYDLFDAQOQYPTLLRIYRDNTTSSLSLSLYTT 233
DB 205 RGLIVHSTEPSVNYDLFDAQOQYNTLLRIYRDNKTINSENNHIDIYLYTS 257

RESULT 24
US-08-474-349A-113
Sequence 113, Application US/08474349A
Patent No. 633395
GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
TITLE OF INVENTION: VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 113:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein

US-08-474-349A-113

Query Match 77.8%; Score 948; DB 4; Length 257;

Best Local Similarity 76.4%; Pred. No. 3.1e-93;

Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNNSKAITSEKSDAQFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNNEKAKTENKESHQDQFLQHTILFKGFFTD 84
QY 61 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 BEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 145 BEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYEDNTTISSTLSISLYLTT 233
DB 205 RGLIVFHTSTPVSNYDLFGAQQGYNTLLRIYRDNKTINSENHDIYLYTS 257

RESULT 25

US-08-470-896-113

; Sequence 113, Application US/08470896

; Patent No. 6479055

; GENERAL INFORMATION:

; APPLICANT: Bolognesi, Dani P.

; APPLICANT: Matthews, Thomas J.

; APPLICANT: Wild, Carl T.

; APPLICANT: Barney, Shawn O.

; APPLICANT: Lambert, Dennis M.

; APPLICANT: Petteway, Stephen R.

; APPLICANT: Langlois, Alphonse J.

; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION

; OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

; TITLE OF INVENTION: TRANSMISSION

; NUMBER OF SEQUENCES: 273

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/470,896

; FILING DATE: 06-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7872-020

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 113:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 257 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

US-08-470-896-113

Query Match

77.8%; Score 948; DB 4; Length 257;

Best Local Similarity 76.4%; Pred. No. 3.1e-93;

Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNNSKAITSEKSDAQFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNNEKAKTENKESHQDQFLQHTILFKGFFTD 84
QY 61 HPWYNDLLVDLGSTAATSEYEGSSVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 BEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 145 BEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNKTINSENHDIYLYTT 233
DB 205 RGLIVFHTSTPVSNYDLFGAQQGYNTLLRIYRDNKTINSENHDIYLYTS 257

RESULT 26

US-08-485-546A-113

; Sequence 113, Application US/08485546A

; Patent No. 6518013

; GENERAL INFORMATION:

; APPLICANT: Bolognesi, Dani P.

; APPLICANT: Matthews, Thomas J.

; APPLICANT: Wild, Carl T.

; APPLICANT: Barney, Shawn O.

; APPLICANT: Lambert, Dennis M.

; APPLICANT: Petteway, Stephen R.

; APPLICANT: Langlois, Alphonse J.

; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE

; FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS

; TITLE OF INVENTION: TRANSMISSION

; NUMBER OF SEQUENCES: 214

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/485,546A

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Coruzzi, Laura A.

; REGISTRATION NUMBER: 30,742

; REFERENCE/DOCKET NUMBER: 7872-028

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (212) 790-9090

; TELEFAX: (212) 869-9741/8864

; TELEX: 66141 PENNIE

; INFORMATION FOR SEQ ID NO: 113:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 257 amino acids

; TYPE: amino acid

; STRANDEDNESS:

; TOPOLOGY: unknown

; MOLECULE TYPE: protein

US-08-485-546A-113

Query Match

77.8%; Score 948; DB 4; Length 257;

Best Local Similarity 76.4%; Pred. No. 3.1e-93;

Matches 178; Conservative 21; Mismatches 34; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKSAQOFLNTLTLFKGFFTG 60
 Db 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHDOFLQHTILFKGFFTD 84
 QY 61 HPWYNDLLVDLGSTAAITSEYEGSSVDLYGAYGYQCAGGTPNKTKACMYGGVTLHDNNRLT 120
 Db 85 HSWYNDLLVDLDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTKACMYGGVTLHDNNRLT 144
 QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 180
 Db 145 EEKVPINLWIDGKQNTVPLETVTKNKNVTVOELDLQARRYLQEKYKLYNSDVFDEGKQV 204
 QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNTTISSTLSISLYTT 233
 Db 205 RGLIVFHTSTEPSVNYDLFGAQGYSTNLLRIYRDNTKNTINSENMHIDIYLYTS 257
 RESULT 27
 US-08-446-918A-4
 ; Sequence 4, Application US/08446918A
 ; Patent No. 5705151
 ; GENERAL INFORMATION:
 ; APPLICANT: Dow, Steve W.
 ; APPLICANT: Elmslie, Robyn E.
 ; TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
 ; NUMBER OF SEQUENCES: 12
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sheridan Ross & McIntosh
 ; STREET: 1700 Lincoln Street, Suite 3500
 ; CITY: Denver
 ; STATE: Colorado
 ; COUNTRY: U.S.A.
 ; ZIP: 80203
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/446,918A
 ; FILING DATE: 18-MAY-1995
 ; CLASSIFICATION: 552
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kovarik, Joseph E.
 ; REGISTRATION NUMBER: 33,005
 ; REFERENCE/DOCKET NUMBER: 2879-29
 ; TELEPHONE: (303) 863-9700
 ; TELEFAX: (303) 863-0223
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 233 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-446-918A-4
 Query Match 77.5%; Score 944; DB 1; Length 233;
 Best Local Similarity 76.3%; Pred. No. 7.1e-93;
 Matches 177; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
 QY 2 EKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKSAQOFLNTLTLFKGFFTG 61
 Db 2 EKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHDOFLQHTILFKGFFTD 61
 QY 62 PWYNDLLVDLGSTAAITSEYEGSSVDLYGAYGYQCAGGTPNKTKACMYGGVTLHDNNRLTE 121
 Db 62 SWYNDLLVDLDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTKACMYGGVTLHDNNRLTE 121
 QY 122 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 181
 Db 122 EEKVPINLWIDGKQNTVPLETVTKNKNVTVOELDLQARRYLQEKYKLYNSDVFDEGKQV 181
 QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNTTISSTLSISLYTT 233
 Db 181 RGLIVFHTSTEPSVNYDLFGAQGYSTNLLRIYRDNTKNTINSENMHIDIYLYTS 257
 RESULT 29
 US-08-896-933-23
 ; Sequence 23, Application US/08896933
 ; Patent No. 6221351
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.

QY 182 GLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNTTISSTLSISLYTT 233
 Db 182 GLIVFHTSTEPSVNYDLFGAQGYSTNLLRIYRDNTKNTINSENMHIDIYLYTS 233
 RESULT 28
 US-08-580-806-4
 ; Sequence 4, Application US/08580806
 ; Patent No. 5935568
 ; GENERAL INFORMATION:
 ; APPLICANT: Dow, Steve W.
 ; APPLICANT: Elmslie, Robyn E.
 ; APPLICANT: Potter, Terence A.
 ; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Sheridan Ross & McIntosh
 ; STREET: 1700 Lincoln Street, Suite 3500
 ; CITY: Denver
 ; STATE: Colorado
 ; COUNTRY: U.S.A.
 ; ZIP: 80203
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/580,806
 ; FILING DATE:
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Connell, Gary J.
 ; REGISTRATION NUMBER: 32,020
 ; REFERENCE/DOCKET NUMBER: 2879-29-C1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (303) 863-9700
 ; TELEFAX: (303) 863-0223
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 233 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-580-806-4
 Query Match 77.5%; Score 944; DB 2; Length 233;
 Best Local Similarity 76.3%; Pred. No. 7.1e-93;
 Matches 177; Conservative 21; Mismatches 34; Indels 0; Gaps 0;
 QY 2 EKSEINEKDLRKSELOQTALGNLKOIYYNSKAITSEKSAQOFLNTLTLFKGFFTG 61
 Db 2 EKSEINEKDLRKSELOQTALGNLKOIYYNEKAKTENKESHDOFLQHTILFKGFFTD 61
 QY 62 PWYNDLLVDLGSTAAITSEYEGSSVDLYGAYGYQCAGGTPNKTKACMYGGVTLHDNNRLTE 121
 Db 62 SWYNDLLVDLDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTKACMYGGVTLHDNNRLTE 121
 QY 122 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 181
 Db 122 EEKVPINLWIDGKQNTVPLETVTKNKNVTVOELDLQARRYLQEKYKLYNSDVFDEGKQV 181
 QY 182 GLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNTTISSTLSISLYTT 233
 Db 182 GLIVFHTSTEPSVNYDLFGAQGYSTNLLRIYRDNTKNTINSENMHIDIYLYTS 233
 RESULT 29
 US-08-896-933-23
 ; Sequence 23, Application US/08896933
 ; Patent No. 6221351
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.

; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 ; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
 ; FILE REFERENCE: 09629/005002
 ; CURRENT APPLICATION NUMBER: US/08/896,933
 ; CURRENT FILING DATE: 1997-07-18
 ; EARLIER APPLICATION NUMBER: 08/252,978
 ; EARLIER FILING DATE: 1994-06-02
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 23
 ; LENGTH: 232
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-08-896-933-23

Query Match 76.5%; Score 931.5; DB 3; Length 232;
 Best Local Similarity 76.0%; Pred. No. 1.5e-91;
 Matches 177; Conservative 21; Mismatches 34; Indels 1; Gaps 1;
 QY 1 SEKSEINEKDLRKXSELOGTALGNLKOIYYNKAITSSEKSADQFLTNTLLFKGFTG 60
 DB 1 SEKSEINEKDLRKXSELOGTALGNLKOIYYNKAITSSEKSADQFLTNTLLFKGFTG 59
 QY 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYOCAGTGNKTAACMYGGVTLHNNRLT 120
 DB 60 HSWYNDLLVDFSDKIDVKYKGGKVDLYGAYGYOCAGTGNKTAACMYGGVTLHNNRLT 119
 QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVEQDLQARHYLHGKFLYNSDSFGKVKQ 180
 DB 120 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVEQDLQARHYLHGKFLYNSDSFGKVKQ 179
 QY 181 RGLIVFHSSEGSTVSYDLFDAGQYPTDILLRIYRDNNTTISLSISLYTT 233
 DB 180 RGLIVFHTSTEPSVNDLFGAGQYNTLLRIYRDNNTTINSENHIDIYLYTS 232

RESULT 30
 US-09-314-235-23
 ; Sequence 23, Application US/09314235
 ; Patent No. 6338845
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 ; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
 ; FILE REFERENCE: 09629/005004
 ; CURRENT APPLICATION NUMBER: US/09/314,235
 ; CURRENT FILING DATE: 1999-05-18
 ; EARLIER APPLICATION NUMBER: 08/896,933
 ; EARLIER FILING DATE: 1997-07-18
 ; EARLIER APPLICATION NUMBER: 08/252,978
 ; EARLIER FILING DATE: 1994-06-02
 ; EARLIER APPLICATION NUMBER: 07/891,718
 ; EARLIER FILING DATE: 1992-06-01
 ; EARLIER APPLICATION NUMBER: US91/00342
 ; EARLIER FILING DATE: 1991-01-17
 ; EARLIER APPLICATION NUMBER: 07/466,577
 ; EARLIER FILING DATE: 1990-01-17
 ; EARLIER APPLICATION NUMBER: 07/416,530
 ; EARLIER FILING DATE: 1989-10-03
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 23
 ; LENGTH: 232
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-314-235-23

Query Match 76.5%; Score 931.5; DB 4; Length 232;
 Best Local Similarity 76.0%; Pred. No. 1.5e-91;
 Matches 177; Conservative 21; Mismatches 34; Indels 1; Gaps 1;
 QY 1 SEKSEINEKDLRKXSELOGTALGNLKOIYYNKAITSSEKSADQFLTNTLLFKGFTG 60

DB 1 SEKSEINEKDLRKXSELOGTALGNLKOIYYNKAITSSEKSADQFLTNTLLFKGFTG 59
 QY 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYOCAGTGNKTAACMYGGVTLHNNRLT 120
 DB 60 HSWYNDLLVDFSDKIDVKYKGGKVDLYGAYGYOCAGTGNKTAACMYGGVTLHNNRLT 119
 QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVEQDLQARHYLHGKFLYNSDSFGKVKQ 180
 DB 120 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVEQDLQARHYLHGKFLYNSDSFGKVKQ 179
 QY 181 RGLIVFHSSEGSTVSYDLFDAGQYPTDILLRIYRDNNTTISLSISLYTT 233
 DB 180 RGLIVFHTSTEPSVNDLFGAGQYNTLLRIYRDNNTTINSENHIDIYLYTS 232

RESULT 31
 US-09-144-776B-2
 ; Sequence 2, Application US/09144776B
 ; Patent No. 6399332
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Ulrich,
 ; Mark A. Olson
 ; Sina Bavari
 ; TITLE OF INVENTION: Bacterial Superantigen
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Charles H. Harris
 ; STREET: US Army MRC - 504 Scott Street
 ; MCMR-JA (Charles H. Harris-Patent
 ; Acty)
 ; CITY: FORT DETRICK
 ; STATE: MARYLAND
 ; COUNTRY: USA
 ; ZIP: 21702-5012
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh 7.5
 ; SOFTWARE: Microsoft Word 6.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/144,776B
 ; FILING DATE: 01-Sep-1998
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/882,431
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Charles H. Harris
 ; REGISTRATION NUMBER: 34,616
 ; REFERENCE/DOCKET NUMBER: <Unknown>
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 619-2065
 ; TELEFAX: (301) 619-7714
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 257
 ; TYPE: Amino Acid
 ; STRANDEDNESS: Unknown
 ; TOPOLOGY: Unknown
 ; MOLECULE TYPE: Peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-144-776B-2

Query Match 75.9%; Score 925; DB 4; Length 257;
 Best Local Similarity 75.1%; Pred. No. 8.9e-91;
 Matches 175; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKXSELOGTALGNLKOIYYNKAITSSEKSADQFLTNTLLFKGFTG 60
 DB 25 SEKSEINEKDLRKXSELOGTALGNLKOIYYNKAITSSEKSADQFLTNTLLFKGFTG 84
 QY 61 HPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYOCAGTGNKTAACMYGGVTLHNNRLT 120

Db 85 HSWNDLLVRFDSDKIDVYKGGKVDLYGAVAGYOCAGTGNKTACMYGGVTLDHNNRLT 144
QY 121 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EKKVPINLWIDGKQNTVPLETVKTKNKQNTVQELDLQARRYLOEKYLNLSVDVFDGKVQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNTTISSTLSLSLYLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFQAQOQYNTLLRIYRDNTKINSENHDIYLYTS 257

RESULT 32
US-09-144-776B-4
; Sequence 4, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Att'y)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-144-776B-4

Query Match 75.6%; Score 921; DB 4; Length 233;
Best Local Similarity 75.0%; Pred. No. 2e-90;
Matches 174; Conservative 21; Mismatches 37; Indels 0; Gaps 0;
QY 2 EKSEINEKDLRKSELOGTALGNLQIYYNKAITSSEKSADOFLLTLFKGFFFTGH 61
Db 2 EKSEINEKDLRKSELOGTALGNLQIYYNKAITENKESHDQFRQLTLFKGFFTDH 61
QY 62 PWTNDDLVLGSLTAATSEYEGSSVDLYGAYGQCAGGTPNKTACMYGGVTLDHNNRLTE 121
Db 62 SWNDLLVRFDSDKIDVYKGGKVDLYGAVAGYOCAGGTPNKTACMYGGVTLDHNNRLTE 121

QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 181
Db 122 EKKVPINLWIDGKQNTVPLETVKTKNKQNTVQELDLQARRYLOEKYLNLSVDVFDGKVQ 181
QY 182 GLIVFHSSEGSTVSYDLFDAQOQYPTLLRIYRDNTTISSTLSLSLYLYTT 233
Db 182 GLIVFHTSTEPSVNYDLFQAQOQYNTLLRIYRDNTKINSENHDIYLYTS 233
RESULT 33
US-08-896-933-25
; Sequence 25, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-08-896-933-25
Query Match 49.7%; Score 605; DB 3; Length 228;
Best Local Similarity 52.0%; Pred. No. 1.3e-56;
Matches 117; Conservative 33; Mismatches 75; Indels 0; Gaps 0;
QY 7 INKDLRKSELOGTALGNLQIYYNKAITSSEKSADOFLLTLFKGFFFTGHWN 66
Db 2 VKEKELHKKSELSSTALNNMKHSYADKNPIIGENKSTGDFLENTLLYKKFFTDLINFED 61
QY 67 LLDVLDGSTAATSEYEGSSVDLYGAYGYOCAGGTPNKTACMYGGVTLDHNNRLTEKKVP 126
Db 62 LLINFSKEMAQHFKNVDVYFIRISINCYGGEIDRTACTYGGVTPHEGNLKEKKP 121
QY 127 INLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQGLIVF 186
Db 122 INLWINGVQKESVLDKVCQTDKQNTVQELDLQARRYLOKDLKLYNNNDTLGGKIQGKIEF 181
QY 187 HSSEGSTVSYDLFDAQOQYPTLLRIYRDNTTISSTLSLSLYLY 231
Db 182 DSSDGSKVSYDLFVKGDFPEKQLRIYSONKTLSTEHLDIYLY 226

RESULT 34
US-09-314-235-25
; Sequence 25, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530

```
;
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-314-235-25

Query Match          49.7%; Score 605; DB 4; Length 228;
Best Local Similarity 52.0%; Pred. No. 1.3e-56;
Matches 117; Conservative 33; Mismatches 75; Indels 0; Gaps 0;

QY 7 INEKDLRKSELOQTALCNLKOIYYVNSKATTSSEKSADQFLNTLLFKGFTGHPWYND 66
Db 2 VKKELHKKSLSSTALNNMKGSHVADKNPIIGENKSTGQDFLENTLLYKKFTDLINFED 61
QY 67 LLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTPNTACMYGGVTLHDNNRLTEKKVP 126
Db 62 LLINFNSKEMAHFKPKSNVDYPIRYINCYGGBIDRTACTYGGVTPHEGNKLKERKKIP 121
QY 127 INLWDGKQTVVPIDKVKTSKKEVTVOELDLQARHYLHGRFGLYNSDSFGKVKVQRLIVF 166
Db 122 INLWINGVQKESVDKVDKNTVQELDLQARHYLHGRFGLYNSDSFGKVKVQRLIVF 166
QY 187 HSEGSTSVSYDLFDAQGQVPTLLRIYRDNNTTISTSLISLXLY 231
Db 182 DSDGSKVSYDLFVKGDFPEKQLRIYSDNKTLSLTHLHIDVLY 226

RESULT 35
US-09-144-776B-19
; Sequence 19, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MPMC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-144-776B-19

Query Match          29.7%; Score 362; DB 4; Length 82;
Best Local Similarity 79.3%; Pred. No. 2.8e-31;
Matches 65; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 43 SADQFLNTLLFKGFTGHPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTPN 102
Db 1 SDQQLFNTLLFKGFTGHPWYNDLLVDLGSKDANKYKGVKVDLYGAYGYQCAGGTPN 60
QY 103 KTACMYGGVTLHDNNRLTEKK 124
Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 36
US-09-144-776B-17
; Sequence 17, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MPMC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-144-776B-17

Query Match          29.7%; Score 362; DB 4; Length 82;
Best Local Similarity 79.3%; Pred. No. 2.8e-31;
Matches 65; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 43 SADQFLNTLLFKGFTGHPWYNDLLVDLGSTAAATSEYEGSSVDLYGAYGYQCAGGTPN 102
```



```
; Sequence 29, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-314-235-29

Query Match      22.2%; Score 270.5; DB 4; Length 221;
Best Local Similarity 33.8%; Pred. No. 8.1e-21;
Matches 76; Conservative 42; Mismatches 88; Indels 19; Gaps 10;

QY      16  SELQGTAL-GNLKQIYY-YNSKAIT-SSEKSAQDQFLNTLLFKGFFTHGHPWYNDLLVDLG 72
Db      7  SOLHRSVLXNLQNIYFLYEGDPVTHENVKSVQDQLSHDLIYN---VSGPNYDKLTELK 63

QY      73  STAATSEYEGSVLDYGAAYGYQC-AGGTPNKTAQMGVTLHDNNRLTEKKVPINLWI 131
Db      64  NQEMATLFDKKNVDIYGVVEYHLCVLCENASRSACIYGGVTNHEGHNLEIPKKIWKVSI 123

QY      132 DGKQTTVPIDKVKTSKKEVTVOELDLQARHVLHGKFGLYNSDSFGGKVQGLIVFHSSEG 191
Db      124 DGIO-SLSFD-IFTNKQWTAQELDYKVRKYLTDNKLQYNGP--SKYETGYIKFIPKNK 179

QY      192 STVSVDLPD----AQGOYPTLLRIYRDNTTISSTLSISLYLT 232
Db      180 ESFWEDLPPEPEFTQSKY----LMYKDNETLDSNTSQIEVYLT 220

RESULT 41
US-08-973-391C-13
; Sequence 13, Application US/08973391C
; Patent No. 6632441
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoehr, Jennifer
; APPLICANT: Chlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973,391C
; CURRENT FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes

; Sequence 29, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-314-235-29

Query Match      22.0%; Score 268.5; DB 4; Length 251;
Best Local Similarity 32.5%; Pred. No. 1.6e-20;
Matches 77; Conservative 45; Mismatches 96; Indels 19; Gaps 10;

QY      4  SBEINEKDLRKKESELQGTAL-GNLKQIYY-YNSKAIT-SSEKSAQDQFLNTLLFKGFFTHG 60
Db      25  SQEFAQQDPDPSQLHRSVLXNLQNIYFLYEGDPVTHENVKSVQDQLSHDLIYN---VS 81

QY      61  HPWYNDLLVDLGSTAATSEYEGSVLDYGAAYGYQC-AGGTPNKTAQMGVTLHDNNRL 119
Db      82  GPNYDKLTELKQEMATLFDKKNVDIYGVVEYHLCVLCENASRSACIYGGVTNHEGHN 141

QY      120 TEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHVLHGKFGLYNSDSFGGKV 179
Db      142 ETPKKIIVKVSIDGIQ-SLSFD-IFTNKQWTAQELDYKVRKYLTDNKLQYNGP--SKY 197

QY      180 QRGLIVFHSSEGTSVSYDLFD----AQGOYPTLLRIYRDNTTISSTLSISLYLT 232
Db      198 ETGYIKFIPKNKESFWDFPEPEFTQSKY----LMYKDNETLDSNTSQIEVYLT 250

RESULT 42
US-08-446-918A-2
; Sequence 2, Application US/08446918A
; Patent No. 5705151
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmelle, Robyn E.
; TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,918A
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 552
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-29
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-918A-2

Query Match      22.0%; Score 267.5; DB 1; Length 255;
Best Local Similarity 31.7%; Pred. No. 2.1e-20;
Matches 77; Conservative 43; Mismatches 104; Indels 19; Gaps 8;

QY      2  EKSEINEKDLRKKESELQGTALGNLQIYYNSKAITSEKSAQDQFLNTLLFKGFFTHG 61
Db      17  ESQDPKPDDELKSSKFTG-LMENMK-VLYDDNHVSAINVKSIDQELDYDLIVSIKDTKL 74

QY      62  PWNDDLVDLGSTAATSEYEGSVLDYGAAYGYQC-----AGGTPNKTAQMGV 111
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Db 75 GNYDNVRVBFKNDLADKYDKYVDVFGVANYQCYFSSKKTNDINSHQTDKREKTCMYGGV 134
QY 112 TLHNNRLTEEEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYN 171
Db 135 TEHNGNQLDKYRSITVRVEDGK-NLLSFD-VQTNKKKYTAQELDYLTRHYLVKNNKLYE 192
QY 172 SDSFGKVORGLIVFHSSSGSTVSVDLFDQAQGYPD--TLRIYRDNTTISSTLSISLY 229
Db 193 FNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNKNKVDKSKVIEVY 249
QY 230 LYT 232
Db 250 LTT 252

RESULT 43
US-08-580-806-2
; Sequence 2, Application US/08580806
; Patent No. 5935568
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmslie, Robyn E.
; APPLICANT: Potter, Terence A.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,806
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-29-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-580-806-2

Query Match 22.0%; Score 267.5; DB 2; Length 255;
Best Local Similarity 31.7%; Pred. No. 2.1e-20;
Matches 77; Conservative 43; Mismatches 104; Indels 19; Gaps 8;

QY 2 EKSEINEKDLRCKSELOQTALGNLKIYYNSKAITSEKSADQFLNTLLFKGFFTGH 61
Db 17 ESQDPKPKDELHKSRTG-LMENMK-VLYDDNHVSAINVKSIDQFLFDLLIYSKOTKL 74
QY 62 PWNLDLLVGLTAATSEYEGSSVDLYGAYGYQC-----AGTTPNKTCMYGGV 111
Db 75 GNYDNVRVBFKNDLADKYDKYVDVFGVANYQCYFSSKKTNDINSHQTDKREKTCMYGGV 134
QY 112 TLHNNRLTEEEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYN 171
Db 135 TEHNGNQLDKYRSITVRVEDGK-NLLSFD-VQTNKKKYTAQELDYLTRHYLVKNNKLYE 192
QY 172 SDSFGKVORGLIVFHSSSGSTVSVDLFDQAQGYPD--TLRIYRDNTTISSTLSISLY 229

Db 193 FNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNKNKVDKSKVIEVY 249
QY 230 LYT 232
Db 250 LTT 252

RESULT 44
US-08-973-391C-14
; Sequence 14, Application US/08973391C
; Patent No. 6632441
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoehr, Jennifer
; APPLICANT: Orlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973,391C
; CURRENT FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 14
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-973-391C-14

Query Match 21.8%; Score 265.5; DB 4; Length 221;
Best Local Similarity 33.3%; Pred. No. 2.8e-20;
Matches 75; Conservative 42; Mismatches 89; Indels 19; Gaps 10;

QY 16 SELQGTAL-GNLKQIYY-YNSKAIT-SSEKSADQFLNTLLFKGFFTGHFWYNDLLVDLG 72
Db 7 SOLHRSLSVKNLQNIYFLYEGDPVTHENVKSVQQLLSHLIYN---VSGENYDKLKTCLK 63
QY 73 STATSEYEGSSVDLYGAYGYQC-AGTTPNKTCMYGGVTLHNNRLTEEEKVPINLMI 131
Db 64 NOEMATLFDKKNVDIYGEVYHLCYCENABRSACIYGGVTHNEGHNHLEIPKIVKVS 123
QY 132 DGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVORGLIVFHSS 191
Db 124 DGIQ-SLSFD-ISTNKKWMTAQELDYKVKYKLTNDKQLYTNGP--SKYETGYIKFIPK 179
QY 192 STVSVDLFD---AQGYPTLLRIYRDNTTISSTLSISLYLT 232
Db 180 ESFWDFPEPEPTQSKY----LMIYNDNETLDSNTSQIEVYLT 220

RESULT 45
US-08-896-933-27
; Sequence 27, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus

US-08-896-933-27

Query Match 21.7%; Score 264.5; DB 3; Length 239;
 Best Local Similarity 31.1%; Pred. No. 4e-20;
 Matches 76; Conservative 43; Mismatches 104; Indels 21; Gaps 9;

QY 2 EKSEINEKDLRKSELOGTALGNLKOIY--YNSKALTSSEKSAQDQFLNTLLFKGFFT 59
 DB 1 ESQDPDPTDELHKASKFTG-LMENKVKLYDDHYVS---ATKVKSVDRFLAHLIYINISDK 56
 QY 60 GHPWYNLLVDLGGSTAATSEYEGSSVDLYGAYGYQC-----AGGTPNKATCMYGGVT 112
 DB 57 KLNVDKVKTELLNEGLAKKYKDEVDVYGNVYVNCVFFSKDNVGVTKGKTMYGGIT 116
 QY 113 LHDNNRLTEE--KKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKGLY 170
 DB 117 KHEGHNFDNGNLQNLVIRVY-ENKNTISFE-VQTDKKSQVTAQELDIKARNFLINKKNLY 174
 QY 171 NSDSFGGKVQORGLIVFHSSEGSTSVYDLFDAQGOYPD--TLRIYRDNNTTISSTLSISL 228
 DB 175 EFNS--SPYETGYIKFIENNGNTFWYDLMPAPGDKFDQSKYLMYNDKNTVDSKSVKIEV 232
 QY 229 YLYT 232
 DB 233 HLTT 236

RESULT 47
 US-09-144-776B-16
 ; Sequence 16, Application US/09144776B
 ; Patent No. 6399332
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Ulrich,
 ; Sina Bavari
 ; TITLE OF INVENTION: Bacterial Superantigen
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSES: Charles H. Harris
 ; STREET: US Army MPMC -504 Scott Street
 ; MCMR-JA (Charles H. Harris-Patent
 ; Attv)
 ; CITY: FORT DETRICK
 ; STATE: MARYLAND
 ; COUNTRY: USA
 ; ZIP: 21702-5012
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh 7.5
 ; SOFTWARE: Microsoft Word 6.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/144,776B
 ; FILING DATE: 01-Sep-1998
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/882,431
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Charles H. Harris
 ; REGISTRATION NUMBER: 34,616
 ; REFERENCE/DOCKET NUMBER: <Unknown>
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 619-2065
 ; TELEFAX: (301) 619-7714
 ; INFORMATION FOR SEQ ID NO: 16:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 251
 ; TYPE: Amino Acid
 ; STRANDEDNESS: Unknown
 ; TOPOLOGY: Unknown
 ; MOLECULE TYPE: Peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 US-09-144-776B-16

Query Match 21.6%; Score 263.5; DB 4; Length 251;
 Best Local Similarity 32.1%; Pred. No. 5.5e-20;
 Matches 76; Conservative 45; Mismatches 97; Indels 19; Gaps 10;

QY 4 SEINEKDLRKSELOGTALGNLKOIY--YNSKALTSSEKSAQDQFLNTLLFKGFFT 60
 DB 25 SQSVFAQQDPDPSQLHRSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYN---VS 81
 QY 61 HPWYNLLVDLGGSTAATSEYEGSSVDLYGAYGYQC--AGGTPNKATCMYGGVTLHDNNRL 119
 DB 82 GPNYDKLTKELKNQEMATLFDKKNVDIYGVYVHLYLNCENASERSACIIGGVTHNEGNHL 141
 QY 120 TEEKKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKGLYNSDSFGKV 179

us-09-900-766-2.ra1

US-08-896-933-27

Query Match 21.7%; Score 264.5; DB 3; Length 239;
 Best Local Similarity 31.1%; Pred. No. 4e-20;
 Matches 76; Conservative 43; Mismatches 104; Indels 21; Gaps 9;

QY 2 EKSEINEKDLRKSELOGTALGNLKOIY--YNSKALTSSEKSAQDQFLNTLLFKGFFT 59
 DB 1 ESQDPDPTDELHKASKFTG-LMENKVKLYDDHYVS---ATKVKSVDRFLAHLIYINISDK 56
 QY 60 GHPWYNLLVDLGGSTAATSEYEGSSVDLYGAYGYQC-----AGGTPNKATCMYGGVT 112
 DB 57 KLNVDKVKTELLNEGLAKKYKDEVDVYGNVYVNCVFFSKDNVGVTKGKTMYGGIT 116
 QY 113 LHDNNRLTEE--KKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKGLY 170
 DB 117 KHEGHNFDNGNLQNLVIRVY-ENKNTISFE-VQTDKKSQVTAQELDIKARNFLINKKNLY 174
 QY 171 NSDSFGGKVQORGLIVFHSSEGSTSVYDLFDAQGOYPD--TLRIYRDNNTTISSTLSISL 228
 DB 175 EFNS--SPYETGYIKFIENNGNTFWYDLMPAPGDKFDQSKYLMYNDKNTVDSKSVKIEV 232
 QY 229 YLYT 232
 DB 233 HLTT 236

RESULT 46
 US-09-314-235-27
 ; Sequence 27, Application US/09314235
 ; Patent No. 6338845
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 ; AND RELATED COMPOUNDS
 ; FILE REFERENCE: 09629/005004
 ; CURRENT APPLICATION NUMBER: US/09/314,235
 ; EARLIER FILING DATE: 1999-05-18
 ; EARLIER APPLICATION NUMBER: 08/896,933
 ; EARLIER FILING DATE: 1997-07-18
 ; EARLIER APPLICATION NUMBER: 08/252,978
 ; EARLIER FILING DATE: 1994-06-02
 ; EARLIER APPLICATION NUMBER: 07/891,718
 ; EARLIER FILING DATE: 1992-06-01
 ; EARLIER APPLICATION NUMBER: US91/00342
 ; EARLIER FILING DATE: 1991-01-17
 ; EARLIER APPLICATION NUMBER: 07/466,577
 ; EARLIER FILING DATE: 1990-01-17
 ; EARLIER APPLICATION NUMBER: 07/416,530
 ; EARLIER FILING DATE: 1989-10-03
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 27
 ; LENGTH: 239
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-314-235-27

Query Match 21.7%; Score 264.5; DB 4; Length 239;
 Best Local Similarity 31.1%; Pred. No. 4e-20;
 Matches 76; Conservative 43; Mismatches 104; Indels 21; Gaps 9;

QY 2 EKSEINEKDLRKSELOGTALGNLKOIY--YNSKALTSSEKSAQDQFLNTLLFKGFFT 59
 DB 1 ESQDPDPTDELHKASKFTG-LMENKVKLYDDHYVS---ATKVKSVDRFLAHLIYINISDK 56
 QY 60 GHPWYNLLVDLGGSTAATSEYEGSSVDLYGAYGYQC-----AGGTPNKATCMYGGVT 112
 DB 57 KLNVDKVKTELLNEGLAKKYKDEVDVYGNVYVNCVFFSKDNVGVTKGKTMYGGIT 116
 QY 113 LHDNNRLTEE--KKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKGLY 170
 DB 117 KHEGHNFDNGNLQNLVIRVY-ENKNTISFE-VQTDKKSQVTAQELDIKARNFLINKKNLY 174

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Db 142 EIPKIVVYKSIDGQ-SLSFD-IETNKKMVAQELDYKVRKVLTDNKKQLYTNGP--SKY 197
Qy 180 ORGLIVFHSSEGTVDLPD---AQGGYDPTLLRIYRNTTTSISLSLYLT 232
Db 198 ETGVIKFIKPKNESFWDFPEPEFTQSKY---LMIYKDNELDSNTQIEVLT 250

RESULT 48
US-08-896-933-26
; Sequence 26, Application US/0896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPRANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-26

Query Match 21.4%; Score 260.5; DB 3; Length 239;
Best Local Similarity 32.0%; Pred. No. 1.1e-19;
Matches 77; Conservative 41; Mismatches 104; Indels 19; Gaps 8;

Qy 2 EKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSAQDPLTNTLLFKGFFTG 61
Db 1 ESQDPKPKDELHKSSKFTG-LMENMK-VLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKL 58
Qy 62 PWYNDLLVLDLGSTAATSEYEGSSVDLYGAYGYQC-----AGGTPNKTCMYGGV 111
Db 59 GNYDNVRVEFPKNDLADKYKDYVDFGANYYYQCYFSKKTNDINSHQTDKRTCMYGGV 118
Qy 112 TLHDNNRLTEKKVPINLMDIGKQTTVPIDKVKTSKEVTVQELDQARHYLHGKFLYN 171
Db 119 TEHNGQLDKYRSLTVRVFEDGK-NLLSFD-VQTNKKKVTQAELDYLTRHYLVKNKKLYE 176
Qy 172 SDSFGKVGRLIVFHSSEGTVSVDLPDAQGYPD--TLRIYRNTTTSISLSISLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDLPAPGDKFQSKYLMYNDNMVDSKDKVIEVY 233
Qy 230 L 230
Db 234 L 234

RESULT 49
US-09-314-235-26
; Sequence 26, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPRANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; EARLIER FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
```

```
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-314-235-26

Query Match 21.4%; Score 260.5; DB 4; Length 239;
Best Local Similarity 32.0%; Pred. No. 1.1e-19;
Matches 77; Conservative 41; Mismatches 104; Indels 19; Gaps 8;

Qy 2 EKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSAQDPLTNTLLFKGFFTG 61
Db 1 ESQDPKPKDELHKSSKFTG-LMENMK-VLYDDNHVSAINVKSIDQFLYFDLIYSIKDTKL 58
Qy 62 PWYNDLLVLDLGSTAATSEYEGSSVDLYGAYGYQC-----AGGTPNKTCMYGGV 111
Db 59 GNYDNVRVEFPKNDLADKYKDYVDFGANYYYQCYFSKKTNDINSHQTDKRTCMYGGV 118
Qy 112 TLHDNNRLTEKKVPINLMDIGKQTTVPIDKVKTSKEVTVQELDQARHYLHGKFLYN 171
Db 119 TEHNGQLDKYRSLTVRVFEDGK-NLLSFD-VQTNKKKVTQAELDYLTRHYLVKNKKLYE 176
Qy 172 SDSFGKVGRLIVFHSSEGTVSVDLPDAQGYPD--TLRIYRNTTTSISLSISLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDLPAPGDKFQSKYLMYNDNMVDSKDKVIEVY 233
Qy 230 L 230
Db 234 L 234

RESULT 50
US-09-414-276-8
; Sequence 8, Application US/09414276
; Patent No. 6392121
; GENERAL INFORMATION:
; APPLICANT: Mason, Hugh
; APPLICANT: Palmer, Kenneth
; APPLICANT: Hefferon, Kathleen
; APPLICANT: Mor, Tsafir
; APPLICANT: Artzen, Charles
; TITLE OF INVENTION: Gemini Virus Vectors for Gene Expression in Plants
; FILE REFERENCE: 4868/84453
; CURRENT APPLICATION NUMBER: US/09/414,276
; EARLIER FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 266
; TYPE: PRT
; ORGANISM: bean yellow dwarf virus
US-09-414-276-8

Query Match 21.4%; Score 260.5; DB 4; Length 266;
Best Local Similarity 31.1%; Pred. No. 1.3e-19;
Matches 76; Conservative 44; Mismatches 105; Indels 19; Gaps 8;

Qy 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNKAITSSEKSAQDPLTNTLLFKGFFTG 60
Db 27 AESQDPKPKDELHKSSKFTG-LMENMK-VLYDDNHVSAINVKSIDQSLYFDLIYSIKDTK 84
Qy 61 HPWYNDLLVLDLGSTAATSEYEGSSVDLYGAYGYQC-----AGGTPNKTCMYGGV 110
Db 85 LGYDNVRVEFPKNDLADKYKDYVDFGANYYYQCYFSKKTNDINSHQTDKRTCMYGGV 144
Qy 111 VTLDHNNRLTEKKVPINLMDIGKQTTVPIDKVKTSKEVTVQELDQARHYLHGKFLY 170
Db 145 VTEHNGQLDKYRSITVRVFEEDGK-NLLSFD-VQTNKKKVTQAELDYLTRHYLVKNKKLY 202
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QY 171 NSDSFGGKVQGLIVFHSSEGSVSYDLFDAQOYDP--TLRLRYRDNNTTSSISLSL 228
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMWPAQGXKFCQSKYLMYNDKNWVDSKDVKIEV 259
QY 229 YLYT 232
Db 260 YLYT 263

RESULT 51
US-09-144-776B-6
; Sequence 6, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144, 776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 286
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-144-776B-6

Query Match 21.4%; Score 260.5; DB 4; Length 266;
Best Local Similarity 30.7%; Pred. No. 1.3e-19;
Matches 75; Conservative 43; Mismatches 107; Indels 19; Gaps 7;

QY 1 SEKSEENEXDLRKKSLOGTALGNLQIYYNYSKAITSEKSDAQFLNTLLFKGFFTG 60
Db 27 AESQDPKPKDELHKSRF--TGLMEDMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTR 84
QY 61 HPWNLDLLVDLGSATSEYEGSSVDLYGAYGYQC-----AGGTENKTACMYGG 110
Db 85 LGDYDNVRFKKNLADKYDKVDFGANYYYQCYFSEKKTNDINSHQTDKRTKMYGG 144
QY 111 VTLDHNNRLTEKKVPINLMDGKQTTVPIDKVKTSKEVTVQELDQARHYLHGKFGLY 170

Db 145 VTEHNGNQLDKYRSTVRVPEDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHVLVKNKKLY 202
QY 171 NSDSFGGKVQGLIVFHSSEGSVSYDLFDAQO--YDPTLLRIYRDNNTTSSISLSL 228
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMWPAQGXKFCQSKYLMYNDKNWVDSKDVKIEV 259
QY 229 YLYT 232
Db 260 YLYT 263

RESULT 52
US-09-144-776B-10
; Sequence 10, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144, 776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-144-776B-10

Query Match 21.0%; Score 255.5; DB 4; Length 239;
Best Local Similarity 32.1%; Pred. No. 3.7e-19;
Matches 75; Conservative 41; Mismatches 99; Indels 19; Gaps 8;

QY 11 DLRKSEELQGTALGNLQIYYNYSKAITSEKSDAQFLNTLLFKGFFTGHPWYNDLLVD 70
Db 10 ELHKSKFTG-LMENMK-VLYDDNHVSAINVKSIDQFRYFDLIYSIKDTKLGNDYDNRVE 67
QY 71 LGSTATSEYEGSSVDLYGAYGYQCAGG-----TENKTACMYGGVTLHDNNELT 120
Db 68 FKNKDLADKYDKVDFGANYYYQCYFSEKKTNDINSHQTDKRTKMYGGVTEHNGOLD 127
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDQARHYLHGKFGLYNSDSFGKVQ 180

Db 128 KYRSTVAFEDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVNKKLYEFNN--SPYE 183
 QY 181 RGLVHSEGSTSVYDLFDAQGYPD--TLLRIYRNTTISSTLSISLYLT 232
 Db 184 TGYIKFIENIS-FWYDMMPAGKFDQSKYLMYNDKNWDSKDKVIEVLT 236

RESULT 53
 US-09-144-776B-14
 ; Sequence 14, Application US/09144776B
 ; Patent No. 6399332
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Ulrich,
 ; Mark A. Olson
 ; Sina Bavari
 ; TITLE OF INVENTION: Bacterial Superantigen
 ; Vaccines
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Charles H. Harris
 ; STREET: US Army MRC -504 Scott Street
 ; MCMF-JA (Charles H. Harris-patent
 ; Atty)
 ; CITY: FORT DETRICK
 ; STATE: MARYLAND
 ; COUNTRY: USA
 ; ZIP: 21702-5012
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh 7.5
 ; SOFTWARE: Microsoft Word 6.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/144,776B
 ; FILING DATE: 01-Sep-1998
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/882,431
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Charles H. Harris
 ; REGISTRATION NUMBER: 34,616
 ; REFERENCE/DOCKET NUMBER: <Unknown>
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 619-2065
 ; TELEFAX: (301) 619-7714
 ; INFORMATION FOR SEQ ID NO: 14:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 266
 ; TYPE: Amino Acid
 ; STRANDEDNESS: Unknown
 ; TOPOLOGY: Unknown
 ; MOLECULE TYPE: Peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
 US-09-144-776B-14

Query Match 21.0%; Score 255.5; DB 4; Length 266;
 Best Local Similarity 30.2%; Pred. No. 4.3e-19;
 Matches 74; Conservative 45; Mismatches 105; Indels 21; Gaps 9;
 QY 1 SKSBEINKDKRKSELOGTALGNLKQIY--YNNKAITSEKSDADQFLNTLLFKGFF 58
 Db 27 ASQPDPTEDELHAKSKFTG-LMENMKVLYDDHYVS---ATKVKSVDFRAHDLIYNSD 82
 QY 59 TGHFWNLLVDLGGSTAATSEYEGSSVDLYGAYGYQC-----AGTPNKTCMYGGV 111
 Db 83 KKLKNDYKVTLELNEGLAKYKDEVDYGYGNYVYFSSKDNVKGVTGKTCMYGI 142
 QY 112 TLHDNNRLTTEE--KKVPINLWIDGQTTVPIDKVKTSKEVTVOELDLQARHYLHGKGL 169
 Db 143 TKHEGNHFNQNLQNLIRVY-ENKENTISFE-VQTDKKSQVTAQELDIKARNFLINKNL 200

QY 170 YNSDSEGGKVGRLIVFHSSSEGSTSVYDLFDAQGYPD--TLLRIYRNTTISSTLSIS 227
 Db 201 YEFNS--SPYETGYTKFIENNNGTWFYDMMPAGKFDQSKYLMYNDKNWDSKSVKIE 258
 QY 228 LYLYT 232
 Db 259 VHLTT 263
 RESULT 54
 US-09-144-776B-8
 ; Sequence 8, Application US/09144776B
 ; Patent No. 6399332
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Ulrich,
 ; Mark A. Olson
 ; Sina Bavari
 ; TITLE OF INVENTION: Bacterial Superantigen
 ; Vaccines
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Charles H. Harris
 ; STREET: US Army MRC -504 Scott Street
 ; MCMF-JA (Charles H. Harris-patent
 ; Atty)
 ; CITY: FORT DETRICK
 ; STATE: MARYLAND
 ; COUNTRY: USA
 ; ZIP: 21702-5012
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh 7.5
 ; SOFTWARE: Microsoft Word 6.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/144,776B
 ; FILING DATE: 01-Sep-1998
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/882,431
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Charles H. Harris
 ; REGISTRATION NUMBER: 34,616
 ; REFERENCE/DOCKET NUMBER: <Unknown>
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 619-2065
 ; TELEFAX: (301) 619-7714
 ; INFORMATION FOR SEQ ID NO: 8:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 266
 ; TYPE: Amino Acid
 ; STRANDEDNESS: Unknown
 ; TOPOLOGY: Unknown
 ; MOLECULE TYPE: Peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 US-09-144-776B-8

Query Match 20.6%; Score 250.5; DB 4; Length 266;
 Best Local Similarity 30.7%; Pred. No. 1.5e-18;
 Matches 75; Conservative 43; Mismatches 107; Indels 19; Gaps 8;
 QY 1 SEKSEINEKDLKKSELOGTALGNLKQIYYNNKAITSEKSDADQFLNTLLFKGFFTG 60
 Db 27 ASQPDPKPELHKKSKFTG-LMENMK-VLYDDNHVSAINVKSIDQFRVFDLIYSKDTK 84
 QY 61 HPWYNLLVDLGGSTAATSEYEGSSVDLYGAYGYQCAGG-----TPNKTCMYGG 110
 Db 85 LGYDNRVVEFKNLDLADKYKVDVFGANAYYQCAFSSKKTNDINSHQTDKRTCMYGG 144
 QY 111 VTLDHNNRLTTEEKKVINLWIDGQTTVPIDKVKTSKEVTVOELDLQARHYLHGKGLY 170
 Db 145 VTEHNGNQLDKYRSITRVFEDGK-NLLSFD-VQYNNKKVTAQELDYLTRHYLVNKKLY 202

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QY      171 NSDSFGKGQVORGLIVFHSEGSTVSVDLFDAGQGYPD--TLRLRYRDNTTISSTLSLSL 228
Db      203 EFNN--SPYETGYIKFIENENS-FWIDMMPAPGKDFQSKYLLMYNDNKNVDSKDVKIEV 259

QY      229 YLYT 232
Db      260 YLTT 263

RESULT 55
US-08-896-933-21
; Sequence 21, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 21
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-21

Query Match      18.5%; Score 225.5; DB 3; Length 239;
Best Local Similarity 30.2%; Pred. No. 6e-16;
Matches 74; Conservative 43; Mismatches 105; Indels 23; Gaps 11

QY      2      EKSEINEKDLRKKSSELOGTALGNLKQIYYNKAITSSEKSADQPLTTLIFKGFPTGH 61
Db      1      ESQPPKPDDELHKSKFTG-LMENNK-VLYNNDHVSAINVKSINEPFDJLYISIKDTKL 58

QY      62      PYNLDLVDLGSTAATSEYEGSSVDLYGAYGYQC-----AGGTENKTACMYGG 110
Db      59      GNYDNVRVEFKKDLADKYDKYVDVFGANY-YQCYFSKKTNNIDSHENTKKT-CMYGG 116

QY      111     VTLDHNNRLTE-EKKVPINLMDGQTTPIDKVTSSKKEVTVQEQLDLQARIYHLHGKFG 169
Db      117     VTEHGNQLDKYRSITVRVEDGK-NLLSFD-VQTNKKVTAEQLDLYTRHYLVKNKKL 174

QY      170     YNSDSFGGKQVORGLIVFHSSSGSVSDYDLFDAGQGYPD--TLRLRYRDNTTISSTLSLS 227
Db      175     YEFNN--SPYETGYIKFIENENS-FWIDMMPAPGKDFQSKYLLMYNDNKNVDSKDVKIE 231

QY      228     LYLXT 232
Db      232     YLTT 236

RESULT 56
US-09-314-235-21
; Sequence 21, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01

```

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Db 122 SIDGQSLFDFIEQKNG-----NCSRISTYVRKYLTDNKLQYTNP--SKYETGVKIFIP 175
Qy 189 SEGSTVSVDLFD-----AQGVPTDILLRIYRDNNTTISSTLSLSLYLT 232
Db 176 KNKESFWDFPEPEFTQSKY----LMIYKONETLDSNTSQIEVYLTT 219

RESULT 58
US-09-314-235-20
; Sequence 20, Application US/09314235
; Patent No. 633845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-314-235-20

Query Match 18.1%; Score 220; DB 4; Length 220;
Best Local Similarity 28.9%; Pred. No. 2e-15;
Matches 66; Conservative 42; Mismatches 98; Indels 22; Gaps 9;

Qy 14 KXSELOGTALGNLKIYIYNSKATTSB--KSADQFLTNLLFKGFTGHPWYNDLLVD 70
Db 5 KPSQLQRSLNLTFTKIYIFFMRTVLTVTHENVKXVDLLSHDLIYN---VSGPNYDKLKE 61
Qy 71 LGSTAATSEYEGSSVDLYGAVYGYOC-AGGTPNKTACMGYVTLHDNNRLTEKKVPINL 129
Db 62 LKNQEMATLFDKNVDIYGVYHLCYLCEAERSACLYGGVTHNEGNHLEIPKIVVKV 121
Qy 130 WIDGKQT-TVPIDKVKTSKKEVTVDQLQARHYHKGFGLYNSDSFGKVQVQGLIVPHS 188
Db 122 SIDGQSLFDFIEQKNG-----NCSRISTYVRKYLTDNKLQYTNP--SKYETGVKIFIP 175
Qy 189 SEGSTVSVDLFD-----AQGVPTDILLRIYRDNNTTISSTLSLSLYLT 232
Db 176 KNKESFWDFPEPEFTQSKY----LMIYKONETLDSNTSQIEVYLTT 219

RESULT 59
US-09-144-776B-18
; Sequence 18, Application US/09144776B
; Patent No. 639332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
```

```
STREET: US Army MRCM -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 82
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-144-776B-18

Query Match 15.9%; Score 194; DB 4; Length 82;
Best Local Similarity 45.1%; Pred. No. 2.7e-13;
Matches 37; Conservative 13; Mismatches 32; Indels 0; Gaps 0;

Qy 43 SADQFLTNLLFKGFTGHPWYNDLLVLDLGSTAATSEYEGSSVDLYGAVYGYOCAGGTEN 102
Db 1 TGOQFLENTLLYKFFTDLINFEDLLINFENKEMAQHFPSKNVDVYPIRYSINCYGGEID 60
Qy 103 KTACMGYVTLHDNNRLTEKK 124
Db 61 RTACTYGGVTPHEGNLKERKK 82

RESULT 60
US-08-220-378-1
; Sequence 1, Application US/08220378
; Patent No. 5545716
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; APPLICANT: Griggs, Nathan D.
; TITLE OF INVENTION: Superantigen Agonist and Antagonist
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
```



```
/ APPLICATION NUMBER: US/08/220,378
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/941,497
/ FILING DATE: 08-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Saliwanchik, David R.
/ REGISTRATION NUMBER: 31,794
/ REFERENCE/DOCKET NUMBER: UP126.C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 904-375-8100
/ TELEFAX: 904-372-5800
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 45 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-220-378-1

Query Match 15.5%; Score 189; DB 1; Length 45;
Best Local Similarity 84.4%; Pred. No. 3.7e-13;
Matches 38; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKXSELOQTALGNLKIYYNKAITSSEKSD 45
Db 1 SEKSEINEKDLRKXSELOQTALGNLKIYYNKAITSSEKSD 45

RESULT 61
US-08-696-012-1
/ Sequence 1, Application US/08696012
/ Patent No. 5859207
/ GENERAL INFORMATION:
/ APPLICANT: Johnson, Howard M.
/ APPLICANT: Pontzer, Carol H.
/ APPLICANT: Griggs, Nathan D.
/ TITLE OF INVENTION: Superantigen Agonist and Antagonist
/ TITLE OF INVENTION: Peptides
/ NUMBER OF SEQUENCES: 10
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Saliwanchik & Saliwanchik
/ STREET: 2421 N.W. 41st Street, Suite A-1
/ CITY: Gainesville
/ STATE: FL
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/696,012
/ FILING DATE: 12-AUG-1996
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/220,378
/ FILING DATE: 29-MAR-1994
/ APPLICATION NUMBER: US 07/941,497
/ FILING DATE: 08-SEP-1992
/ CLASSIFICATION: 530
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Saliwanchik, David R.
/ REGISTRATION NUMBER: 31,794
/ REFERENCE/DOCKET NUMBER: UP126.C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 904-375-8100
/ TELEFAX: 904-372-5800
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
```

```
/ LENGTH: 45 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-696-012-1

Query Match 15.5%; Score 189; DB 2; Length 45;
Best Local Similarity 84.4%; Pred. No. 3.7e-13;
Matches 38; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKXSELOQTALGNLKIYYNKAITSSEKSD 45
Db 1 SEKSEINEKDLRKXSELOQTALGNLKIYYNKAITSSEKSD 45

RESULT 62
US-08-896-933-30
/ Sequence 30, Application US/08896933
/ Patent No. 6221351
/ GENERAL INFORMATION:
/ APPLICANT: Terman, David S.
/ TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
/ TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
/ FILE REFERENCE: 09629/005002
/ CURRENT APPLICATION NUMBER: US/08/896,933
/ CURRENT FILING DATE: 1997-07-18
/ EARLIER APPLICATION NUMBER: 08/252,978
/ EARLIER FILING DATE: 1994-06-02
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 30
/ LENGTH: 208
/ TYPE: PRT
/ ORGANISM: Streptococcus pyogenes
/ US-08-896-933-30

Query Match 12.3%; Score 150; DB 3; Length 208;
Best Local Similarity 26.3%; Pred. No. 5.8e-08;
Matches 60; Conservative 38; Mismatches 78; Indels 52; Gaps 12;

Qy 33 NSKAITSEKSDQFLTNTLFLKGFFTGHPW--YNDLLVLDLGTAA---TSYEGSS--- 84
Db 1 DSKDLSNVKS-----DLLYA--YTTPDYKDCRVNFSTHTLNIDTQYRKDYVI 51
Qy 85 -----VDLYGAYGYQCAGTTPNKATCMYGGVTLHDNNRLTEKKVPI 127
Db 52 SSEMSEYASQKFKRDDHVDVGLFYILNSHTG-----EVIYGITPAQNNKVNH--KLLG 104
Qy 128 NLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHVLHGKFLYNSDS--FGKVGQGLIV 185
Db 105 NLFISGESQOQNNLNKILEKDIVTFQEDIFKIRKYLMDNYKIYDATSPYVSGRIBIG--- 161
Qy 186 FHSSEGSTVSYDLFDA--QGQVPDTLLRIYRDNNTTISSTLS-ISLYL 230
Db 162 --TKDGKHEQIDLFDSPNEGFSDIFAK-YKDNRIINNMKNFSHPDIYL 206

RESULT 63
US-09-314-235-30
/ Sequence 30, Application US/09314235
/ Patent No. 6338845
/ GENERAL INFORMATION:
/ APPLICANT: Terman, David S.
/ TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
/ TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
/ FILE REFERENCE: 09629/005004
/ CURRENT APPLICATION NUMBER: US/09/314,235
/ CURRENT FILING DATE: 1999-05-18
/ EARLIER APPLICATION NUMBER: 08/896,933
/ EARLIER FILING DATE: 1997-07-18
/ EARLIER APPLICATION NUMBER: 08/252,978
/ EARLIER FILING DATE: 1994-06-02
```

EARLIER APPLICATION NUMBER: 07/891,718
EARLIER FILING DATE: 1992-06-01
EARLIER APPLICATION NUMBER: US91/00342
EARLIER FILING DATE: 1991-01-17
EARLIER APPLICATION NUMBER: 07/466,577
EARLIER FILING DATE: 1990-01-17
EARLIER APPLICATION NUMBER: 07/416,530
EARLIER FILING DATE: 1989-10-03
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 30
LENGTH: 208
TYPE: PRT
ORGANISM: Streptococcus pyogenes
US-09-314-235-30

Query Match 12.3%; Score 150; DB 4; Length 208;
Best Local Similarity 26.3%; Pred No. 5.8e-08;
Matches 60; Conservative 38; Mismatches 78; Indels 52; Gaps 12;
QY 33 NSKAITSEKSDQFLNTLTKGFTGHPW-YNDLLVDLGSTAA-----TSEYEGSS--- 84
Db 1 DSKKDISNVKS-----DLLVA--YTTPDYDKCRVNFSTHTLNIDTQKRGKDYII 51
QY 85 -----VDLYGAYGYQCAGTGNKTKACMYGVTLHDNNRLTEKKVPI 127
Db 52 SSEMSYEASQKPRDDHVDVGLFVILNSHTG-----EYIYGITPAQNNKNVH--KLLG 104
QY 128 NLWIDGKQTTVIDKTKTSKKEVTVQELDLQARHYLHGKFLGYNDS--FGKQVQRGLIV 185
Db 105 NLFISGESQNNLNKILEKIDVTQEDIFKIRKLYMDNYKIYDATSPVSGRIEIG-- 161
QY 186 FHSSEGSTSVYDLFA--QCGPDPILLRIYRNTTISSTLS-ISLYL 230
Db 162 --TKDGKHEQIDLFDSNPEGRSDIFAK-YKDNRIINKNFNSHFDIYL 206

RESULT 64
US-08-896-933-34
Sequence 34, Application US/08896933
Patent No. 6221351
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 34
LENGTH: 27
TYPE: PRT
ORGANISM: Staphylococcal
US-08-896-933-34

Query Match 10.8%; Score 131; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKXSELOGTALGNLK 27
Db 1 SEKSEINEKDLRKXSELOGTALGNLK 27

RESULT 65
US-09-314-235-34
Sequence 34, Application US/09314235
Patent No. 6338845
GENERAL INFORMATION:
APPLICANT: Terman, David S.

TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/005004
CURRENT APPLICATION NUMBER: US/09/314,235

CURRENT FILING DATE: 1999-05-18
EARLIER APPLICATION NUMBER: 08/896,933
EARLIER FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
EARLIER APPLICATION NUMBER: 07/891,718
EARLIER FILING DATE: 1992-06-01
EARLIER APPLICATION NUMBER: US91/00342
EARLIER FILING DATE: 1991-01-17
EARLIER APPLICATION NUMBER: 07/466,577
EARLIER FILING DATE: 1990-01-17
EARLIER APPLICATION NUMBER: 07/416,530
EARLIER FILING DATE: 1989-10-03
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 34
LENGTH: 27
TYPE: PRT
ORGANISM: Staphylococcal
US-09-314-235-34

Query Match 10.8%; Score 131; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 2.8e-07;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKXSELOGTALGNLK 27
Db 1 SEKSEINEKDLRKXSELOGTALGNLK 27

RESULT 66
US-08-838-413A-22
Sequence 22, Application US/08838413A
Patent No. 6075119
GENERAL INFORMATION:
APPLICANT:
APPLICANT:
TITLE OF INVENTION: PEPTIDES USEFUL FOR
TITLE OF INVENTION: REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,413A
FILING DATE: 07-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MORRIS, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2016-4010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)758-4800
TELEFAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:

LENGTH: 24
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE: PEPTIDE
US-08-838-413A-22

Query Match 10.4%; Score 127; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 6.2e-07;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 KKEVTQELDQARHYLHGKFGLY 170
Db 1 KKEVTQELDQARHYLHGKFGLY 24

RESULT 67

US-08-378-5
Sequence 5, Application US/08220378
Patent No. 5545716

GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.

APPLICANT: Pontzer, Carol H.

APPLICANT: Griggs, Nathan D.

TITLE OF INVENTION: Superantigen Agonist and Antagonist

TITLE OF INVENTION: Peptides

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: FL

COUNTRY: USA

ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/220,378

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/941,497

FILING DATE: 08-SEP-1992

ATTORNEY/AGENT INFORMATION:

NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 31,794

REFERENCE/DOCKET NUMBER: UF126.C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 904-375-8100

TELEFAX: 904-372-5800

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-220-378-5

Query Match 10.3%; Score 126; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 NKTACMYGGVTLHDNNRLTEKK 124
Db 1 NKTACMYGGVTLHDNNRLTEKK 23

RESULT 68

US-08-696-012-5

Sequence 5, Application US/08696012
Patent No. 5859207
GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/696,012

FILING DATE: 12-AUG-1996

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/220,378

FILING DATE: 29-MAR-1994

APPLICATION NUMBER: US 07/941,497

FILING DATE: 08-SEP-1992

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 31,794

REFERENCE/DOCKET NUMBER: UF126.C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 904-375-8100

TELEFAX: 904-372-5800

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 23 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-696-012-5

Query Match 10.3%; Score 126; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 7.4e-07;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 NKTACMYGGVTLHDNNRLTEKK 124
Db 1 NKTACMYGGVTLHDNNRLTEKK 23

RESULT 69

US-08-220-378-6

Sequence 6, Application US/08220378

Patent No. 5545716

GENERAL INFORMATION:

APPLICANT: Johnson, Howard M.

APPLICANT: Pontzer, Carol H.

APPLICANT: Griggs, Nathan D.

TITLE OF INVENTION: Superantigen Agonist and Antagonist

TITLE OF INVENTION: Peptides

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESSEE: Saliwanchik & Saliwanchik

STREET: 2421 N.W. 41st Street, Suite A-1

CITY: Gainesville

STATE: FL

COUNTRY: USA

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;
;
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/220,378
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,497
; FILING DATE: 08-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UFI26.C1
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-220-378-6

Query Match 10.2%; Score 124; DB 1; Length 29;
Best Local Similarity 78.6%; Pred. No. 1.7e-06;
Matches 22; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSK 148
Db 1 EEKVPINLWIDGKQNTVPLETVKTKK 28

RESULT 70
US-08-696-012-6
; Sequence 6, Application US/08696012
; Patent No. 5859207
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; APPLICANT: Griggs, Nathan D.
; TITLE OF INVENTION: Superantigen Agonist and Antagonist
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,012
; FILING DATE: 12-AUG-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/220,378
; FILING DATE: 29-MAR-1994
; APPLICATION NUMBER: US 07/941,497
; FILING DATE: 08-SEP-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
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;
;
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UFI26.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-696-012-6

Query Match 10.2%; Score 124; DB 2; Length 29;
Best Local Similarity 78.6%; Pred. No. 1.7e-06;
Matches 22; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSK 148
Db 1 EEKVPINLWIDGKQNTVPLETVKTKK 28

RESULT 71
US-09-144-776B-24
; Sequence 24, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Acty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/892,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-144-776B-24

Query Match 9.2%; Score 112; DB 4; Length 79;
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Best Local Similarity 32.1%; Pred. No. 0.00016;
Matches 25; Conservative 17; Mismatches 32; Indels 4; Gaps 2;

QY 43 SADQFLNTLLFKGFFTHGHPWYNDLLVDLGSSTAATSEYEGSSVDLYGAYGYQC-AGTTP 101
Db 1 SVDQLSHDLIYN--VSGPNYDKLTKELKQEMATLFKDKNDVIYGVETIYHLCYCENA 57

QY 102 NKTACMYGGVTLHDNNRL 119
Db 58 ERSACIYGGVTNHEGNHL 75

RESULT 72
US-09-144-776B-20
; Sequence 20, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; VACCINES
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army WPMC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144, 776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-144-776B-20

Query Match 9.2%; Score 111.5; DB 4; Length 89;
Best Local Similarity 33.3%; Pred. No. 0.00021;
Matches 29; Conservative 15; Mismatches 32; Indels 11; Gaps 2;
QY 43 SADQFLNTLLFKGFFTHGHPWYNDLLVDLGSSTAATSEYEGSSVDLYGAYGYQC----- 96
Db 1 SIDQFLYFDLIYSIKDKLGNVDNRVFEKKNLADKYDKYDVFQANY-YQCYFSKKT 59
QY 97 ----AGGTPNKTCMYGGVTLHDNNRL 119
Db 60 NDINSHQTDREKTCMYGGVTEHNGNL 86

RESULT 73
US-08-220-378-4
; Sequence 4, Application US/08220378
; Patent No. 5845716
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; APPLICANT: Griggs, Nathan D.
; TITLE OF INVENTION: Superantigen Agonist and Antagonist
; Peptides
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/220,378
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,497
; FILING DATE: 08-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF126.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 22 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-220-378-4
Query Match 9.0%; Score 110; DB 1; Length 22;
Best Local Similarity 95.0%; Pred. No. 3.6e-05;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 85 VDLGYGYGYQCAGGTPNKT 104
Db 3 VDKYGYGYQCAGGTPNKT 22
RESULT 74
US-08-696-012-4
; Sequence 4, Application US/08696012
; Patent No. 5859207
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; APPLICANT: Griggs, Nathan D.
; TITLE OF INVENTION: Superantigen Agonist and Antagonist
; Peptides
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA

ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,012
FILING DATE: 12-AUG-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/220,378
FILING DATE: 29-MAR-1994
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08-SEP-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF126.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-696-012-4

Query Match 9.0%; Score 110; DB 2; Length 22;
Best Local Similarity 95.0%; Pred. No. 3.6e-05;
Matches 19; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 85 VDLYGAYGYQCAGGTPNKT 104
DB 3 VDKYGAYGYQCAGGTPNKT 22

RESULT 75
US-08-220-378-2
Sequence 2, Application US/08220378
Patent No. 5545716
GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,378
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF126.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-220-378-2

Query Match 8.8%; Score 107; DB 1; Length 28;
Best Local Similarity 66.7%; Pred. No. 0.00011;
Matches 18; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 40 SEKSADQFLTNLLFKGFTGHPWYND 66
DB 2 NKESHQFLQHTILFKGFTDHSWYND 28

Search completed: August 12, 2004, 13:34:03
Job time : 11.2135 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 12, 2004, 13:26:25 ; Search time 7.37083 Seconds
(without alignments)
3040.721 Million cell updates/sec

Title: US-09-900-766-3

Perfect score: 1238

Sequence: 1 SEKSEENKDLRKKSLEQG.....RDNKTENSENHIALYLYTT 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR_78.*

1: PIR1.*

2: PIR2.*

3: PIR3.*

4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1210	97.7	257	A28179	enterotoxin E prec
2	1037	83.8	257	A28664	enterotoxin A prec
3	992	80.1	260	C89984	enterotoxin P [imp
4	663	53.6	258	A33953	enterotoxin D prec
5	453.5	36.6	258	H89968	enterotoxin Se [i
6	380.5	30.7	260	C89969	enterotoxin Se [i
7	339.5	27.4	242	C89969	extracellular ente
8	333	26.9	240	C89991	extracellular ente
9	310	25.0	239	D89969	enterotoxin SEM [i
10	304.5	24.6	266	ENSAB6	enterotoxin B prec
11	302.5	24.4	266	S11885	enterotoxin C3 - S
12	288.5	24.1	266	A60114	enterotoxin C-2 pr
13	283.5	22.9	251	S129659	exotoxin type A pr
14	270.5	21.8	236	S18789	exotoxin A precurs
15	270.5	21.8	266	ENSAC1	enterotoxin C-1 pr
16	268.5	21.7	236	S18783	exotoxin type A pr
17	263.5	21.3	236	S18786	exotoxin type A pr
18	256	20.7	258	C89968	extracellular ente
19	234	18.9	250	A26152	streptococcal pyro
20	200	16.2	157	A89942	hypothetical prote
21	194	15.7	136	A89969	enterotoxin YENT2
22	175.5	14.2	235	A30509	exotoxin C precurs
23	136	11.0	62	H89941	hypothetical prote
24	125	10.1	133	C89969	enterotoxin Yent1
25	105.5	8.5	234	XCSAS1	toxic shock syndro
26	104.5	8.4	232	F89807	exotoxin 13 [imp
27	103.5	8.4	234	C89969	toxic shock syndro
28	101	8.2	1634	E64410	DNA-directed DNA p
29	99	8.0	631	S70908	transferrin-bindin

30	98.5	8.0	231	2	D89807	exotoxin 11 [imp
31	97.5	7.9	232	2	E89807	exotoxin 12 [imp
32	94	7.6	227	2	G89807	exotoxin 14 [imp
33	91	7.4	411	2	A11161	flagellar hook pro
34	91	7.4	411	2	A11520	flagellar hook pro
35	89.5	7.2	194	2	AC1553	B. subtilis YJbK p
36	89	7.2	226	2	G89806	exotoxin 6 [imp
37	88.5	7.1	227	2	C89808	exotoxin 15 [imp
38	88.5	7.1	324	2	T03276	GAG protein - Yeas
39	88.5	7.1	413	2	S59650	hypothetical prote
40	88.5	7.1	816	2	C88196	protein ZK1127.7 [
41	88	7.1	203	2	C89803	hypothetical prote
42	88	7.1	617	2	E96793	hypothetical prote
43	87.5	7.1	409	2	E69886	processing protein
44	87.5	7.1	634	2	T08145	myrosinase-binding
45	87.5	7.1	956	2	T08144	myrosinase-binding
46	87.5	7.1	1014	2	H71602	protein with DnaJ
47	87	7.0	1419	1	DVZQF	multidrug resistan
48	87	7.0	2167	2	AF1489	cell wall-associat
49	86.5	7.0	614	2	D86342	hypothetical prote
50	86.5	7.0	856	2	B81399	probable periplasm
51	86.5	7.0	2971	2	T08026	hypothetical prote
52	86	6.9	853	2	G90559	trse-like protein
53	86	6.9	1090	2	AG1749	glycosidase homolo
54	85.5	6.9	291	2	G86903	cell shape determi
55	85.5	6.9	573	2	AH1793	ABC transporter, A
56	85	6.9	241	2	C89888	hypothetical prote
57	85	6.9	617	2	T10102	diphosphate-fructo
58	85	6.9	679	2	G71615	phospholipase A2-1
59	85	6.9	1014	2	T30545	major surface glyc
60	85	6.9	6486	2	T31076	tyrocidine synthet
61	84.5	6.8	573	2	AF1418	ABC transporter, A
62	84.5	6.8	637	2	S35523	E1 protein - human
63	84.5	6.8	993	2	A97334	type II restrictio
64	84	6.8	241	2	T07067	beta-fructofuranos
65	84	6.8	333	2	A95882	hypothetical prote
66	84	6.8	552	2	T41863	chitinase chi-A or
67	84	6.8	562	2	S01312	chitinase chi-A or
68	84	6.8	616	1	A40457	replication protei
69	84	6.8	1902	1	B44858	lactocepin (EC 3.4
70	84	6.8	1948	2	S00485	gene 11-1 protein
71	83.5	6.7	507	2	S36595	L1 protein - human
72	83.5	6.7	547	2	S49815	transferrin-bindin
73	83.5	6.7	668	2	J00773	penicillin-binding
74	83.5	6.7	668	2	J00774	penicillin-binding
75	83.5	6.7	668	2	T44118	penicillin-binding
76	83.5	6.7	804	2	G90571	hypothetical prote
77	83	6.7	438	2	S42581	neutral metallopro
78	83	6.7	476	2	H82177	conserved hypothet
79	83	6.7	556	2	A11394	arginyl tRNA synth
80	83	6.7	631	2	S70910	transferrin-bindin
81	83	6.7	914	2	T08081	probable myrosinas
82	83	6.7	988	2	T08102	myrosinase-binding
83	83	6.7	1353	2	T27404	hypothetical prote
84	83	6.7	2910	2	T29156	DNA-directed RNA p
85	82.5	6.7	328	2	F64187	p-aminobenzoate sy
86	82.5	6.7	638	2	AH0340	putative autotransp
87	82.5	6.7	1520	2	T23620	hypothetical prote
88	82.5	6.7	2441	2	D71623	erythrocyte membra
89	82	6.6	292	2	B89807	exotoxin 9 [imp
90	82	6.6	520	2	D83845	hypothetical prote
91	82	6.6	1217	2	T21403	hypothetical prote
92	82	6.6	2380	2	E71604	hypothetical prote
93	82	6.6	5005	2	F82884	hypothetical prote
94	81.5	6.6	356	2	A89807	exotoxin 8 [imp
95	81.5	6.6	381	2	B89886	hypothetical prote
96	81.5	6.6	555	2	S71365	ovule development
97	81.5	6.6	609	2	F90160	membrane conserved
98	81.5	6.6	672	1	S73438	MG032 homolog B01
99	81.5	6.6	819	2	G89801	hypothetical prote
100	81	6.5	272	2	D86671	transposase of IS1

ALIGNMENTS

RESULT 1

A28179
 enterotoxin E precursor - Staphylococcus aureus
 C:Species: Staphylococcus aureus
 C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 15-Oct-1999
 C:Accession: A28179
 R:Couch, J.L.; Soltis, M.T.; Betley, M.J.
 J. Bacteriol. 170, 2954-2960, 1988
 A:Title: Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gene.
 A:Reference number: A28179; MUID:88257005; PMID:3384800
 A:Accession: A28179
 A:Molecule type: DNA
 A:Residues: 1-257 <COU>
 A:Cross-references: GB:M21319; NID:G153001; PIDN:AAA26617.1; PID:G153002
 C:Superfamily: enterotoxin B

Query Match 97.7%; Score 1210; DB 2; Length 257;
 Best Local Similarity 97.9%; Pred. No. 6e-93;
 Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
 DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFFTG 84
 QY 61 HPWYNDLLVDSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
 DB 85 HPWYNDLLVDSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 144
 QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKQV 180
 DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKQV 204
 QY 181 RGLIVFHSSEGSVSYDLFDAQGYPTTLRIYRDKNKTINSENHLALYLYTT 233
 DB 205 RGLIVFHSSEGSVSYDLFDAQGYPTTLRIYRDKNKTINSENHLALYLYTT 257

RESULT 2

A28664
 enterotoxin A precursor - Staphylococcus aureus
 C:Species: Staphylococcus aureus
 C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 15-Oct-1999
 C:Accession: A28664; A29566
 R:Betley, M.J.; Mekalanos, J.J.
 J. Bacteriol. 170, 34-41, 1988
 A:Title: Nucleotide sequence of the type A staphylococcal enterotoxin gene.
 A:Reference number: A28664; MUID:88086892; PMID:3335483
 A:Accession: A28664
 A:Molecule type: DNA
 A:Residues: 1-257 <BET>
 A:Cross-references: GB:M18970; NID:G153120; PIDN:AAA26681.1; PID:G153121
 A:Experimental source: strain FRI337
 R:Huang, I.Y.; Hughes, J.L.; Bergdoll, M.S.; Schantz, E.J.
 J. Biol. Chem. 262, 7006-7013, 1987
 A:Title: Complete amino acid sequence of staphylococcal enterotoxin A.
 A:Reference number: A29566; MUID:87222293; PMID:3384106
 A:Accession: A29566
 A:Molecule type: protein
 A:Residues: 25-241, 'S', 243-257 <HUA>
 C:Genetics:
 A:Gene: entA
 A:Map position: 6
 C:Superfamily: enterotoxin B

Query Match 83.8%; Score 1037; DB 2; Length 257;
 Best Local Similarity 83.3%; Pred. No. 1.3e-78;
 Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFFTG 60

DB 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFFTG 84
 QY 61 HPWYNDLLVDSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
 DB 85 HSWYNDLLVDFSDKIDVYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 144
 QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKQV 180
 DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKQV 204
 QY 181 RGLIVFHSSEGSVSYDLFDAQGYPTTLRIYRDKNKTINSENHLALYLYTT 233
 DB 205 RGLIVFHSSEGSVSYDLFDAQGYPTTLRIYRDKNKTINSENHLALYLYTT 257

RESULT 3

C89984
 enterotoxin P [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: C89984
 R:Kuroda, M.; Ohba, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani, U.; Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Hama, A.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: C89984
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-260 <KUR>
 A:Cross-references: GB:BA000018; PID:G13701743; PIDN:BAB43036.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: sep
 C:Superfamily: enterotoxin B

Query Match 80.1%; Score 992; DB 2; Length 260;
 Best Local Similarity 78.5%; Pred. No. 7.3e-75;
 Matches 183; Conservative 18; Mismatches 32; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
 DB 28 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFFTG 87
 QY 61 HPWYNDLLVDSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
 DB 88 HQWYNDLLVDSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 147
 QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKQV 180
 DB 148 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNSDSFGKQV 207
 QY 181 RGLIVFHSSEGSVSYDLFDAQGYPTTLRIYRDKNKTINSENHLALYLYTT 233
 DB 208 RGLIEFHPSSGDSVGYDLFDAQGYPTTLRIYRDKNKTINSENHLALYLYTT 260

RESULT 4

A33953
 enterotoxin D precursor - Staphylococcus aureus
 C:Species: Staphylococcus aureus
 C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 15-Oct-1999
 C:Accession: A33953
 R:Bayles, K.W.; Iandolo, J.J.
 J. Bacteriol. 171, 4799-4806, 1989
 A:Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin I
 A:Reference number: A33953; MUID:89359112; PMID:2549000
 A:Accession: A33953
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-258 <BAY>
 A:Cross-references: GB:M28521; NID:G1492109; PIDN:AAB06195.1; PID:G758691

C;Superfamily: enterotoxin B

Query Match 53.6%; Score 663; DB 2; Length 258;
Best Local Similarity 55.0%; Pred. No. 1.4e-47;
Matches 127; Conservative 33; Mismatches 71; Indels 0; Gaps 0;

QY 1 SEKSEENELDKKKSELQGTALGNLKOIYYNEKAITENKESDDOLENTLLPKGFTTG 60
Db :
26 NEWIDSVKRELHKHKSLSSTALNNMKHSYADKNPIIGENKSGDGFLENTLLYKKEFFTD 85
QY 61 HPVYNDDLVLGSKSDATNKYKGKKVDLYGAYGVQCAGGTPNKTACMGVGTVLLHDNNRLT 120
Db :
86 LINFEDLLINFSKEMAQHFKSNVDVYPRIYSINCVGGIEDRTACTYGGVTHEGKLK 145
QY 121 EEKVPINLMIDGQTTPVIDKVTKSKEVTVQVELDLQARHYLHGKFGLYNSDSFGKVQ 180
Db :
146 ERKKIPINLMINGQVEKVSVDKVTQDKKNTVQVELDAQARRYLOLKLYNNDTLGGKIQ 205
QY 181 RGLIVFHSSRGSTSVSYDLFDAQQGYPDTLIRIYRDNKTINSNLHLAIYLY 231
Db :
206 RGKIEPDSOGSKVSYDLFDVGDFPEKQLRIYSDNKTLSTEHLHDIYLY 256

RESULT 5

H89968
enterotoxin SeN [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: H89968
R;Kuroda, M.; Ohka, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizukani-Yui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A;Reference number: A89758; UID:21311952; PMID:11418146
A;Accession: H89968
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-258 <KUR>
A;Cross-references: GB:BA000018; PID:g13701618; PIDN:BAB42911.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: sen
C;Superfamily: enterotoxin B

Query Match 36.6%; Score 453.5; DB 2; Length 258;
Best Local Similarity 40.8%; Pred. No. 3.2e-30;
Matches 95; Conservative 45; Mismatches 78; Indels 15; Gaps 6;

QY 6 EINEKLRKKSELQGTALGNLKOIYYNEKAIT-----ENKESDDOLENTLLPKGFTTG 60
Db :
32 EVDPKOLKKSLDSSKLFNLTS--YYTD--ITWLDESINKISTDQLLNLTILKNIKDIS 87
QY 61 HPVYNDDLVLGSKSDATNKYKGKKVDLYGAYGVQCAGGTPNKTACMGVGTVLLHDNNRLT 120
Db :
88 VLKTSLSKFVFNSSDLANQFKNINILYLGFNKVCGLTEETKSLCYGGVTIHGNDQLD 147
QY 121 EEKVPINLMIDGQTTPVIDKVTKSKEVTVQVELDLQARHYLHGKFGLYNSDSFGKVQ 180
Db :
148 EEKVIQNVNPFKDGQGEGFV--IKTKAKAVTVQELDTKVRFLKENLYKIYNKDT--GNIQ 203
QY 181 RGLIVFHS--SEGSTVSYDLFDAQQGYPDTLIRIYRDNKTINSNLHLAIYLY 231
Db :
204 KGCIFFSHNHQDQSFFYDYDLNVKGSVGAEFFQFYSDNRVTSSNYHIDVFLY 256

RESULT 6

E89969
enterotoxin SeO [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: E89969
R;Kuroda, M.; Ohka, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura,

ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant *Staphylococcus aureus*.
A:Reference number: A89758; MUID:213111952; PMID:11418145
A:Accession: E89969
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-260 <KUR>
A:Cross-references: GB:BA000018; PID:gl3701623; PIDN:BA842916.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: seo
C:Superfamily: enterotoxin B

Query Match 30.7%; Score 380.5; DB 2; Length 260;
Best Local Similarity 39.5%; Pred. No. 3.7e-24;
Matches 96; Conservative 31; Mismatches 87; Indels 29; Gaps 8;

QY 8 NEKD-----LEKKSELOCTALGNLKQIYYNE---KAITENKESDDQFLENTLLFKGFF 58
DB 29 NEEDPKIESCKSSVDPIALHNNDYINNRFTTVKSIIVSTE---KFLDFFDLFKSI- 84
QY 59 TGHFW-----YNDLLVLDGSKDATNKYKGKKVDLYGAYGYQCAGGTPNKTACMYGV 111
DB 85 --NWLDSIAEFKDLKVEFSSAISKEFLGTVDIYGYVYKAHCHGEHQVDTACTYGV 141
QY 112 TLHNNRLTEKKVPINLWIDGQTTVIDKVTSKKEVTVQELDLQARHYLHGKGLYN 171
DB 142 TPHENNKLSPEKNIGVAYKDNVNTFI--VTTDKKVTAGELDIKVKTKLNAYKLY- 198
QY 172 SDSFGGKVGQRLIVFHSEGSTVS--YDLFDAQGYPTLIRIYRDNKTINSNLHIALY 229
DB 199 -DRMTSDVQKGYINFHSHSEKSEFYDLFYKGNLPQOYLQIYNDNKTIDSSDXYHIVY 257
QY 230 LYT 232
DB 258 LFT 260

RESULT 7
C89969
extracellular enterotoxin type I precursor [imported] - *Staphylococcus aureus* (strain N31)
C:Species: *Staphylococcus aureus*
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
R:Accession: C89969
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Hiramatsu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant *Staphylococcus aureus*.
A:Reference number: A89758; MUID:213111952; PMID:11418145
A:Accession: C89969
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-242 <KUR>
A:Cross-references: GB:BA000018; PID:gl3701621; PIDN:BA842914.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: sei
C:Superfamily: enterotoxin B

QY 123 KKVPIINLWIDGKOTTPIDKVKTSKEVTQELDLQARHYLHGKFLYNSDSFG-GK--- 178
 Db 117 RKPIINLWNGKHKTISTDKIATNKKLVTAQIDVKRLRYLQEEYNIYGHNTGKGEY 176
 QY 179 -----VORGIVPHSSEGTSTVSDLFDAQQGPDTLLRIYRDNKTINSENLI 226
 Db 177 YKSKFYGFNGKVLPHLNNEKSFSDYLTGDTGLPVSPLKIYEDNKIIESEKFL 232

RESULT 8

G89991
 extracellular enterotoxin L [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: G89991
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Oi, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: G89991
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-240 <KUR>
 A:Cross-references: GB:BA000018; PID:g13701803; PIDN:BAB43096.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: sel
 C:Superfamily: enterotoxin B

Query Match 26.9%; Score 333; DB 2; Length 240;
 Best Local Similarity 35.0%; Pred. No. 2.9e-20;
 Matches 77; Conservative 37; Mismatches 72; Indels 34; Gaps 6;

QY 24 GNLKQIY-----YNEKAITENKESDQFLNTLLFKGFTGHPWYND-LLVPLGSKDATN 78
 Db 31 GNLRNFYTKYEVNLRKNVXDKNSPESHRL-----YKXNDILYAFDNEYITS 79
 QY 79 KYRGKVDLYGAYGYQCAGGTPTNKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQT 138
 Db 80 DLKGNVDVFGISYKY---GNSRT--IYGVTKAENKLDSPRIPIINLIINGKHQTV 133
 QY 139 PIDKVTSKKEVTQELDLQARHYLHGKFLY-----NDSFGGKVGQGLIVF 186
 Db 134 TTKSVSTDKQWVTAQIDVKRLRYLQEEYNIYGHNTGKGEYTSKFPYSGFDKGVVF 193
 QY 187 HSSEGTSTVSDLFDAQQGPDTLLRIYRDNKTINSENLI 226
 Db 194 HMDGNSFSDLYFTGVLGPESFLKIYKDKTVDSQFHL 233

RESULT 9

D89969
 enterotoxin SEM [imported] - Staphylococcus aureus (strain N315)
 C:Species: Staphylococcus aureus
 C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
 C:Accession: D89969
 R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogura, A.; Mizutani-Oi, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
 Lancet 357, 1225-1240, 2001
 A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
 A:Reference number: A89758; MUID:21311952; PMID:11418146
 A:Accession: D89969
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-239 <KUR>
 A:Cross-references: GB:BA000018; PID:g13701622; PIDN:BAB42915.1; GSPDB:GN00149
 A:Experimental source: strain N315
 C:Genetics:
 A:Gene: sem

C:Superfamily: enterotoxin B

Query Match 25.0%; Score 310; DB 2; Length 239;
 Best Local Similarity 32.1%; Pred. No. 2.3e-18;
 Matches 70; Conservative 40; Mismatches 82; Indels 26; Gaps 5;

QY 23 LGMNKQIYYNEKAITENK--ESDDQFLNTLLFKGFTGHPWYNDLLVPLGSKDATNKY 80
 Db 24 VGVNLNLFNYGSYPFIEDHQISINPENNLHSQLVFS-----MDNSTVTAEFKVDDVKKF 77
 QY 81 KGKVDLYGAYGYQCAGGTPTNKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQTVP 140
 Db 78 KNHADVIGLSYGYCL-----KNKIYGGVTL-AGDYLEKSRRIPLNWNGEHQTIST 131
 QY 141 DKVTSKKEVTQELDLQARHYLHGKFLY-----NDSFGGKVGQGLIVFHS 188
 Db 132 DKVSTNKKLVTAQIDVKRLRYLQEEYNIYGHNTGKGEYTSKFPYSGFNAGKILFHL 191
 QY 189 SEGSTVSDLFDAQQGPDTLLRIYRDNKTINSENLI 226
 Db 192 NDGSSFSYDLFDGTGTQGAESFLKIYNDNKIVETEKFHL 229

RESULT 10

ENSAB6

enterotoxin B precursor - Staphylococcus aureus

C:Species: Staphylococcus aureus

C:Date: 24-Apr-1994 #sequence_revision 15-Oct-1996 #text_change 18-Jun-1999

C:Accession: S27360; A92065; S27240; A01815

R:Jones, C.L.; Khan, S.A.

J. Bacteriol. 166, 29-33, 1986

A:Title: Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus.

A:Reference number: S27360; MUID:86168029; PMID:3957869

A:Accession: S27360

A:Molecule type: DNA

A:Cross-references: EMBL:M1118; NID:g152999; PIDN:AAA88550.1; PID:g153000

A:Experimental source: strain S6

R:Huang, I.Y.; Bergdoll, M.S.

J. Biol. Chem. 245, 3518-3525, 1970

A:Title: The primary structure of staphylococcal enterotoxin B. III. The cyanogen bromide

A:Reference number: A92065; MUID:71007902; PMID:5470821

A:Accession: A92065

A:Molecule type: protein

A:Residues: 28-55, 'NND', 59-68, 'NE', 71, 'FDLIYL', 78-117, 119-127, 'N', 129, 'D', 131-132, 'ENT', 1

A:Experimental source: strain S-6

R:Huang, I.Y.; Bergdoll, M.S.

J. Biol. Chem. 245, 3511-3517, 1970

A:Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, composition

A:Reference number: A92064; MUID:71007901; PMID:5470820

A:Contents: annotation; chymotryptic peptides

R:Huang, I.Y.; Bergdoll, M.S.

J. Biol. Chem. 245, 3493-3510, 1970

A:Title: The primary structure of staphylococcal enterotoxin B. I. Isolation, composition

A:Reference number: A92063; MUID:71007900; PMID:5470819

A:Contents: annotation; tryptic peptides

R:Schantz, E.J.; Roessler, W.G.; Wagman, J.; Spero, L.; Dunne, D.A.; Bergdoll, M.S.

Biochemistry 4, 1011-1016, 1965

A:Title: Purification of staphylococcal enterotoxin B.

A:Reference number: A90548; MUID:66035792; PMID:4953912

A:Contents: annotation; biological source of protein

R:Alakhov, V.Y.; Klinisky, E.Y.; Kolosov, M.I.; Maurer-Fogy, I.; Moskaleva, E.Y.; Sveshnik

Eur. J. Biochem. 209, 823-828, 1992

A:Title: Identification of functionally active fragments of staphylococcal enterotoxin B.

A:Reference number: S27240; MUID:93049338; PMID:1425690

A:Accession: S27240

A:Molecule type: protein

A:Residues: 28-42, 128-148 <ALA>

C:Superfamily: enterotoxin B

C:Keywords: enterotoxin; extracellular protein; toxin

F:1-27/Domain: signal sequence #status predicted <SIG>

F:28-266/Product: enterotoxin B #status experimental <MAT>

F:120-140/Disulfide bonds: #status experimental

A;Experimental source: Streptococcus pyogenes strain MGAS156 isolate Nebraska unassigned
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 A;Accession: S18784
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 9-244 <NEA>
 A;Cross-references: EMBL:X61556; NID:G47291; PIDN:CAA43754.1; PID:G47292
 A;Experimental source: Streptococcus pyogenes strain MGAS165 isolate Minnesota unassigned
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 A;Accession: S18785
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 9-244 <NEZ>
 A;Cross-references: EMBL:X61559; NID:G47293; PIDN:CAA43757.1; PID:G47294
 A;Experimental source: Streptococcus pyogenes strain MGAS167 isolate Texas unassigned
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 A;Accession: S18791
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 9-244 <NEY>
 A;Cross-references: EMBL:X61555; NID:G47309; PIDN:CAA43753.1; PID:G47310
 A;Experimental source: Streptococcus pyogenes strain MGAS327 isolate Arizona unassigned
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 A;Accession: S18796
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 9-244 <NEO>
 A;Cross-references: EMBL:X61557; NID:G47319; PIDN:CAA43755.1; PID:G47320
 A;Experimental source: Streptococcus pyogenes strain MGAS493 isolate France unassigned
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 A;Accession: S18797
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 9-244 <NEH>
 A;Cross-references: EMBL:X61558; NID:G47321; PIDN:CAA43756.1; PID:G47322
 A;Experimental source: Streptococcus pyogenes strain MGAS494 isolate France unassigned
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 A;Accession: S18800
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 9-228 <NES>
 A;Cross-references: EMBL:X61554; NID:G47327; PIDN:CAA43752.1; PID:G47328
 A;Experimental source: Streptococcus pyogenes strain MGAS500 isolate New Zealand unassigned
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 C;Genetics:
 A;Gene: speA1
 C;Superfamily: enterotoxin B
 C;Keywords: exotoxin
 F;1-30/Domain: signal sequence #status predicted <SIG>
 F;31-251/Product: exotoxin type A #status predicted <MAT>

Query Match 22.9%; Score 283.5; DB 1; Length 251;
 Best Local Similarity 33.8%; Pred. No. 3.9e-16;
 Matches 80; Conservative 44; Mismatches 94; Indels 19; Gaps 10;

Qy 4 SEINEKDLAKKSELQGTAL-GNLKQIY--YNEKAITENKESDDQFLENTLFGKFFTG 60
 Db 25 SQEVFAQQDPPSGLHSSLSLVKLNQIYFLYEGDPVTHENVKSVDDLSDLIYN---VS 81
 Qy 61 HPWYNDLLVGLGSKDATNKYKGGVDLYGAYGYQC-AGGTPNKTACMYGGVTLHDNNRL 119
 Db 82 GPNYDKLTKELKQEMATLPKKNVDIYGYEYHLCVLCENASARSACIYGGVTHNHNHL 141
 Qy 120 TEKKVPINLWIDQKTTVPIDKVKSKKVTVOELDLQARHVLHGKFGLYNSDSFGK 179
 Db 142 EIPKNILVKVSDIGIQ-SLSFD-IEITNKWMTAQELDYKVRKLTDNKQLYTNGP--SKY 197
 Qy 180 QRGILVPHSSEGSVTSYDLFD---AQGQYPTDLLRIYRDNTKNTINSENHIALYLT 232
 Db 198 ETGYIKFIPKNKSFWDFFPEFTQSKY----LMYKDNETLDSNTSQIEVLTT 250

RESULT 14

S18789
 exotoxin A precursor (allele 4) - Streptococcus pyogenes (strain MGAS262 isolate Californ
 N;Alternate names: scarlet fever toxin
 C;Species: Streptococcus pyogenes
 A;Variety: strain MGAS262 isolate California
 C;Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 16-Jul-1999
 C;Accession: S18789
 J;Exp. Med. 174, 1271-1274, 1991
 A;Title: Characterization and clonal distribution of four alleles of the speA gene encodi
 A;Reference number: S18782; MUID:92044323; PMID:1940804
 A;Accession: S18789
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-236 <NEL>
 A;Cross-references: EMBL:X61573; NID:G47303; PIDN:CAA43771.1; PID:G47304
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
 C;Genetics:
 A;Gene: speA
 C;Superfamily: enterotoxin B
 C;Keywords: exotoxin
 F;1-22/Domain: signal sequence (fragment) #status predicted <SIG>
 F;23-236/Product: exotoxin A (fragment) #status predicted <MAT>

Query Match 21.8%; Score 270.5; DB 2; Length 236;
 Best Local Similarity 33.0%; Pred. No. 4.3e-15;
 Matches 75; Conservative 41; Mismatches 100; Indels 11; Gaps 7;

Qy 4 SEINEKDLAKKSELQGTAL-GNLKQIY--YNEKAITENKESDDQFLENTLFGKFFTG 60
 Db 17 SQEVFAQQDPPSGLHSSLSLVKLNQIYFLYEGDPVTHENVKSVDDLSDLIYN---VS 73
 Qy 61 HPWYNDLLVGLGSKDATNKYKGGVDLYGAYGYQC-AGGTPNKTACMYGGVTLHDNNRL 119
 Db 74 GLNYDKLTKELKQEMATLPKKNVDIYGYEYHLCVLCENASARSACIYGGVTHNHNHL 133
 Qy 120 TEKKVPINLWIDQKTTVPIDKVKSKKVTVOELDLQARHVLHGKFGLYNSDSFGK 179
 Db 134 EIPKNILVKVSDIGIQ-SLSFD-IEITNKWMTAQELDYKVRKLTDNKQLYTNGP--SKY 189
 Qy 180 QRGILVPHSSEGSVTSYDLFDQAGQYPTDLLRIYRDNTKNTINSENHIALYLT 226
 Db 190 ETGYIKFIPKNKSFWDFFPEFTQSKY----LMYKDNETLDSNTSQIEVLTT 236

RESULT 15

ENSAC1
 enterotoxin C-1 precursor - Staphylococcus aureus
 C;Species: Staphylococcus aureus
 C;Date: 15-Nov-1994 #sequence_revision 05-Jan-1996 #text_change 18-Jun-1999
 C;Accession: S06356; A01816
 R;Bohach, G.A.; Schlievert, P.M.
 Mol. Gen. Genet. 209, 15-20, 1987
 A;Title: Nucleotide sequence of the staphylococcal enterotoxin C-1.
 A;Reference number: S06356; MUID:88038352; PMID:2823067
 A;Accession: S06356
 A;Molecule type: DNA
 A;Residues: 1-266 <BOH>
 A;Cross-references: EMBL:X05815; NID:G46566; PIDN:CAA29260.1; PID:G46567
 J;Schmidt, J.J.; Spero, L.
 J. Biol. Chem. 258, 6300-6306, 1983
 A;Title: The complete amino acid sequence of Staphylococcal enterotoxin C-1.
 A;Reference number: A01816; MUID:83213327; PMID:6189824
 A;Accession: A01816
 A;Molecule type: Protein
 A;Residues: 28-75, 117, 78-176, 'N', 178-266 <SCH>
 C;Genetics:
 A;Gene: entC1
 C;Superfamily: enterotoxin B
 C;Keywords: enterotoxin
 F;1-27/Domain: signal sequence #status predicted <SIG>
 F;28-266/Product: enterotoxin C-1 #status experimental <MAT>
 F;120-137/Disulfide bonds: #status experimental

Query Match 21.8%; Score 270.5; DB 1; Length 266;
Best Local Similarity 31.3%; Pred. No. Se-15;
Matches 76; Conservative 49; Mismatches 101; Indels 17; Gaps 8;

Qy 1 SEKSEINEKDLRKSELQGTALGNLRFQIYYVNEKAITENKESDDOPLENTLLFKGFFTG 60
:
Db 27 AESQDPDPTDELHKASKFTG-LMENMKVLVDHVSATKV-KSVDFELADHLIYNISDKK 84
:
Qy 61 HPWTNLDLVLGSKDANKVKYKKVDLYIGAYGVQC-----AGTPNKTCMYGGVTLL 113
:
Db 85 LKNYDKRYKTLLNGGLAKKYKDEVDVYGNSYNYNCVFSSKDNVGKVTGKTCTMGGITK 144
:
Qy 114 HDNNRLTEE--KKVPINLWDGKTTVPIDIKWTSKKEVTVOQLDLQARHYLHGKFGLYN 171
:
Db 145 HEGNHFDNGNLQNVLIRVY-ENKENTISFE-VQTDKKSVAQAELDIAKRNFLINKNLYE 202
:
Qy 172 SDSFGKGVRGLIVFHSESGSTVSYDLFDAQQGYPD--TLRLTYRDNKNTINSNHALY 229
:
Db 203 FNS--SPVETGIYKFIENNNGTWFMDMPAPGKFDQSKYLMMYNDNKTVDSKSVKIEVH 260
:
Qy 230 LYT 232
| | | | |
Db 261 LTT 263
| | | | |

RESULT 16
S18783
exotoxin type A precursor (allele 3) - Streptococcus pyogenes phage (strain MGAS158 isol
N;Alternate names: scarlet fever toxin
C;Species: Streptococcus pyogenes phage
A;Variety: strain MGAS158 isolate Nebraska; strain MGAS485 isolate Yugoslavia; strain MG
C;Date: 29-Jan-1993 sequence revision 29-Jan-1993 #text_change 16-Jul-1999
C;Accession: S18793; S18793; S18794; S18801; S18798
R;Neelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991
A;Title: Characterization and clonal distribution of four alleles of the speA gene encod
A;Reference number: S18782; PMID:92044323; PMID:1940804
A;Accession: S18783
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEL>
A;Cross-references: EMBL:X61568; NID:g47289; PIDN:CAA43766.1; PID:g47290
A;Experimental source: strain MGAS158 isolate Nebraska assigned phase
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18793
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEA>
A;Cross-references: EMBL:X61569; NID:g47313; PIDN:CAA43767.1; PID:g47314
A;Experimental source: strain MGAS485 isolate Yugoslavia unassigned phase
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18794
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEZ>
A;Cross-references: EMBL:X61570; NID:g47315; PIDN:CAA43768.1; PID:g47316
A;Experimental source: strain MGAS491 isolate United Kingdom unassigned phase
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18801
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEY>
A;Cross-references: EMBL:X61571; NID:g47323; PIDN:CAA43769.1; PID:g47324
A;Experimental source: strain MGAS495 isolate Germany unassigned phase
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A;Accession: S18798
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-236 <NEB>

A,Cross-references: EMBL:X61565; NID:g47311; PIDN:CMAA3763.1; PID:g47312
A,Experimental source: strain MGAS480 isolate Yugoslavia unassigned phage
A,A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A,Accession: S18795
A>Status: nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Residues: 1-236 <NES>
A,Cross-references: EMBL:X61566; NID:g47317; PIDN:CMAA3764.1; PID:g47318
A,Experimental source: strain MGAS492 isolate United Kingdom unassigned phage
A,A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A,Accession: S18799
A>Status: nucleic acid sequence not shown; translation not shown
A,Molecule type: DNA
A,Residues: 1-236 <NES>
A,Cross-references: EMBL:X61567; NID:g47325; PIDN:CMAA3765.1; PID:g47326
A,Experimental source: strain MGAS496 isolate Germany unassigned phage
A,A>Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C,Genetics:
A,Gene: speA2
C,Superfamily: enterotoxin B
C,Keywords: exotoxin
F,i-1-22/Domain: signal sequence (fragment) #status predicted <SIG>
F,i-23-236/Product: exotoxin type A (fragment) #status predicted <MAT>

Query Match 21.3%; Score 263.5; DB 2; Length 236;
Best Local Similarity 32.9%; Pred. No. 1.6e-14;
Matches 76; Conservative 43; Mismatches 93; Indels 19; Gaps 10;

QY 4 SSEEINEKDLRKSEIQGTAL-GNLKQIYY-YNEKAIT-ENKESDDQFLNTLLFKGFTG 60
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 17 SOEVEFAQQDPDPSQLRSRLVKNLQNIFYLEGDFVTENVKSYDQLSHDLIYN--VS 73
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 61 HPWANDLLVLGSKDATNKYGKKVDLYGAYVQC-AGGPNTACMYGGVTLHDNNRL 119
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 74 GPNYDKLTTELKNQEWAFLFDKXNDVIYSVEYHYLCYENAESACIYGVTVNEG NHL 133
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 120 TBEKVPIINLWDIGKQTTPVIDKVKTSKEVTVQSLELDLOARHYLHGKPLGYNDSFGKV 179
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 134 ETPKIKIVKVSIDGIQ-SLSFD-IETNKKMVTAQELDYKVRKYLTDNKQLYTNGP--SKY 189
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
QY 180 QGLVLVFHSSSESTVSYDLFD---AQCGVPDTLLRIYRDNKTINSENLIHI 226
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
DB 190 ETGYTKFIPIKNKSFWFDFPEPETQSKI----LMYKDNETLSDSNTSQI 236
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

RESULT 18
G89968
extracellular enterotoxin type G precursor [imported] - Staphylococcus aureus (strain I
C,Species: Staphylococcus aureus
C,Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C,Accession: G89968
ma, A.: Kuratani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.
C.: Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A,tittle: Whole genome sequencing of methicillin-resistant staphylococcus aureus.
A,Reference number: A89758; PMID:12131952; PMID:11418146
A,Accession: G89968
A>Status: preliminary
A,Molecule type: DNA
A,Residues: 1-258 <KUR>
A,Cross-references: GB:BA000018; PID:gl3701617; PIDN:BAB42310.1; GSPDB:GN00149
A,Experimental source: strain N315
C,Genetics:
A,Gene: seg
C,Superfamily: enterotoxin B

Query Match 20.7%; Score 256; DB 2; Length 258;
Best Local Similarity 29.6%; Pred. No. 7.7e-14;
Matches 74; Conservative 50; Mismatches 84; Indels 42; Gaps 12;

QY 3 KSEINEKDLRKSEIQGTALGNLKQIYY---YNEKAITENKESDDQFLNTLLFKGFTT 59
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :
| : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | :

A;Cross-references: GB:BA000018; PID:gl3701400; PIDN:BA42694.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA1430

Query Match 16.2%; Score 200; DB 2; Length 157;
Best Local Similarity 35.6%; Pred. No. 1.8e-09;
Matches 42; Conservative 20; Mismatches 54; Indels 2; Gaps 2;

QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDOLENTLLPKGFTG 60
DB 42 TNSASAIYSDLHKKSPDKSLGNK--MSFINTQL--ENKNTNDRLLKHDLDFHDMFN 99
QY 61 HPWYNDLLVDLGSQDATNKYKGGKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNR 118
DB 100 VASKKDFKVEFENEALSKKFNKNDIYAGSYSECHGATNKQCSGGVTLSDNNK 157

RESULT 21
A89969
enterotoxin YENT2 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: A89969
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; PMID:21311952; PMID:11418146
A;Accession: A89969
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-136 <KUR>
A;Cross-references: GB:BA000018; PID:gl3701619; PIDN:BA42912.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: Yent2

Query Match 15.7%; Score 194; DB 2; Length 136;
Best Local Similarity 34.1%; Pred. No. 4.8e-09;
Matches 46; Conservative 27; Mismatches 52; Indels 10; Gaps 5;

QY 103 KTACMYGGVTLHDNRLLTEKKV--PINLW----DGKTTVPIDKVTSKKEVTVOELDL 157
DB 2 KKTCTGGVTEHDGQIDKNSTDSNHLIKVYENERSLSFD--IPTNKKNTAQAIEDY 60
QY 158 QARHVLHGKFGLYNGDSFGKVGQGLIVFHSSEGSTVSVDLFDAGQ--YPTDLLRIYRD 215
DB 61 KVRNLLKHKNLYEFS--SPYETGYIKFEGSGHSFYDLMPESGKFFYTKYLLIYND 118
QY 216 NKTINSENHIALYL 230
DB 119 NKTVESKSNINVEHL 133

RESULT 22
A30509
exotoxin C precursor - Streptococcus pyogenes
C;Species: Streptococcus pyogenes
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 17-Mar-2000
C;Accession: A30509
R;Coshorn, S.C.; Schlievert, P.W.
Infect. Immun. 56, 2518-2520, 1988
A;Title: Nucleotide sequence of streptococcal pyrogenic exotoxin type C.
A;Reference number: A30509; PMID:8814303; PMID:3045005
A;Accession: A30509
A;Molecule type: DNA
A;Residues: 1-235 <GCS>
A;Cross-references: GB:M35514; NID:gl53820; PIDN:AA427017.1; PID:gl53821
C;Superfamily: enterotoxin B
C;Keywords: exotoxin

Query Match 14.2%; Score 175.5; DB 2; Length 235;
Best Local Similarity 25.4%; Pred. No. 3.2e-07;
Matches 60; Conservative 37; Mismatches 74; Indels 65; Gaps 11;

QY 47 FLENTLLFKGFTGH-----PWYNDLLVDLGSKDA-----TNK 79
DB 11 FIITVILISTYFTYHQSDSKDISNVKSLLYAYITPYDKDCRVNFTTHTLNDTOK 70
QY 80 YGKG-----KVDLYGAYGYQCAGGTENKTACMYGGVTLHDNRLL 119
DB 71 YRGKDYIISSEMSYEASQKFKRDDHVDVFGFLVILNSHTG-----EYIYGITPAQNNKV 125
QY 120 TEKKVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHVLHGKFGLYNSDS--FG 177
DB 126 NH--KLGNLFTSGESQQNLNKKIILEKDIVTFOEIDFKIRKYLMDNYKIYDATSPYVG 183
QY 178 KVQKGLIVFHSSEGSTVSVDLFD--OGQVPTLLRIYRDNKTINSEN--HIALYL 230
DB 184 RIBIG-----TKDGKHEQIDLFDSPNEGTRSDIFAK--YKDNRIINWKNFSDIYL 233

RESULT 23
H89941
hypothetical protein SA1429 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: H89941
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; PMID:21311952; PMID:11418146
A;Accession: H89941
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-62 <KUR>
A;Cross-references: GB:BA000018; PID:gl3701399; PIDN:BA42693.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA1429

Query Match 11.0%; Score 136; DB 2; Length 62;
Best Local Similarity 37.5%; Pred. No. 0.00012;
Matches 21; Conservative 16; Mismatches 19; Indels 0; Gaps 0;

QY 176 GKVKQGLIVFHSSEGSTVSVDLFDAGQGPDTLLRIYRDNKTINSENHIALYL 231
DB 5 GGDIVKGVYKHNDQCNVEYDFYNLNGEYGEVLEKMYADNKTINRDKLHLDIYLF 60

RESULT 24
B89969
enterotoxin Yent1 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C;Accession: B89969
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A;Reference number: A89758; PMID:21311952; PMID:11418146
A;Accession: B89969
A;Status: Preliminary
A;Molecule type: DNA
A;Residues: 1-133 <KUR>
A;Cross-references: GB:BA000018; PID:gl3701620; PIDN:BA42913.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: Yent1

Query Match 10.1%; Score 125; DB 2; Length 133;

QY 175 FGG--KVORGLIVFHSSRGSTVSVDL-----FPAQQYQPTLLRIYRDNKTINSE 222
Db 190 TGGYWKIT-----MNDGSTYQSDLSKKFYNTKEPINT---DEIKTIBAE 232

RESULT 28
E64410
DNA-directed DNA polymerase (EC 2.7.7.7) family B, intein containing precursor - Methanococcus jannaschii
N:Contains: DNA endonuclease (EC 3.1.1.1) PI-I; DNA endonuclease (EC 3.1.1.1) PI-II; DNA
C:Species: Methanococcus jannaschii
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 13-Sep-1998
C:Accession: E64410
R:Bult, C.J.; White, O.; Olsen, G.J.; Zhou, L.; Fleischmann, R.D.; Sutton, G.G.; Blake,
Reich, C.J.; Overbeek, R.; Kirkness, E.F.; Weinstock, K.G.; Merrick, J.M.; Glodek, A.;
raon, J.D.; Sadow, P.W.; Hama, M.C.; Cotton, M.D.; Roberts, K.M.; Hurst, M.A.
Science 273, 1058-1073, 1996
A:Authors: Kaine, B.P.; Borodovsky, M.; Klenk, H.P.; Fraser, C.M.; Smith, H.O.; Woese, C.
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MUID:96337999; PMID:8686087
A:Accession: E64410
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1634 <BUL>
A:Cross-references: GB:U67532; GB:L77117; NID:G1591559; PID:G1591563; TIGR:MJ0885; PID:G
A:Map position: REV816304-811400
C:Genetics:
A:Start codon: TTG
A:Function:
A:Description: as DNA-directed DNA polymerase, catalyzes the polymerization of DNA at th
C:Function: <EN1>
A:Description: as DNA endonuclease PI-Mjai, catalyzes the hydrolysis of internal phospho
C:Function: <EN2>
A:Description: as DNA endonuclease PI-Mjai, catalyzes the hydrolysis of internal phosph
C:Superfamily: DNA-directed DNA polymerase KOD
C:Keywords: endonuclease; hydrolase; nucleotidyltransferase; protein splicing
F:1-425/Domain: 1359-1634/Product: DNA-directed DNA polymerase family B #status predicted
F:1-425/Domain: DNA-directed DNA polymerase family B extein 1 #status predicted <XT1>
F:426-794/Product: DNA endonuclease PI-I (pol B extein 1) #status predicted <MAT2>
F:795-882/Domain: DNA-directed DNA polymerase family B extein 2 #status predicted <XT2>
F:883-1358/Product: DNA endonuclease PI-II (pol B extein 2) #status predicted <MAT3>
F:1358-1634/Domain: DNA-directed DNA polymerase family B extein 3 #status predicted <XT3>
F:426-794/Cross-link: peptide (Arg-Ser) #status predicted
F:882-1359/Cross-link: peptide (Arg-Ser) #status predicted

Query Match 8.2%; Score 101; DB 2; Length 1634;
Best Local Similarity 22.9%; Pred. No. 5.5;
Matches 53; Conservative 33; Mismatches 79; Indels 66; Gaps 10;

QY 12 LRKSELQGTALGNLKQIYYNEKAITENKESDDQFLENTLLFKGFTTGHFWYNDLVDL 71
Db 614 VRRKKGTKAITLGCACKDYLKIEELKNKE---KYLFPNAIL-RGFEGDGYVNTVRRAV 669

QY 72 GSKDATNKYKCK-----VDLYGAYGYQCAGTPTNCTACMYGGVTLHDNNRLTEKKVP 126
Db 670 VVNGTNNYDKIKFIASLDRLGKYSF-----YTSYSEERGGKKRYV 713

QY 127 INLWIDGKQTTVPIDKVKTS-----KKEVTVQELDQARHYLHGKFLGNSD----- 173
Db 714 IEITSGK-----DLKFSILISFISRRKNLLNEIRQKTLKIGDYGFDLDDVCVS 766

QY 174 --SFGKV-----QRLIVFHSSEGS-TVSVDLEDAQGYPDIL 209
Db 767 LESYKGEVYDTLGRPPYFANGILTHNSLPYSIIISYNI-----SPDIL 811

RESULT 29
S70908
transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB29)
C:Species: Haemophilus influenzae
A:Variety: strain SB29
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C:Accession: S70908; S73321
R:Loosmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.B.

Mol. Microbiol. 19, 575-586, 1996
A:Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes.
A:Reference number: S70901; MUID:96228706; PMID:8830248
A:Accession: S70908
A:Molecule type: DNA
A:Residues: 1-631 <LOO>
A:Cross-references: EMBL:U15055
A:Experimental source: strain SB29, clone DS-1090-3-2
R:Loosmore, S.M.
submitted to the EMBL Data Library, September 1994
A:Reference number: S73320
A:Accession: S73321
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-250, 'L', 352-349, 'RTDATTN', 357-631 <LOW>
A:Cross-references: EMBL:U15055; NID:G1223948; PIDN:AAC43931.1; PID:G1223949
A:Experimental source: strain SB29, clone DS-1090-3-2
C:Genetics:
A:Gene: tbp2
C:Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor an
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-631/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match 8.0%; Score 99; DB 2; Length 631;
Best Local Similarity 21.0%; Pred. No. 2.5;
Matches 56; Conservative 31; Mismatches 60; Indels 120; Gaps 12;

QY 14 KGELOGTALGNLKQIYYNEKAITENKESDDQFLENTLLFKGFTTGHFWYNDLVDL 60
Db 190 QRYSLFSGAFG-----AYNRRSAISDIDN-----LENNLKNGAGLTSEFTVNFGTKKLTG 240

QY 61 HPWYNL-----LVDLGSKDATNKYKCK-----KVDLYGAY 91
Db 241 KLYNERETNNKLOKRXKHELVDIADIYSNFRGKVKFTQKDSQEHFTSEGTLEGGF 300

QY 92 YGQCAGTPTNCTACMYGGVTLHDNNRL-----TEKKVPINLWIDGKQTTVPID 141
Db 301 YG-----PNGEE---LGGKFLAGDNRVGFVSAXEETKDKKLSRETLDGLKLTFTKTK 351

QY 142 K-----VKTSSKEVTVQELD-----LQARHYLHG-- 165
Db 352 KTDAKTAANAKTDERNFTTKDIPSGEADYLLIDNVFVLPFPEENTNDFTSRHHKVGDK 411

QY 166 -----KFLYNSDSFGGK 178
Db 412 TYKVEACKNLSVYKFGMYEDPLNGE 438

RESULT 30
D89807
exotoxin 11 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: D89807
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kato, C.; Sekimizu, K.; I
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramat, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: D89807
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-231 <KUR>
A:Cross-references: GB:BA000018; PID:G13700317; PIDN:BA841615.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: set11

Query Match 8.0%; Score 98.5; DB 2; Length 231;
Best Local Similarity 23.6%; Pred. No. 0.77;
Matches 55; Conservative 29; Mismatches 96; Indels 53; Gaps 10;

QY 2 EKSEINE-----KLRKSELQGTALGNL--KQIYYNEKAITENKESDDQFLENTLLFK 55
Db 32 EKQERYOHLYDIKOLRYYSSESFBFNSGKVENYNSVVRFNQEK-----QNHQLF- 85
QY 56 GFPTGHPWYNDLIVDLSGSKDATNKYK---GKKVDLYGAYYQACAGTTPNKTCMYGV 111
Db 86 -----LLGKD-KDKYKGLGQNVFVKELI-----DPNGRLSTVGV 122
QY 112 TLHNNRLTEKKVPINLMDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGFLYN 171
Db 123 TKNNKSSETNTHLFYNK-VYGNLSDASIDSLINKKEVSLKELDFKIRKQJVEKYGLYK 181
QY 172 SDSFGKVGKQGLVPHSSSEGSTVSVDLFDAGQGYPTLLRIYRDNKNTINSEN 224
Db 182 -----GTTKVGKTTINLKEKEVIDLGK-----LQFERMGVDVLSKDI 221
RESULT 31
E89807
exotoxin 12 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 14-Apr-2003
C;Accession: E89807
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: E89807
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-232 <XUR>
A;Cross-references: GB:BA000018; PID:g13700318; PIDN:BAB41616.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: set12
C;Superfamily: toxic shock syndrome toxin
Query Match 7.9%; Score 97.5; DB 2; Length 232;
Best Local Similarity 25.6%; Pred. No. 0.93;
Matches 63; Conservative 26; Mismatches 98; Indels 53; Gaps 11;
QY 3 KSEINEK-DLRKSELQGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 24 ENQSVNAKGYEKMRNLYDT--NKLHQYSGPSYELTNVSGSQGYDYNVLLF----- 75
QY 61 HPWYNDLVLGSKDATNKYKGGK-----VDLYGAYYQACAGTTPNKTCMYG 109
Db 76 NQONKQFQVFLGKD-ENKYEKTHGLDPAVPELVLDLGRIFS-----VS 120
QY 110 GVTLDHNNRLTEKKVPINLW----IDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGK 166
Db 121 GVTGNVKSIFESLRTP-NLLVKKIDDKDGFSDIFFEQKEVSLKELDFKIRKLLIKK 179
QY 167 FGLYNSDPSFGKVGKQGLVPHSSSEGSTVSVDLFDAGQGYPTLLRIYRDNKNTINSEN 224
Db 180 YKLYE-----GSADKGRIVNMKNENKYEIDLSDK-----LDPERMADVINEQI 224
RESULT 32
E89807
exotoxin 14 [imported] - Staphylococcus aureus (strain N315)
C;Species: Staphylococcus aureus
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 14-Apr-2003
C;Accession: E89807
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A;Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: E89807

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-227 <KUR>
A;Cross-references: GB:BA000018; PID:g13700320; PIDN:BAB41618.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: set14
C;Superfamily: toxic shock syndrome toxin
Query Match 7.68%; Score 94; DB 2; Length 227;
Best Local Similarity 25.9%; Pred. No. 1.8;
Matches 52; Conservative 31; Mismatches 76; Indels 42; Gaps 9;
QY 8 NEKDLRKSELQGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYND 66
Db 33 NQKSVNKHDK-----EALYRYTYGKTWEMKNISALKHGKNNLRFK--PRGIKIQLV 81
QY 67 LLVDLGSKDATNKYK-----KKVDLYGAYYQACAGT--PNKTACMYGVTVLHDNN 117
Db 82 LPGAQKSKFOQRSYEGLDVFFVQEKRDKHDIFY---TVGGVIQNNKTS-----GWSAPIL 134
QY 118 RLTEKKVPINLMDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGG 177
Db 135 NISKEK-----GEDAFVKGYPYIKKEKTLKELDYKLRKHLIEKYLKTKISKOG 185
QY 178 KVQRGLIVPHSSSEGSTVSVDL 198
Db 186 RVKISL-----XDGSPYNDL 201
RESULT 33
A11161
flagellar hook protein FlgE homolog lmo0697 [imported] - Listeria monocytogenes (strain I
C;Species: Listeria monocytogenes
C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C;Accession: A11161
R;Glaser, P.; Prangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Psihi, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlend,
A;Title: Comparative genomics of Listeria species.
A;Reference number: A51077; MUID:21537279; PMID:11679669
A;Accession: A11161
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-411 <GLA>
A;Cross-references: GB:NC 003210; PIDN:CAC98775.1; PID:g16410086; GSPDB:GN00177
A;Experimental source: strain BGD-e
C;Genetics:
A;Gene: lmo0697
Query Match 7.4%; Score 91; DB 2; Length 411;
Best Local Similarity 20.9%; Pred. No. 6.6;
Matches 55; Conservative 39; Mismatches 81; Indels 88; Gaps 14;
QY 32 YNEKAITENKESDDQFLENTLL--LFKGFFTG-HPW-----YNDLIVD--LGSKDATNK 79
Db 34 YKQSVVFN-----DLLYQNTMGSVAGGLYAGTNPMSFGSGSKIGAILTDTAGSPSTGR 89
QY 80 YKGGKVDLYGAYYQACAGTTPNKTCMYGVTVLHDNNRLTEK----- 123
Db 90 NKDAALQGRGFFIAGDNAGG--NIVYTRDGSFAVDNNYLLTQGGKYVMGYATDKGNVL 147
QY 124 -----KVPINLMDGKQT-----TVPIDKVKTSKEVTVQELDLQARHYLHGKFL 169
Db 148 NGNLQIP-QIPLNSAIPGEATKNGSLNIFLD---WGEKDTISSELSVY----- 193
QY 170 YNSDSFGG--KVQRGLIVPHSSSEGSTVSVDL-----FDACQY--PD 207
Db 194 ---DNAGGKHLQYMKAAATPDASGVSYEIQMDGKALTTPPVYTGTLNNAQGLNPD 250

Qy 208 TLLRIYRDNKTIINSENHLIALYL 230
Db 251 ALKNI-QINSTVNGKQVNMGLNL 272

RESULT 34
AC1520
flagellar hook protein FlgE homolog lin0705 [imported] - *Listeria innocua* (strain Clip11262)
C/Species: *Listeria innocua*
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C/Accession: AC1520
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournan, A.; Maok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AC1520
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-411 <GLA>
A/Cross-references: GB:AL592022; PIDN:CAC95937.1; PID:gl6413157; GSPDB:GN00178
A/Experimental source: strain Clip11262
C/Genetics:
A/Gene: lin0705

Query Match 7.4%; Score 91; DB 2; Length 411;
Best Local Similarity 20.9%; Pred.No.6.6;
Matches 55; Conservative 39; Mismatches 81; Indels 88; Gaps 14;

Qy 32 YNEKAITENKESDDQFLENTL-LFKGFFTG-HPW-----YNDLLVD--LGSKDATNK 79
Db 34 YKQSVFVN---DLLYQNTGVSAGLYAGTNPMFGSGSKIGALTIDYTAGSPFSTGR 89
Qy 80 YGKKKVDLYGAYGYQCAGTPNKTAOMYGGVTLHDNNRLTEK-----123
Db 90 NKDAALQGRGFFIAGDNAGG-NIVYTRDGSFAVSDNNYLLTQQGKYVMGYATDKNGNVL 147
Qy 124 -----KVPINLWIDKQT-----TVPIDKVKTSKEVTVOELDQARHVLHGKFG 169
Db 148 NGNLQPTQIPLNSAIPGEAKNGSLGNIFLD---WGEKDTISSELSVY-----193
Qy 170 YNSDSFGG--KVQRGILVFHSSGSTVSYDL-----FDAQGY--PD 207
Db 194 --DNAGGKHLQVNMKAATPDASGNVSVEYETQMDGKALTPVTGTLNVAQGLTNFD 250
Qy 208 TLLRIYRDNKTIINSENHLIALYL 230
Db 251 ALKNI-QINSTVNGKQVNMGLNL 272

RESULT 35
AC1553
B. subtilis YjbK protein homolog lin0964 [imported] - *Listeria innocua* (strain Clip11262)
C/Species: *Listeria innocua*
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Oct-2003
C/Accession: AC1553
R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournan, A.; Maok, C.; Schluster, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of *Listeria* species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AC1553
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-194 <GLA>
A/Cross-references: GB:AL592022; PIDN:CAC96195.1; PID:gl6413423; GSPDB:GN00178
A/Experimental source: strain Clip11262

```

C/Genetics:
A/Gene: lin0964
C/Superfamily: uncharacterized stand-alone CYTH domain protein

      Query Match      7.2%: Score 89.5; DB 2; Length 194;
      Best Local Similarity 21.9%: Pred. No. 3.4;
      Matches 52; Conservative 34; Mismatches 88; Indels 63; Gaps 12

Qy 3 KSEETNEKDLRKKSELQGTALGNLKQIYYNEKAITENKESDQFLNTLLFKGFTGHP 62
Db 3 KELETEFNRLTKSEY-----DRLIEDFRIKEDDFEQT-----N 37

Qy 63 WYNDLLVLDSKDATNKYKGGKVDLYGAVYCYQCAGGTNNKTACMYGGVTLHDNNRLTEE 122
Db 38 FYLD-TADFGLKERNALSALRIKLETO-----YQLTKTPEARGLM-----ETQILAAD 85

Qy 123 KKVPINLWIDGQTVTPIDKVTKSKSVTVQELDQARHVLHGKFGLYNSDSPGKVKVQG 182
Db 86 QATAIT---DG--ANIPGVPVDRTLTKSIGINHSDQV-----FGSLTIRAEKDYKKG 133

Qy 183 LIVFHSS-EGSTVSYDL-----PDAQQYFPDLLRIYR-----DNKTINSENLHI 226
Db 134 LLVFDKNFVGSISDFLEIYEVSDYDKGKEIFDKLLKEYQITNHPAENKVARFVN-HV 189

RESULT 36
G89806
exotoxin 6 [imported] - Staphylococcus aureus (strain N31:5)
C/Species: Staphylococcus aureus
C/Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 14-Apr-2003
C/Accession: G89806
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui
ma, A.; Mizukuni-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Seki
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A/Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A/Reference number: A89758; MUID:213111952; PMID:11418146
A/Accession: G89806
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-226 <R>
A/Cross-references: GB:BA000018; PID:gl3700312; PIDN:BABA1610.1; GSPDB:GN00149
A/Experimental source: strain N315
C/Genetics:
A/Gene: set6
C/Superfamily: toxic shock syndrome toxin

```

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Query Match          7.2%; Score 89; DB 2; Length 226;
Best Local Similarity 22.5%; Pred. No. 4.6;
Matches 49; Conservative 36; Mismatches 65; Indels 68; Gaps 11

Qy      8 NEKDLRKESELCQTALGNLKIYYNNEKAITENKESDDQPLENTLIFKGFFFTCHPW---- 63
        |||::||:::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      24 NVQSQAATEVKKQSESELK--HYIN-KPLVERLN-----VTGIRKTEKG 65

Qy      64 --YNDLLVD-----LGS-KDANTKYKKGVLDLYGYGYOCAGGTPNKTACMYGGVT 112
        |||::||:::||::||::||::||::||::||::||::||::||::||::||::||
Db      66 KDYIDVIDENVQYSILVSGDKFKPDGDSNTIDVF-----ILREGDSQATNYSIGGVT 120

Qy      113 LHDNNRLTEEKVPINWIDGQCTTVIDKVTSKKE-----VTVEQLDLQAR 160
        |||::||:::||::||::||::||::||::||::||::||::||::||::||::||
Db      121 -----KTN SQPIDVIHT--FILEIKKGKEPQSSLQIYKEDISUKELDYRUR 167

Qy      161 HYLHGKFLGYNDSFGGKVQRGLIVFHSSEGSTVSVDL 198
        |||::||:::||::||::||::||::||::||::||::||::||::||::||::||
Db      168 ERAIKOHGLYNG-----LKQGIIITIMKDGKSHITDL 200

```

RESULT 37
C89908
exorxin 15 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:date: 10-May-2001 #sequence revision 10-May-2001 #text change 14-Apr-2003

A>Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: C89196
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-816 <STO>
A:Cross-references: GB:AB93429.1; PID:AB93429.1; PID:g1330372; GSPDB:GN00020; CESP:ZK1127.
A>Note: strong similarity to DNA topoisomerase II
C:Genetics:
A:Gene: ZK127.7
A:Map position: 2

Query Match 7.1%; Score 88.5; DB 2; Length 816;
Best Local Similarity 21.9%; Pred. No. 25;
Matches 51; Conservative 30; Mismatches 59; Indels 93; Gaps 13;

QY 19 QGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG-----PWNDLLVDLG 72
DB 462 QGTGTGWTNPNPRELVN-----IKRLIAGEPQKALAPWYN----- 502

QY 73 SKDATNKYKGVLDYGAIVGYQCAGGTGNTKACMGVTLHDNNRLTEKKYPIINLW-- 130
DB 503 -----FRGLIIOI-----DPSRFAC-YGEVSLDNTI-EITEPIKQWTO 541

QY 131 -----IDG-----KQTTVPIDKVTSKKVTYQEL-----DLQARHYLHGKFG 169
DB 542 DYKEKVLGLMESDCKSPVVD-YKEVHTDTTVKVVVQLSPGKRLERLQDQLHQVF-- 598

QY 170 YNSDSFGKQVQGLIVHSSSGSVVDLFDACQYEDTLIRIYRDNKTINSE 222
DB 599 -----KLOAVI-----NTTCWVLFDAAG-----WLRTYSPEAITQE 630

RESULT 41
C89803
hypotheical protein SA0357 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: C89803
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Ogud
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: C89803
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-203 <KUP>
A:Cross-references: GB:BA000018; PID:g13700284; PID:BA041582.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA0357

Query Match 7.1%; Score 88; DB 2; Length 203;
Best Local Similarity 21.1%; Pred. No. 4.9; Mismatches 53; Indels 100; Gaps 12;
Matches 50; Conservative 34

QY 1 SEKSEINEKDLRKSLEQGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 37 TONSSSVQDKLQKVEEVPNN-----SEKLVKK----- 65

QY 61 HPWNDLLVDLGSKDATNKYKGVLDYGAIVGYQCAGGTGNTKACMGVTLHDNNRL 119
DB 66 -----LYDRYSKDTIN-----GSKNKRNVWYGERPLNENQ-- 96

QY 120 TEKKVPINLWDGQTTVPIDKVTSKKE-----VTQELDLQARHYLHGKFGLYNS 172
DB 97 -----VRIHEGTYTA--DRYVTPKNTLNKEVTVLKLDELHIIR-FAHISYGLY-- 144

QY 173 DSFGKQVQGLIVHSSSGSVVDLFDACQYEDTLIRIYRDNKTINSEN 224
DB 145 --MGEHLPGKNIVINTKDG-----GKY--TLESHELQKDRNPKINTADI 186

RESULT 42
E96793

hypotheical protein F14G6.15 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Sep-2003

C:Accession: E96793

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.

C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maity, R.; Marziani,

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: E96793

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-617 <STO>

C:Genetics:

A:Gene: F14G6.15

A:Map position: 1

C:Superfamily: pyrophosphate-dependent phosphofructokinase, PfpB type; 6-phosphofructokiir

Query Match 7.1%; Score 88; DB 2; Length 617;
Best Local Similarity 30.2%; Pred. No. 19;
Matches 26; Conservative 9; Mismatches 35; Indels 16; Gaps 3;

QY 74 KDATNKYKGVLDYGAIVGYQCAGGTGNTKACMGVTLHDNNRLTE 122

DB 412 KEGT--YKGGKNATCHFFGYQARGLSKFPCDDYAVLGHVCHYLAAGLNGYATVTN 469

QY 123 KKVPIINLWDGQTTVPIDKVTSKK 148

DB 470 LKSPVKNW--KCGAAPISAMWTKR 492

RESULT 43
E69886

processing proteinase homolog ymxG - Bacillus subtilis
C:Species: Bacillus subtilis

C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 20-Jun-2000

C:Accession: E69886; B46665; S34595

R:Kuster, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berterc

C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Choi

A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.

Nature 390, 249-256, 1997

A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallerc

iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.;

Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,

A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel,

Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle,

Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,

A:Authors: Schleich, S.; Scoffone, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror,

akeuchi, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, K.; Tosato, V.; Uchiyama,

T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.

A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.

A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.

A:Reference number: A69580; MUID:19804033; PMID:9384377

A:Accession: E69886

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-409 <KUN>

A:Cross-references: GB:Z99112; GB:ALC09126; NID:q2633902; PIDN:CAB13544.1; PID:g2634043

A:Experimental source: strain 168

R:Chen, N.Y.; Jiang, S.Q.; Klein, D.A.; Paulus, H.

J. Biol. Chem. 268, 9448-9465, 1993

A:Title: Organization and nucleotide sequence of the Bacillus subtilis diaminopimelate op

se.

A;Reference number: A46665; MUID:93252813; PMID:8098035
A;Accession: B46665
A;Molecule type: DNA
A;Residues: 30-269, 'LE', 272-359, 'Q', 361-409 <CHE>
A;Cross-references: EMBL:LC08471; NID:g142823; PIDN:AAA2379.1; PID:g142824
C;Genetics:
A;Gene: ymxG
C;Superfamily: mitochondrial processing peptidase alpha chain

Query Match 7.1%; Score 87.5; DB 2; Length 409;
Best Local Similarity 22.4%; Pred. No. 13;
Matches 55; Conservative 43; Mismatches 79; Indels 65; Gaps 15;

QY 10 KDLRK--KSELOGTALGNLQIYYNEKAITENKESDDOFLNTLLFKGFTTGHFWYND 66
DB 198 KDVEKWFGEYAEAKGKATG-LEKPEFTEK-LTRKKETEQAHLL--CLGFKGLEVGHERIYD 253
QY 67 LLV--DLGSKDATNKY-----KGRKVDLYGAYGYOCAGTGNKTAQMYGGVTLHDNN 117
DB 254 LIVLNNVLGSMSSRLFDQVREDKGLAYSIVSHSYEDSG-----MLTIYGTGANQLQ 308
QY 118 RLTEKKVPINLWIDKQTTVPIDKVTSSKE-VTVQELDLQARHYLHGKFLGNSDSFG 176
DB 309 QLSE-----TIQ-ETLALTKRDGITSKELE-NSKEQMKGSL-MLSLESTN 350
QY 177 GKVORG-----LIVFHSSEGSTVSYDLFDAQGYPDTLRLIYRDNKTINSENLH-IALYL 230
DB 351 SKMSRNGKHELLGKKH-----TLDEIINELNAVNLERNVNGLARQL 391
QY 231 YT 232
DB 392 FT 393

RESULT 44
T08145
myrosinase-binding protein 2 - rape (fragment)
C;Species: Brassica napus (rape)
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 08-Oct-1999
C;Accession: T08145
R;Taipalensuu, J.; Falk, A.; Ek, B.; Rask, L.
Eur. J. Biochem. 243, 605-611, 1997
A;Title: Myrosinase-binding proteins are derived from a large wound-inducible and repeti
A;Reference number: Z16379; MUID:97210758; PMID:9057822
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-634 <TAI>
A;Cross-references: EMBL:U59444; NID:g1655825; PIDN:AAC08049.1; PID:g1655826
A;Experimental source: cv. 20516 of Svalof's Karat; immature seed, 30 days after pollinat

Query Match 7.1%; Score 87.5; DB 2; Length 634;
Best Local Similarity 22.4%; Pred. No. 22;
Matches 64; Conservative 27; Mismatches 86; Indels 109; Gaps 15;

QY 10 KDLRKSELOGTALGNLQ--IYYNEKAITENKESDDOFLNTLLFKG-FTTGHFWYND 66
DB 178 KDGKVEIREHGTNRGQKFEFSDVPNDNIVAVGGSYDHIYFTYDTLLIKSLYFTTSGFTS 237
QY 67 LLVDLGSKDAT-----NKYK-----GKVDLYGAYY--GYOCA-GGTENKTACMY 108
DB 238 PL--FGEKTGTDFEFGENRGKLLGFHGRAGYDAIGAIFHTGSGGEGGDPK----- 290
QY 109 GGVTLHDNNRLTEKKVPI-----NLWIDGKQ-----TTVPIDKV 143
DB 291 GG-----PKPVVPVKGPLGGDRGNFNDVGDGKRVAADEFSVTYIKIEV 340
QY 144 KTSKKEV-----TVQELDLQ-----ARHYLH 164
DB 341 KDGKVEIREHGTNRGQKFEFSDVPNDNFTAVGGSYDHIYFTYDTLLIKSLYFTTSGFTS 400
QY 165 GKFLYNSDSFGGKVORG--LIVFHSSEGSTVSYDLFDAQGYPD 208

Db 401 PLFGEMKGTFFPKGENGEKLI GFHGRAGHAI-----DAIGAIFDT 441

RESULT 45
T08144
myrosinase-binding protein 1 - rape
C;Species: Brassica napus (rape)
C;Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 08-Oct-1999
C;Accession: T08144
R;Taipalensuu, J.; Falk, A.; Ek, B.; Rask, L.
Eur. J. Biochem. 243, 605-611, 1997
A;Title: Myrosinase-binding proteins are derived from a large wound-inducible and repeti
A;Reference number: Z16379; MUID:97210758; PMID:9057822
A;Accession: T08144
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-956 <TAI>
A;Cross-references: EMBL:U59443; NID:g1655823; PIDN:AAC08048.1; PID:g1655824
A;Experimental source: cv. 20516 of Svalof's Karat; immature seed, 30 days after pollinat

Query Match 7.1%; Score 87.5; DB 2; Length 956;
Best Local Similarity 22.4%; Pred. No. 37;
Matches 64; Conservative 27; Mismatches 86; Indels 109; Gaps 15;

QY 10 KDLRKSELOGTALGNLQ--IYYNEKAITENKESDDOFLNTLLFKG-FTTGHFWYND 66
DB 487 KDGKVEIREHGTNRGQKFEFSDVPNDNIVAVGGSYDHIYFTYDTLLIKSLYFTTSGFTS 546
QY 67 LLVDLGSKDAT-----NKYK-----GKVDLYGAYY--GYOCA-GGTENKTACMY 108
DB 547 PL--FGEKTGTDFEFGENRGKLLGFHGRAGYDAIGAIFHTGSGGEGGDPK----- 599
QY 109 GGVTLHDNNRLTEKKVPI-----NLWIDGKQ-----TTVPIDKV 143
DB 600 GG-----PKPVVPVKGPLGGDRGNFNDVGDGKRVAADEFSVTYIKIEV 649
QY 144 KTSKKEV-----TVQELDLQ-----ARHYLH 164
DB 650 KDGKVEIREHGTNRGQKFEFSDVPNDNFTAVGGSYDHIYFTYDTLLIKSLYFTTSGFTS 709
QY 165 GKFLYNSDSFGGKVORG--LIVFHSSEGSTVSYDLFDAQGYPD 208
DB 710 PLFGEMKGTFFPKGENGEKLI GFHGRAGHAI-----DAIGAIFDT 750

RESULT 46
H71602
protein with DnaJ domain (RESA-like) PFB0920w - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Accession: H71602
R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.;
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: H71602
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1014 <GAR>
A;Cross-references: GB:AE001425; GB:AE001362; NID:g3845310; PIDN:AAC71973.1; PID:g3845311
A;Experimental source: clone 3D7
C;Genetics:
A;Gene: PFB0920w
C;Superfamily: dnaJ amino-terminal homology
F:677-742/Domain: dnaJ amino-terminal homology <DNJ>

Query Match 7.1%; Score 87.5; DB 2; Length 1014;
Best Local Similarity 23.0%; Pred. No. 40;
Matches 50; Conservative 35; Mismatches 77; Indels 55; Gaps 10;

QY 6 EINKDLRKSELOGTALGNLQIYYNEKAITENKESDDOFLNTLLFKGFTTGHFW-- 63

```

Db      218 EFVENEKEKYLLKG-----FLYKNNKFKMKNKYTDE-----YPPRKXKNW 259
Qy      64 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGVTLHDNRLTEEK 123
Db      260 YNDLIYK-GSKDLEKLNKMFYEWY-----KQENLNLEEYR 294
Qy      124 KVPINLWIDGQRTVPIDKVKTSKEVTVQELD-LQARHVLHGKFGLYNSD-SFGGKQVR 181
Db      295 RLVLVCRGTGKAL---YNYVENTCKEIIHSDDLIIKNKGSNNMKGLYNNYKNGK--- 348
Qy      182 GLIVFHSSEGSTVSYDLFDAQGGVDPDTLLRIYRDNKT 218
Db      349 -NIPFNTS-SSIDNKKLYNFGKFNPMCFNEDSLT 383

RESULT 47
DVZQF
N;Multidrug resistance protein - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 19-Jan-2001
C;Accession: S18204; A32547
R;Trigilia, T.; Foote, S.J.; Kemp, D.J.; Cowman, A.F.
Mol. Cell. Biol. 11, 5244-5250, 1991
A;Title: Amplification of the multidrug resistance gene pfmdr1 in Plasmodium falciparum
A;Reference number: S18204; PMID:92017800; PMID:1922044
A;Accession: S18204
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-1419 <TRI>
A;Cross-references: EMBL:X56851; NID:G9935; PIDN:CAA04180.1; PID:G9936
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1990
R;Foote, S.J.; Thompson, J.K.; Cowman, A.F.; Kemp, D.J.
Cell 57, 921-930, 1989
A;Title: Amplification of the multidrug resistance gene in some chloroquine-resistant is
A;Reference number: A32547; PMID:89286297; PMID:2701941
A;Accession: A32547
A;Molecule type: mRNA
A;Residues: 1-1419 <FOO>
A;Cross-references: GB:M29154; GB:M24322; NID:G160398; PIDN:AAA29646.1; PID:G160399
C;Superfamily: multidrug resistance protein; ATP-binding cassette homology
C;Keywords: ATP; duplication; glycoprotein; nucleotide binding; P-loop; transmembrane
P;1-632,655-1276/Region: duplication
F;396-638/Domain: ATP-binding cassette homology <ABC1>
F;413-420/Region: nucleotide-binding motif A (P-loop)
F;583-587/Region: nucleotide-binding motif B
F;1144-1387/Domain: ATP-binding cassette homology <ABC2>
F;1161-1168/Region: nucleotide-binding motif A (P-loop)
F;1332-1336/Region: nucleotide-binding motif B

Query Match      7.0%; Score 87; DB 1; Length 1419;
Best Local Similarity 21.8%; Pred.No. 67;
Matches 65; Conservative 37; Mismatches 112; Indels 84; Gaps 15;
Qy      3 KSEIINEKD-----LRKSELQGTALGNLXQI-----YYYN--EKAT 38
Db      955 KSKIEIKKENNMSGVFAPSSDENMFKDPSFIQIAFTNMTVINYGLIEDYFCNLIEKAD 1014
Qy      39 -ENKESDDQFLENTLLPKGFPTGHP-----WYNDLLVDLGS-----KDA-----T 77
Db      1015 YKNGQKRRIIIVNAALW-GFQSQAQLFINSPAYWFGSLIKRGITILVDDEMKSLFTFT 1073
Qy      78 NKYKGGKVDLYG-----AYYQCA-----GGTPNKTCACMYGGVTLHP--NN 117
Db      1074 GSYAGKMLSLGSDSENAKLSPEKYPIMLIRKSNIDVRDDGIRINKNLIRKGVDIKDNWF 1133
Qy      118 RLTEKKVPI---NLMTDGGQTTVPIDKVKTSK---EVTQVELDLQASHYL-----HGK 166
Db      1134 RYISRPNVPIYKNLSFTCDSKTTAIYGETSGSKSTFWNLLRFPYDLKNDHILKNDWTN 1193
Qy      167 FGLYNSDSFGKVGORGLIVFHSSEGSTVSYDLFDAQGGVDPDTLLRIYRDNKTINSENL 224
Db      1194 FQDYQNNNNSLVLKNNNEFNGSGSAEDYTVFNNGE-----ILLDDINI DYNL 1244

```

RESULT 48
AFI489
cell wall-associated protein precursor wapa (B. subtilis) homolog lin0454 [imported] - Lj
C/Species: Listeria innocua
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C/Accession: AFI489
E/Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dissurget, O.; Entian, K.D.; Psihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schluter, T.; Simoes, N.; Tierres, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlant,
A./Title: Comparative genomics of Listeria species.
A/Reference number: AB1077; MUID:21537279; PMID:11679669
A/Accession: AFI489
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-2167 <GLA>
A/Cross-references: GB:AU92022; PIDN:CAC95686.1; PID:g16412895; GSPDB:GN00178
A/Experimental source: strain Clip11262
C/Genetics:
A/Gene: lin0454

Query Match 7.0%; Score 87; DB 2; Length 2167;
Best Local Similarity 24.0%; Pred. No. 1.1e+02;
Matches 56; Conservative 27; Mismatches 86; Indels 64; Gaps 14;

Qy 30 YYYNEKAITENKESDDQPLENTLIFKGFTGHP--WYNDL----LYDLGSKDATNKY-KG 82
| | | : | : | : | : | : | : | : | : | : | : | :
Db 1671 YYXDKPKDNKNKGTKVGE-VAINHGDTAKTSYTYNLDNRTRVNDSKNAYFEDEF 1729
| | | : | : | : | : | : | : | : | : | : | : | :

Qy 83 KKVDLY-----GAPYGQCAGGTNPKTACMYGGVTLLHDNNRLTE--EKKVPLINLMIDGX 134
| | | : | : | : | : | : | : | : | : | : | : | :
Db 1730 GNINVYTAGNGTAANYTSDTKVTNAALISSASGQTILDENVTYDAASNRTSIDNQDGK 1789
| | | : | : | : | : | : | : | : | : | : | : | :

Qy 135 QTTVPIDKKVKTSKEVTVQEILDLQRHYHLHGFELNSDFSGKVORGLIVFHSSEGSTV 194
| | | : | : | : | : | : | : | : | : | : | : | :
Db 1790 --TTYEDAVNLTKR-TLPD-----GVFKATYTDGFGNRTQ---VAISGETKI 1834
| | | : | : | : | : | : | : | : | : | : | : | :

Qy 195 --SYD-----LFDAQGYPTDLLRIYRDKNKTINGENLHIALVLYT 232
| | | : | : | : | : | : | : | : | : | : | : | :
Db 1835 DASINDGNQLVSNGEALTYPDANG-----NRTSDGK-----ITYT 1869
| | | : | : | : | : | : | : | : | : | : | : | :

RESULT 49
DB6342
hypothetical protein F9HI6.6 - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 15-Sep-2003
C/Accession: DB6342
R/Theologis, A.; Eckert, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A/Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, B.; Kim, C.S.C.
C.A.; Li, J.H.; Ly, X.; Lin, X.; Liu, Z.A.; Luo, J.S.; Maiti, R.; Marziali,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A/Authors: Salberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, I.
ker, M.; Wu, D.; Yu, G.; Fraser, C.N.; Venter, J.C.; Davis, R.W.
A/Title: Sequence and analysis of chromosome 1 of the plant Arabidopsi.s.
A/Reference number: AS6141; MUID:21016719; PMID:11130712
A/Accession: DB6342
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-614 <STO>
A/Cross-references: GB:AE005172; NID:g4836893; PIDN:AAD30596.1; GSPDB:GN00141
C/Genetics:
A/Map position: 1
C/Superfamily: pyrophosphate-dependent phosphofructokinase, PfkB type; 6-phosphofructoki

Query Match 7.0%; Score 86.5; DB 2; Length 614;


```
Db 390 -----KRSSIIIFINK--STNKKDLIKLQNE-----NIKNANLINIKINCL 428
QY 231 YT 232
Db 429 YT 430

RESULT 53
AG1749
Glycosidase homolog lin2540 [imported] - Listeria innocua (strain Clip11262)
C:Species: Listeria innocua
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
C:Accession: AG1749
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AG1749
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1090 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC97767.1; PID:gl6415062; GSPDB:GN00178
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin2540

Query Match 6.9%; Score 86; DB 2; Length 1090;
Best Local Similarity 22.5%; Pred. No. 58;
Matches 47; Conservative 35; Mismatches 61; Indels 66; Gaps 14;

QY 33 NEKAITENKESDDOFLNTLLFKGFF---TGHP-----WY-NDLLVLDLGSKDATNKY 80
Db 491 DDNTVYGEORNDY----MSQGSADDTGAGYRVPASQWFGNLLDFTNKDAVNW 546
QY 81 KGKK-----VDLYGAYYQCAGGTPNKATACMYGGVTLHDNNRLTEKKVPINLWID 132
Db 547 TSQREYLLTDVIGID-----GFKTDGG-----EMVWGREDTTFSGEKGQEMR----- 587
QY 133 GKQTVPIDKVKY---SKKEVTVELDLOARHYLHG--KFGLYNS-----DSFGSKYQ 180
Db 588 ---NRYPTDYSSVDFPAKSNPEAVSF--SRSGTGAQKSGIYWSGQDTTFDSFQASVK 643
QY 181 RGLIVFHSSEGSTVSY---DLFDAQGOVP 206
Db 644 AGL-----SASTSGVSYAWMDAGFTGNYP 668

RESULT 54
G86903
cell shape determining protein [imported] - Lactococcus lactis subsp. lactis (strain IL1
C:Species: Lactococcus lactis subsp. lactis
C>Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: G86903
R:Boilotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrli
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: G86903
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-291 <STO>
A:Cross-references: GB:AE005176; PID:gl2725299; PIDN:AAK06329.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: mreC

Query Match 6.9%; Score 85.5; DB 2; Length 291;
Best Local Similarity 20.0%; Pred. No. 12;
Matches 46; Conservative 26; Mismatches 67; Indels 91; Gaps 8;
```

```
QY 23 LGNLKQIYYNEKAIT-----ENK-----ESDDOFLNTLLFKGFFTGH----- 61
Db 69 LSNLMDTYQQOQSLKTQLAKSKDDDDNKLSEBENKELKALKLOETLTDYQTVAAANVIT 128
QY 62 ----PWNDLLVDLGSKDATNKYGGKVDLYGAYYQCAGGTPNKATACMYGGVTLHDNN 117
Db 129 REPSSWNDTLVIDSGKD-----GLTGMVWANGGV-----G 162
QY 118 RLTFE-----EKKVPINLWIDGKQTVPIDKVKTSKKEVTVOELDLQAR 160
Db 163 RVTQVKNKSKVALLSSSGKIDNKIPRIESDQSPYIGILSSYDSQOEAYVVKNIDSQ-- 220
QY 161 HYLHGRFGLYNSDFGKQVQKGLIVFHSSEGSVSYVDLFDAGQYDPDILL 210
Db 221 -----GKFKNGDSVFTSLGINS-----SQGTSPSGLL 249

RESULT 55
AH1793
ABC transporter, ATP-binding protein homolog lin2894 [imported] - Listeria innocua (strai
C:Species: Listeria innocua
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001
C:Accession: AH1793
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AH1793
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-573 <GLA>
A:Cross-references: GB:AL592022; PIDN:CAC98120.1; PID:gl6415429; GSPDB:GN00178
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin2894
C:Superfamily: Escherichia coli ABC transporter mdla; ATP-binding cassette homology

Query Match 6.9%; Score 85.5; DB 2; Length 573;
Best Local Similarity 23.8%; Pred. No. 29;
Matches 46; Conservative 29; Mismatches 81; Indels 37; Gaps 8;

QY 22 ALGNLKKQI--YYNEKAITENKESDDOFLNTLLFKGF---FTGH--PWYNDLLVD----- 70
Db 298 ALISLARITEVLETPDIYENAPEQDLGIEFRNVSFKYDGDTPALEDISFKANVG 357
QY 71 --LGSKDATNKYGGKVDLYGAYYQCAGGTPNKATACMYGGVTLHDNNRLTEKKVPIN 128
Db 358 EMVGIVGATGSGKSTLAQLIPLY-----DPTGEVIGTGTLNKDINKKTLRSTVSFV 410
QY 129 LMTDQKQTVPIDKVKTSKKEVTVOELD-----LQARHYLHGRFGLYNS-----DSFG 177
Db 411 LQRAILFSTIADNRHGHKKQATIDEMEHASKIAQKSFIDKQAKLYEAFVSERGNFSG 470
QY 178 -----KVQRGLT 184
Db 471 GQKQRLSITRGVI 483

RESULT 56
C89888
hypothetical protein SA1011 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: C89888
R:Kuroda, M.; Ohca, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; I
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
```

A;Title: Whole genome sequencing of metacillin-resistant *Staphylococcus aureus*.
A;Reference number: A89758; MUID:21311952; PMID:11418146
A;Accession: C89888
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-241 <KUR>
A;Cross-references: PID:G13700967; PIDN:BA842263.1; GSPDB:GN00149
A;Experimental source: strain N315
C;Genetics:
A;Gene: SA1011
C;Superfamily: toxic shock syndrome toxin

Query Match 6.9%; Score 85; DB 2; Length 241;
Best Local Similarity 23.9%; Pred. No. 11;
Matches 44; Conservative 31; Mismatches 63; Indels 46; Gaps 10;
QY 63 WYNDLLVGLSKD--ATNKYKGGKVDLYG-----AYYGQ---CAGGTNKTACMYG 109
Db 84 WSHIQV-FGSESWGNINQLRNKYVDIFGTKDIEDTVEGYWTYDETFTGGVTPAAT----- 137
QY 110 GVTLHDNNRLTEKKVPINLWIDGKQTV--PIDKVKTSKEVTVQELDLQARHYLHGKF 167
Db 138 -----SSDKPYRLFLKYSKQQTIGGHEFYKGNKPVLTILKELDFRIQRLINK 187
QY 168 GLYNSDFGKVGQRGJLVFHSSEGSTVSVDLPDAQOQYDPTLLRIYRDKNTI--NSENLI 226
Db 188 KLTN-----GEFNKGQIKI--TAGNNYITDL-----SKKLKLTDTNRYVKNPNAQI 233
QY 227 ALYL 230
Db 234 EVIL 237

RESULT 57

T10102
diphosphate-fructose-6-phosphate 1-phosphotransferase (EC 2.7.1.90) alpha chain - castor
N;Alternate names: 6-phosphofructokinase (pyrophosphate)
C;Species: Ricinus communis (castor bean)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 15-Sep-2003
C;Accession: T10102
R;Todd, J.F.; Blakeley, S.D.; Dennis, D.T.
Gene 152, 181-186, 1995
A;Title: Structure of the genes encoding the alpha- and beta-subunits of castor pyrophosphatase
A;Reference number: Z16949; MUID:95137384; PMID:7835697
A;Accession: T10102
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-617 <TOD>
A;Cross-references: EMBL:Z32849; NID:G483546; PIDN:CAA83682.1; PID:G483547
C;Genetics:
A;Supernotes: 30/3; 88/2; 126/1; 151/1; 189/1; 211/3; 239/3; 257/3; 284/3; 316/1; 340/3; 371/1
C;Superfamily: pyrophosphate-dependent phosphofructokinase, PfFB type; 6-phosphofructokinase
C;Keywords: phosphotransferase

Query Match 6.9%; Score 85; DB 2; Length 617;
Best Local Similarity 30.2%; Pred. No. 35;
Matches 26; Conservative 9; Mismatches 35; Indels 16; Gaps 3;

QY 74 KDATNKYKGGKVDLYGAYGYQCAGGTNKTACMYGGVT-----LHDNNRLTEE 122
Db 412 KEGT--YKGGKFNACHFFGQARGSLPSKFDYAYVLGHICYHVLAAGLNGYMATATN 469
QY 123 KQVPINLWIDGKQTVPIDKVKTSKK 148
Db 470 LKPNVKNKRCG---AAPIAAMTVKR 492

RESULT 58

G71615
phospholipase A2-like a/b fold hydrolase PF0410c - malaria parasite (*Plasmodium falciparum*)
C;Species: *Plasmodium falciparum*
C;Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C;Accession: G71615

R;Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.;
Science 282, 1126-1132, 1998
A;Title: Chromosome 2 sequence of the human malaria parasite *Plasmodium falciparum*.
A;Reference number: A71600; MUID:99021743; PMID:9804551
A;Accession: G71615
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-679 <GAR>
A;Cross-references: GB:AE001393; GB:AE001362; NID:G3845175; PIDN:AA71871.1; PID:G384517;
A;Experimental source: clone 3D7
C;Genetics:
A;Gene: PF0410c

Query Match 6.9%; Score 85; DB 2; Length 679;
Best Local Similarity 19.3%; Pred. No. 39;
Matches 50; Conservative 35; Mismatches 112; Indels 62; Gaps 7;

QY 3 KSEINEKDLRKSELOQTALGNLKQIYYNEXAITENKESDDQFLENTLLFKGFTGHP 62
Db 185 KNEETSNYNLNNEINKICKYNLQDTLLDSDNSERRNSKEKIKNTNYDNLQNK 244
QY 63 WYNDLLV-DLGSKDATNKY-----KQKVDLYGAYGYQCAGGTNKTAC 106
Db 245 YTNISILYDDDDKNNTEYTCFTKEDQIRVPSQKKYIYLNKY-----DNATL- 294
QY 107 MYGVTLHDNNRLTEKKVPINLWIDGKQTVPIDKVKTSKEVTVQELD-----L 157
Db 295 ---DLNVHTYNSLQMSILCKYLLYCKYNNHPRDPTFFKPKVPSILSDGGILITSL 351
QY 158 QARHYLHGK-----FGLYNSDSFGKVGQRLIVFHSSEGSTVSVDLPDAQ 202
Db 352 LVLNLEALRKEIGSDDIKLIDCFDMVCGTSAGLISALL-----REIDLQDVS 402
QY 203 GQYDPTLLRIYRDKNTINS 221
Db 403 NMWPTTIKKVFEGRNRIIS 421

RESULT 59

T30545
major surface glycoprotein - *Pneumocystis carinii* (fragment)
C;Species: *Pneumocystis carinii*
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 15-Jun-2001
C;Accession: T30545
R;Mei, Q.; Turner, R.E.; Sorial, V.; Klivington, D.; Angus, C.W.; Kovacs, J.A.
Infect. Immun. 66, 4268-4273, 1998
A;Title: Characterization of major surface glycoprotein genes of human *Pneumocystis carinii*
A;Reference number: Z17905; MUID:98380374; PMID:9712777
A;Accession: T30545
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-1014 <MEI>
A;Cross-references: EMBL:AF038556; NID:G3560524; PID:G3560525; PIDN:AA34980.1
A;Experimental source: f.sp. hominis
C;Genetics:
A;Gene: msg1
C;Superfamily: *Pneumocystis carinii* major surface glycoprotein MSG100

Query Match 6.9%; Score 85; DB 2; Length 1014;
Best Local Similarity 26.3%; Pred. No. 64;
Matches 45; Conservative 27; Mismatches 63; Indels 36; Gaps 9;

QY 2 EKSEINE---KDLRKSELOQTALGNLKQIYYN-----EKAITENKESDDQFLENT 51
Db 328 EKCKKILEDKCKLKEHDIING-----LCEDYNANKDKKKCELSSTDIETCKFFISKT 382
QY 52 LLFKGFTGH-----PWYNDLLVGLGSKDATNKYKGGKVDLYGAYGYQCAGGTNPK-- 103
Db 383 LMIHFGGNGKNDGIIKAGN-LSTFLSNKDKT-----KLESYCLYFEKSCRSSETACKNI 435
QY 104 -TACMYGQVTLHDNNRLTEKKVPIN-----LWIDGKQTVPIDKVKTSKKE 149

Db 436 RAACYKRGDLTLANEVLQKEMRGLHGSNKTWLSGFQKKL-IEVCKVKYKE 485

RESULT 60

T31076

tyrocidine synthetase 3 - Brevibacillus brevis

C:Species: Brevibacillus brevis

C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 01-Dec-2000

C:Accession: T31076

R:Mootz, H.D.; Marahiel, M.A.

J. Bacteriol. 179, 6843-6850, 1997

A:Title: The tyrocidine biosynthesis operon of Bacillus brevis: Complete nucleotide sequence

A:Reference number: 220969; MUID:98012987; PMID:9352938

A:Accession: T31076

A:Status: preliminary

A:Superfamily: translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-6486 <MOO>

A:Cross-references: EMBL:AF004835; NID:G2623770; PID:G2623773; PIDN:AA045930.1

C:Genetics:

A:Gene: tycC

C:Function:

A:Pathway: tyrocidine biosynthesis

C:Superfamily: acyl carrier protein homology; acetate-CoA ligase homology

C:Keywords: carrier protein; phosphopantetheine; phosphoprotein

F:510-950/Domain: acetate-CoA ligase homology <ACLI>

F:1546-1987/Domain: acyl carrier protein homology <ACP1>

F:1546-1987/Domain: acetate-CoA ligase homology <ACLI>

F:2005-2073/Domain: acyl carrier protein homology <ACP2>

F:2583-3025/Domain: acetate-CoA ligase homology <ACP2>

F:3043-3111/Domain: acyl carrier protein homology <ACLI>

F:3043-3111/Domain: acyl carrier protein homology <ACP3>

F:3621-4060/Domain: acetate-CoA ligase homology <ACP3>

F:4078-4146/Domain: acyl carrier protein homology <ACP4>

F:4636-5104/Domain: acetate-CoA ligase homology <ACP4>

F:5122-5190/Domain: acyl carrier protein homology <ACLI>

F:5122-5190/Domain: acyl carrier protein homology <ACP5>

F:5702-6147/Domain: acetate-CoA ligase homology <ACP6>

F:6165-6233/Domain: acyl carrier protein homology <ACP6>

F:1000, 2037, 3075, 4110, 5154, 6197/Binding site: phosphopantetheine (Ser) (covalent) #statu

Query Match 6.9%; Score 85; DB 2; Length 6486;

Best Local Similarity 20.5%; Pred. No. 6.6e+02;

Matches 50; Conservative 42; Mismatches 76; Indels 76; Gaps 12;

Qy 16 SELOQTALGNLKOIY-----YYNEKAITENKESDDQFLENTLLFKGFTGH--PWY 64

Db 789 ASMQPVPVGSIGEMVIAGDGVAKYFNPELTKFKFDINPRPCTKYR---TGLAKWL 845

Qy 65 NDILVD-LGSKDANKYKGVKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEK 123

Db 846 PDGMEVAGRDYQVKIRHRIEM-----GBI-----ETRLTQHE 880

Qy 124 KVPINLWIDGKQTTVPIDKVKT-----SKKEVTVOELDLQARHYLHGKFLYNSD 173

Db 881 AV-----KEAVVIVEKDESGQNVLYALVSRERLVAEL-----REFLGRLLPSYMP 928

Qy 174 SF-----GKQVORGLIVFHSSEGSTVSYDLPDA-CQQPPTLLRTYRDNKTINS 221

Db 929 SFFIRLAPILTANGKVERKLL--PKPAGAVTGTAVAPQNEIAKLAEIWOQVLGISQ 986

Qy 222 ENLH 225

Db 987 VGIH 990

RESULT 61

AF1418

ABC transporter, ATP-binding protein homolog lmc2751 [imported] - Listeria monocytogenes

C:Species: Listeria monocytogenes

C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-2001

C:Accession: AF1418

R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; Jones, L.M.; Karsst, U.

Science 294, 849-852, 2001

A:Authors: Krefth, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat ok, C.; Schluter, T.; Simoes, N.; Tietz, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AF1418

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-573 <GLA>

A:Cross-references: GB:NC_003210; PIDN:CAD00964.1; PID:gl6412251; GSPDB:GN00177

A:Experimental source: strain EGD-e

C:Genetics:

A:Gene: lmc2751

C:Superfamily: Escherichia coli ABC transporter mlaA; ATP-binding cassette homology

Query Match 6.8%; Score 84.5; DB 2; Length 573;

Best Local Similarity 23.8%; Pred. No. 35;

Matches 46; Conservative 29; Mismatches 81; Indels 37; Gaps 8;

Qy 22 ALGNLKOI--YYNEKAITENKESDDQFLENTLLFKGF--FTGH--PWYNDLLVD---- 70

Db 298 ALISLKRITVLETPDITYNENAPQDLEGTVEFRNVSKYDGDTPALEDISFKASVG 357

Qy 71 --LGSKDANKYKGVKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKVPI 128

Db 358 EMGIVGATGSGKSTLAQLIPRLY-----DPTGEVIIGTGNLKDINKTLRSTVSV 410

Qy 129 LWIDGKQTTVPIDKVKTSKEVTVOELD-----LQARHYLHGKFLYNS-----DSFG 177

Db 411 LQRAILFSGTIADNLRHGKDATAEEMHASKIAQAKFIDKQAKLYEAPVSEGRNFGS 470

Qy 178 -----KVORGLI 184

Db 471 GQKQLSITRGVI 483

RESULT 62

S36523

E1 protein - human papillomavirus type 35H

C:Species: human papillomavirus type 35H

C:Date: 09-Dec-1993 #sequence_revision 26-Jul-1996 #text_change 26-Aug-1999

C:Accession: S36523

R:Delius, H.; Hofmann, B.

Submitted to the EMBL Data Library, August 1993

A:Description: Primer-directed sequencing of human papillomavirus types.

A:Reference number: S36469

A:Accession: S36523

A:Molecule type: DNA

A:Residues: 1-637

A:Cross-references: EMBL:X74477; NID:g396997; PIDN:CAA52563.1; PID:g397000

A:Experimental source: strain 35H

C:Superfamily: papillomavirus E1 protein

C:Keywords: early protein; nucleus

Query Match 6.8%; Score 84.5; DB 2; Length 637;

Best Local Similarity 20.9%; Pred. No. 40;

Matches 53; Conservative 41; Mismatches 91; Indels 69; Gaps 11;

Qy 21 TALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGHFWYNDLLVDLGSKQATNKY 80

Db 310 TAMSNISEV-----DGETPEWIRQTVLQHSF-----NDALFDL-SEMVQWAY 351

Qy 81 KKKVDLYGAYGYQCAGGTPNKTACMY-----GGVTLHDNNRLTEKKVPI 129

Db 352 DNDFFDSDIAKYQALET--NSNACAFKLSQAKIVKDCATCMCHYKAEKREMTMSQ 410

Qy 130 WIDGKQTTVPID-KVTSKEVTVOELDLQA-----RHYLHGK-----FGLYNSDSF 175

Db 411 WIKRCEKVDGDDWRDIVRFLRYQQVDFVAFLSALKNELHGVKPKNCILLYGAPNT--- 467

Qy 176 GKQVQGLIVFHSSEGSTVSY-----DLFDAQ-----GQVPTLLIRYR 214

Db 468 -GKSLFGLMFLQALITVYNSKSHFWLQPLQYDAKIAMLDDATSPCWAYIDQYLRLAL 526

QY 215 DNKTINSENHIAL 228
Db 527 DGNPISLDVKKHAL 540

RESULT 63

A97334
type II restriction enzyme, methylase chain [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
C:Accession: A97334
R:Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clostridium acetobutylicum
A:Reference number: A96900; MUID:21359325; PMID:21359325

A:Accession: A97334

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-993 <KUR>

A:Cross-references: GB:AE001437; PIDN:AAK81460.1; PID:G15026629; GSPDB:GN00168

A:Experimental source: Clostridium acetobutylicum ATCC824

C:Genetics:

A:Gene: CAC3535

Query Match 6.8%; Score 84.5; DB 2; Length 993;

Best Local Similarity 22.9%; Pred. No. 69;

Matches 47; Conservative 33; Mismatches 62; Indels 63; Gaps 11;

QY 14 KXSELOGTALGNLKOYYNEKAITENKESDDQFLENTLLFKGFTTGHFWYNDLVDLGS 73

Db 663 KRKVESVVLGNLW-----ALVANK--DD-----MSLVK 690

QY 74 KQATNRYK-GKKYDLYGAYGYQCAGGTENKTAACMYGGVTLHDNNRLTEKKVP-INLWID 132

Db 691 KMYRNSVXMGKEVELN--GIOTSAERP-----PIYFSDKEILESELYFKIKKK 739

QY 133 GKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGELNSDFGKGQVGLVIF-HSSEG 191

Db 740 DKQYIIIEKNILKKYFVLUKKEKNL-----GSYDIFDTNRP-----IIFPINHEG 784

QY 192 STVSYDLFDAQGGQYPTLLRIYRDN 216

Db 785 KL--VDLNTMETEYPNT-LRYLMDN 806

RESULT 64

T07067
beta-fructofuranosidase (EC 3.2.1.26) LIN5 - tomato (fragment)
N:Alternate names: invertase
C:Species: Lycopersicon esculentum (tomato)
C:Date: 30-Apr-1999 #sequence_revision 30-Apr-1999 #text_change 21-Jul-2000
C:Accession: T07067
R:Godt, D.E.; Roitsch, P.
Plant Physiol. 115, 273-282, 1997
A:Title: Regulation and tissue-specific distribution of mRNAs for three extracellular in
A:Reference number: Z15997; MUID:97451780; PMID:9306701

A:Accession: T07067

A>Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-241 <OOD>

A:Cross-references: EMBL:X91389; NID:g1771149; PIDN:CAA62734.1; PID:g1771150

A:Experimental source: cultivar MoneyMaker; leaf

C:Genetics:

A:Gene: LIN5

C:Superfamily: beta-fructofuranosidase

C:Keywords: cell wall; glycosidase; hydrolase

Query Match 6.8%; Score 84; DB 2; Length 241;

Best Local Similarity 21.2%; Pred. No. 13;

Matches 55; Conservative 28; Mismatches 76; Indels 100; Gaps 13;

QY 26 LKQIYYNEKAITENKESDDQFLENTLLFKGFTTGHFWYNDLVDLGSKDAIN----- 78

Db 1 LHLFYQYNPK-----GSWGNIIWAHSVSKDLINWIHLEPA 36

QY 79 KYGKKVDLYGAYGYQCAGGT-NKTAACMYGGVTLHDNNRLTEKKVPINL-----W 130

Db 37 IYFSKKFDKYGTSWGSSTI--LPNNKPVIIYGVDSYNNQV-QNYAIPANLSDPFLRKW 93

QY 131 I--DGKQTTVPIDKV-KTSKKEVTVOELD-----L 157

Db 94 IKPNNNPLIVPDSINSINRTEPRDPTTAMWGQGLWRILIASMRKHGWMALLYRSRDFMKWI 153

QY 158 QASHYHLHGKFLYN--SDSFGKVGQSGIVFHSSEGSTVSVDLFDACQGYPTDLLRIYR 214

Db 154 KAQHPLHSSNTNGWECDFPF-----VLFNSTNGLDVSY-----RG-----K 191

QY 215 DNKTINSENHIALYLYTT 233

Db 192 NVKYLKNSLDVARFDYTT 210

RESULT 65

A99582
hypothetical protein MYPV 5610 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 03-Aug-2001
C:Accession: A99582
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galisson, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A99512; MUID:21267165; PMID:11353084

A:Accession: A99582

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-333 <KUR>

A:Cross-references: GB:AL445566; PID:g14089976; PIDN:CAC13734.1; GSPDB:GN00153

A:Experimental source: strain UAB CTIP

C:Genetics:

A:Gene: MYPV 5610

A:Genetic code: SGC3

C:Superfamily: DNA-directed RNA polymerase alpha chain

Query Match 6.8%; Score 84; DB 2; Length 333;

Best Local Similarity 23.5%; Pred. No. 19;

Matches 38; Conservative 24; Mismatches 38; Indels 62; Gaps 9;

QY 25 NLKOIY-YNKEAITENK-----BDDQFLENTLLFKGFTTGHFWYNDLLV 69

Db 82 NVKNHVLVDYDENIFEDNKIYRGVIETKNEKITSSDLKFPENP-----EI 125

QY 70 DLGSKD---ATNKYKGGKVDLYGAY---GYCAGGTPTNKTAACMYGGVTLHDNNRLTEE 122

Db 126 EIVNKDLLEIATN--NGOKPFWEVYFHVGRGY-----ISFENKKLIEE 167

QY 123 KKVPINLWID-GKQTTV-----PIDKVTSKKEVTVOELDLQ 158

Db 168 KVALLNSTIKRGKFLAIDSFSPVERKVKVQVEINSSSLNIE 209

RESULT 66

T41863
chitinase chi-A orf126 - Bombyx mori nuclear polyhedrosis virus (isolate T3)
C:Species: Bombyx mori nuclear polyhedrosis virus, BmSNPV
A:Variety: isolate T3
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jul-2000
C:Accession: T41863
R:Gomi, S.; Majima, K.; Maeda, S.
J. Gen. Virol. 80, 1323-1337, 1999
A:Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
A:Reference number: Z22020; MUID:99281911; PMID:10355780
A:Accession: T41863
A>Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-552 <KAM>

A;Cross-references: EMBL:L33180; NID:g3745835; PIDN:AA063792.1; PID:g3745945
A;Experimental source: isolate T3
C;Superfamily: Serratia marcescens chitinase

Query Match 6.8%; Score 84; DB 2; Length 552;
Best Local Similarity 24.3%; Pred. No. 36;
Matches 45; Conservative 23; Mismatches 69; Indels 48; Gaps 11;

QY 32 YNEKAI---TENKESDDOFLNTLLFKGFFTGHPWYNLLVLDGSKDQATNKYKGGKVDLY 88
DB 359 YDKIAVNYAQAQSLDKILFMTYDFKG-----AWSN---TDLGVQITTVAPSNSEELY 410
QY 89 GAYGYQC---AGGPNKT---ACMYG---GVTLHDN-NRLTEKKVPIN-LWIDKQOT 136
DB 411 TTHYAVDALLEGQVDPNKIIIVGVAMYGRTGVTNTNGNYFSGTGNGPVSQWEDG--- 467
QY 137 TVPIDKVTSKKEVTVQSLDLQARHYLHGKGLYNSDSFGKGVORGLIVFHSSEGSTVSY 196
DB 468 -----VVDYROIQDLNNY-----VITFDS-----AAQASVVPKSKGDLISF 505
QY 197 DLFDA 201
DB 506 DSVD 510

RESULT 67
S01312
alpha-amylase (EC 3.2.1.1) B - Dictyoglomus thermophilum
C;Species: Dictyoglomus thermophilum
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 22-Jun-1999
C;Accession: S01312
R;Horiouchi, S.; Fukusumi, S.; Ohshima, T.; Beppu, T.
R; J. Biochem. 176, 243-253, 1988
A;Title: Cloning and expression in Escherichia coli of two additional amylase genes of a
unaine-plus-cytosine contents.
A;Reference number: S01312; MUID:88329076; PMID:2458257
A;Accession: S01312
A;Molecule type: DNA
A;Residues: 1-562 <HOR>
A;Cross-references: EMBL:X13199; NID:g2690; PIDN:CA331586.1; PID:g2691
A;Note: the sequence from Fig. 9 is inconsistent with that from Fig. 2 in having 479-ile
A;Note: part of this sequence, including the amino end of the mature protein, was confir
C;Genetics:
C;Gene: amyB
C;Function:
A;Description: catalyzes the hydrolysis of internal 1,4-alpha-D-glucosidic bonds
A;Pathway: glycogen/starch degradation
C;Superfamily: neopullulanase; alpha-amylase core homology
C;Keywords: glycosidase; hydrolase; polysaccharide degradation
P:276-407/Domain: alpha-amylase core homology <AMY>

Query Match 6.8%; Score 84; DB 2; Length 562;
Best Local Similarity 23.0%; Pred. No. 37;
Matches 60; Conservative 31; Mismatches 94; Indels 76; Gaps 15;

QY 25 NLKQIVYNEKA-----ITENKESDDOFL---ENTL---LPK---GFFTGHPWN 65
DB 317 NFWSPFYNLKSEFPETFFGIVETPKTKYVKGFGDGLDFYLFKIRDFPGKRWST 376
QY 66 D---LVLVDGSKDATNKY-----KGGKVDLYGAYGYQCAGGTPNKT 104
DB 377 KBFVXKMDLEKPYGNKFKRISFLENHDSNRLFWAKOKKLLRLASIFQSI-----NAI 431
QY 105 ACMYGGV-----TLHDNRLTEKKVPINLWIDKQITVPID---KVKTSKKEVT 151
DB 432 PIYINGQMGCSQYRDILEGNTLTHHARLPID-NSDDKQDKELIDFVQLVKIRKHPA 490
QY 152 VOELDLQARHYLHGKGLYNSD--SFGGKVQ-RGLIVFHSSEGSTVSYDLFDAQOQYPT 208
DB 491 LYK-----GTFPIFSDWISFIKETQESILVLINIEDKE---EIFNLNGTYRDL 537
QY 209 LL-RIYRDNKTINSENHLAL 228

Db 538 FSGNIYTNLSKLGPMASHLL 558

RESULT 68

A40457
replication protein A1 - human
N;Alternate names: replication protein A 70K chain
C;Species: Homo sapiens (man)
C;Date: 28-Feb-1992 #sequence_revision 27-Oct-1995 #text_change 07-May-1999
C;Accession: A40457; A44501
R;Erdile, L.F.; Heyer, W.D.; Kolodner, R.; Kelly, T.J.
J. Biol. Chem. 266, 12090-12098, 1991
A;Title: Characterization of a cDNA encoding the 70-kDa single-stranded DNA-binding subur
A;Reference number: A40457; MUID:91268092; PMID:2050703
A;Accession: A40457
A;Molecule type: mRNA
A;Residues: 1-216, A', 218-616 <ERD>
A;Cross-references: GB:M63488
A;Note: parts of the sequence determined by protein sequencing
A;Note: this sequence has been corrected in reference A44501
R;Erdile, L.F.; Heyer, W.D.; Kolodner, R.; Kelly, T.J.
J. Biol. Chem. 268, 2268, 1993
A;Title: Characterization of a cDNA encoding the 70-kDa single-stranded DNA-binding subur
A;Reference number: A44501; MUID:93131993; PMID:8420996
A;Accession: A44501
A;Molecule type: mRNA
A;Residues: 217 <ER2>
A;Cross-references: GB:M63488
A;Note: sequence correction
C;Genetics:
A;Gene: GDB:RPA1
A;Cross-references: GDB:138362; OMIM:179835
A;Map position: 17p13.3-17p13.3
C;Complex: Replication protein A is a trimer of 70K (A1), 32K (A2), and 14K (A3) chains.
C;Function:
A;Description: probable eukaryotic equivalent of prokaryotic single-stranded DNA-binding
probably also has a role in the elongation stage of DNA replication
A;Pathway: DNA replication initiation
A;Note: the single-stranded DNA-binding activity resides in the A1 protein
C;Superfamily: replication protein A1
C;Keywords: DNA replication initiation; single-stranded DNA binding; trimer; zinc finger
P:481-503/Region: zinc finger CCCC motif

Query Match 6.8%; Score 84; DB 1; Length 616;
Best Local Similarity 26.5%; Pred. No. 42;
Matches 59; Conservative 28; Mismatches 66; Indels 70; Gaps 15;

QY 6 EINE-----KDLRKSELOQTALGNLQIYYINEKAITENKESDDOFLNTLLFKGFFTG 60
DB 250 EVNKVYFSGTGLKIANQKFTAVKNDYEMTFNNTSYMPCE--DDHLP-TVQFD--FTG 304
QY 61 HPWVNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACWYGGVTLHDNRLT 120
DB 305 -----ID-----DLENKSKDSLVDLIGICKSYEDA-----TKITVRSNNREV 341
QY 121 EEKVPINLWIDKQITVPID---DKVTSKKEVTVQELDLQARHYLHGKGLYNSDSF 175
DB 342 AKRNIYL-MDTSGKVVTATLWGEDADKFDGSRQPVLAIK-----GARVSD-F 386
QY 176 GKKVQVGLIVFHSSEGSTV-----SYDL---FDAQOQYPD 207
DB 387 GG---RSLSVLS---STIIANPDIPAYKLRGFWDAEGQALD 423

RESULT 69

B44858
lactocepin (EC 3.4.21.96) precursor [validated] - Lactobacillus paracasei (strain NCDO 11
N;Alternate names: cell-envelope-associated proteinase prtP; serine proteinase Lp151
C;Species: Lactobacillus paracasei
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 19-May-2000
C;Accession: B44858; A44850
R;Holck, A.; Naes, H.
J. Gen. Microbiol. 138, 1353-1364, 1992

A:Title: Cloning, sequencing and expression of the gene encoding the cell-envelope-associated protein
A:Reference number: A44858; MUID:92381481; PMID:1512565
A:Accession: B44858
A:Molecule type: DNA
A:Residues: 1-1902 <HOL1>
A:Cross-references: GB:M83946; NID:G149580; PID:AAA25248.1; PID:G149582
A:Note: sequence extracted from NCBI backbone (NCBIN:112261, NCBI:112263)
A:Note: the source is designated as Lactobacillus paracasei subsp. paracasei
A:Accession: C44858
A:Molecule type: protein
A:Residues: 189-196 <HOL2>
A:Naes, H.; Nissen-Meyer, J.
J. Gen. Microbiol. 138, 313-318, 1992
A:Title: Purification and N-terminal amino acid sequence determination of the cell-wall-associated protein
A:Reference number: A44850; MUID:92226694; PMID:1564442
A:Accession: A44850
A>Status: preliminary
A:Molecule type: protein
A:Residues: 189-196 <NAE>
A:Cross-references: PID:AA22052.1; PID:G248666
A:Experimental source: strain NCDO 151
A:Note: sequence extracted from NCBI backbone (NCBIP:94706)
C:Genetics:
A:Gene: prtP
C:Superfamily: lactocepin; subtilisin homology
C:Keywords: hydrolase; serine proteinase; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:23-187/Domain: propeptide #status predicted <PRO>
F:188-1902/Product: serine proteinase, cell-envelope-associated #status experimental <M2>
F:208-634/Domain: subtilisin homology #status atypical <SBT>

Query Match 6.8%; Score 84; DB 1; Length 1902;
Best Local Similarity 25.8%; Pred. No. 1.7e+02;
Matches 51; Conservative 12; Mismatches 69; Indels 66; Gaps 8;

Qy 46 QFLENTLLFK-----GFFTGHPWYNDLLVLDLGSKDATNKYKGVLDLYGAYG 93
Db 805 QFVEGLNFKGSDGSRNLNLYMGFFGD--WND-----GKIVDSLNG-IT 845

Qy 94 YQAGGTPNKTACMGVGVTLHNNRTEKKVPINWIDGKQTVPIDKVKTSKEVTWQ 153
Db 846 YSPAGN-----YGTVPILTNKTHQYVGWMTDADGKQT----- 881

Qy 154 ELDLQARHYLHGKFGLYNSDFGKVGQGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIY 213
Db 882 -VDQAIASFSDKNALYNDISMQYLLRNI-----SNVQVDLDGGGNKVTLLSS-- 930

Qy 214 RDNKTINSENLHLYLY 231
Db 931 STNQTKTYDAHQKYYI 948

RESULT 70
gene 11-1 protein precursor - malaria parasite (Plasmodium falciparum) (fragments)
C:Species: Plasmodium falciparum
C>Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 09-Jun-2000
C:Accession: S00485
R:Scherf, A.; Hilbich, C.; Sieg, K.; Mattei, D.; Mercereau-Pujalon, O.; Mueller-Hill, E.
EMBO J. 7, 1129-1137, 1988
A:Title: The 11-1 gene of Plasmodium falciparum codes for distinct fast evolving repeats
A:Reference number: S00485; MUID:88296416; PMID:2841111
A:Accession: S00485
A:Molecule type: DNA
A:Residues: 1-1315; 1316-1485; 1486-1657; 1658-1729; 1730-1948 <SCH>
A:Cross-references: EMBL:X07453
C:Comment: This protein is associated with the membrane of red blood cells at the schizont stage.
C:Genetics:
A:Gene: 11-1
A:Introns: 71/73
C:Keywords: tandem repeat
F:1-71/Domain: signal sequence #status predicted <SIG>
F:72-1948/Product: gene 11-1 protein (fragments) #status predicted <MAT>

Query Match 6.8%; Score 84; DB 2; Length 1948;
Best Local Similarity 21.5%; Pred. No. 1.8e+02;
Matches 59; Conservative 36; Mismatches 75; Indels 104; Gaps 13;

Qy 8 NEKLRKSEL-----OQTALNLIKQ-----IYYNEK-----AITENKESD 44
Db 15 NGSDKKKSFEVFKIXGTDLKDTKDIRPHFYFIVKIIILSLLIWTVIYNNCSN 74

Qy 45 DQF-----LENTLLFKGF-----FTGHPWYNDLLV-----DLGSKDATNKYKGVKD 86
Db 75 GRYKSTLYIVGNHURFRGFRILAENEYEMTKYKTLWVNIIDNDLGRGNKKIKPRHKKVE 134

Qy 87 LYGAYGYQACAGTPTNKTACMGVGVTLHNN-----RLTEKKVPINL-----WIDGK 134
Db 135 -----INLNDNNLSNESKSKSRKKVKVNLKDNLEKREGK 170

Qy 135 QTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDFGKVGQGLIVFHSSEGSTV 194
Db 171 MK-----RNNKKEKRRKKNKNKNELK-----REYKESYLLDNKSDMDVI 213

Qy 195 SYDLFDAGQYPTDLLRIYRDNKTINSENLHI 226
Db 214 RNDKF-----SYFTLYKKNLFPNSNNYFLHM 239

RESULT 71
L1 protein - human papillomavirus type 9
C:Species: human papillomavirus type 9
C>Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S36595
R:Deilius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A:Description: Primer-directed sequencing of human papillomavirus types.
A:Reference number: S36469
A:Accession: S36595
A:Molecule type: DNA
A:Residues: 1-507
A:Cross-references: EMBL:X74464; NID:G397068; PID:CAA52488.1; PID:G397076
C:Superfamily: papillomavirus L1 protein
C:Keywords: late protein

Query Match 6.7%; Score 83.5; DB 2; Length 507;
Best Local Similarity 20.3%; Pred. No. 36;
Matches 49; Conservative 38; Mismatches 69; Indels 85; Gaps 14;

Qy 42 ESDQFLENTLLF-----KGFTGHPWYNDLLVLDLGSKD-----ATNKYKGVKD 86
Db 23 QSTDEYVERTINIFVHAISDRLLTVGHPY-----DVRSGDQRIEVPKVGSGNQYRAPRIS 77

Qy 87 -----LYGAYGYQACAGT-----NKTACMYG 109
Db 78 LPDPNRFALADMSVYNPDKERLVWACRGIEGRGQPLGVGTSGHPLPNKVRDTESSNYQ 137

Qy 110 GVTLDHNNRTEKKVPINWIDGKQTVPI-----DKVTSKEVTVOELDL-----QAR 160
Db 138 GTTWDDQNTSFDPK-QVQNFIIIG--CIPCLGEHWDAKAVCEKDN-NOLGCLPIELR 192

Qy 161 HYLHGKFGLYNSDFG---GKVGQGLIVFHSSEGSTVSVDLFDAGQYPTLLR---IYR 214
Db 193 NTV-----IEDGMDFDICFGNINNKELSPKSD---VSLDIVDETCKYPTFLTWANDVYG 244

Qy 215 D 215
Db 245 D 245

RESULT 72
transferin-binding protein - Actinobacillus pleuropneumoniae
S49815
C:Species: Actinobacillus pleuropneumoniae
C>Date: 05-Mar-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000

```
e penicillin binding protein part is neither from S. aureus nor from E. coli
C;Superfamily: penicillin-binding protein 2B
C;Keywords: antibiotic resistance; cell wall synthesis
F;403/Active site: Ser #status predicted

Query Match          6.7%; Score 83.5; DB 2; Length 668;
Best Local Similarity 20.4%; Pred. No. 51;
Matches 64; Conservative 44; Mismatches 88; Indels 117; Gaps 15;

QY      7 INEKDLRKSELOG---TALGNLKGIIYYNEK-----AITEKNK 41
       |||::|||::|||::|||::|||::|||::|||::|||::|||
Db     259 INSEELKQR-EYKGYKDDAVIGKKLEKLYDKKLQHEGDYRVTVVDNSNTIAHTLIENK 317

QY     42 ESDDQPLENTLAFKFPTGHPWYNLLDVLGSKDATNKYGKKVDL----YCAYYGYQC 96
       |||::|||::|||::|||::|||::|||::|||::|||::|||
Db     318 KXDGKDIQLTIDAK--VQSKIYNNKMNDYGSGTAIHPQTGELLALVSTPSYDVY---- 369

QY     97 AGGTPNKTACMGGVYLHNHNNELTTEKKVP-TNLMDWGQITVP--LDVKTSKEKVTVQ 153
       |||::|||::|||::|||::|||::|||::|||::|||::|||
Db     370 -----PFMT-GMSNEEYNKLTEDKPEPLNKF---QITSPGSTQKILTAGMLNNK 417

QY    154 ELDAQRYHLHGKFGILYNSDSFGG-----177
       |||::|||::|||::|||::|||::|||::|||::|||::|||
Db    418 TLDDKTSYKIDGK-GWKQDKSGNGYNVTREYVVGNI DLKQAIESSDNIFPARVALELGS 476

QY    178 -KVQRGGLIVFHSEGSTSYVDLFDAQ-----GO-----YPDTLIRIY- 213
       |||::|||::|||::|||::|||::|||::|||::|||::|||
Db    477 KPFEKGMKKLGVEDIPSDYPFPYNAQISKNKLNDEILLADSGVGGQEILINPQQILIYS 536

QY    214 --RDNKTINSENL 224
       |||::|||::|||::|||::|||::|||::|||::|||::|||
Db    537 ALENNGINAPHL 549
```

RESULT 74

```

JQ00774
penicillin-binding protein mecA, low-affinity - Staphylococcus epidermidis
N;Alternate names: penicillin-binding protein 2,
C;Species: Staphylococcus epidermidis
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 26-May-2000
C;Accession: JQ00774
R;Yifell, C.; Tesch, W.; Birch-Mechin, I.; Reynolds, P.E.; Barberis-Maino, L.;
Gene 94, 137-138, 1990
A;Title: Sequence comparison of mecA genes isolated from methicillin-resistant
A;Reference number: JQ00773; MUID:91033056; PMID:2227446
A;Accession: JQ00774
A;Molecule type: DNA
A;Residues: 1-668 <RYF>
A;Cross-references: GB:X52592; NID:946993; PIDN:CAA36828.1; PID:946994
A;Experimental source: strain WT55
C;Genetics:
A;Gene: mecA
C;Superfamily: penicillin-binding protein 2B
F;403/Active site: Ser #status predicted

Query Match      6.7%; Score 83.5; DB 2; Length 658;
Best Local Similarity 20.4%; Pred. No. 51;
Matches 64; Conservative 44; Mismatches 88; Indels 117; Gaps 15;

Qy      7 INEKDLRKSELOG---TALGNLKKIYYNEX-----AITEK 41
      : : : : : : : : : : : : : : : : : : : : : :
Db      259 INSEELKQK-EYKGXDVAIGKKGLEKLYDKLOHEDGVRVTIVDNSNTIAHTLEKK 317

Qy      42 ESDQPLENTLIFKGFTGHPWYNOLLVDLGSKDAFNKYGKKVDL-----YGAYGYQC 96
      : : : : : : : : : : : : : : : : : : : : : :
Db      318 KKGDKDIQLTIDAK---VQKSIYNNKNDYGSSTAHPQTGELLALVSTPSDYV-----369

Qy      97 AGGTPNKTCMGYGGVTLHDNNRLTEKKVP-INLWIDGQTTVP--IDKVKTSKKEVTVQ 153
      : : : : : : : : : : : : : : : : : : : : : :
Db      370 -----PFMY-GMNEFYNNKLTEDKKEPLNKF---QITSPGTSQILTFAMIGLNKK 417

Qy      154 ELDQARHYLHGKFGLYNDSDFG----- 177
      : : : : : : : : : : : : : : : : : : : : : :

```

Db 418 TLDDKTSYKIDGK-GWQKDKSGGVNTRVEVVGNGIDLKQAISSDNIFPARVALELGS 476
QY 178 -KVQRLIVFHSSEGSTVSYDLFDAQ-----GO-----YPTLLRIY- 213
Db 477 KKEFGMKKLGVGEDIPSYFFYNAQISNKNLNEILLADSGYGQGEILINPVQILSIYS 536
QY 214 --RDNKTINSEN 224
Db 537 ALENGNGINAPHL 549

RESULT 75

T44118
penicillin-binding protein 2 [imported] - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 26-May-2000
C:Accession: T44118
R:Itô, T.; Katayama, Y.; Hiramatsu, K.
Antimicrob. Agents Chemother. 43, 1449-1458, 1999
A:Title: Cloning and nucleotide sequence determination of the entire mec DNA of pre-meth
A:Reference number: Z22733; MUID:99278010; PMID:10348769
A:Accession: T44118
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-668 <fpo>
A:Cross-references: EMBL:D86934; PIDN:BAA82220.1
A:Experimental source: strain N315
C:Genetics:
A:Note: mecA
C:Superfamily: penicillin-binding protein 2B

Query Match 6.7%; Score 83.5; DB 2; Length 668;
Best Local Similarity 20.4%; Pred. No. 51;
Matches 64; Conservative 44; Mismatches 88; Indels 117; Gaps 15;
QY 7 INEKDLRKKSELOG---TALGNLKOIYYNKK-----ALTENK 41
Db 259 INSEELKQK-EYKGKDDAVIGKGLKLYDKLQKHEDGYRTIVDDNSNTIAHTLIEKK 317
QY 42 ESDDQFLENTLLPKGPTGHPWYNDLLDLGSKDATNKYKGVLDL-----YCAYYGYQC 96
Db 318 KKGDKDIQLTIDAK---VQKSIYNNMKNDYSGTATHPQTGELLALVSTPSYDVY----- 369
QY 97 AGGTPNKTACMYGGVTLHDNRLTEKKVP-INLWIDGKQTTVP--IDKVKTSKKEVTVQ 153
Db 370 -----PFMY-GMSNEEYNKLTEDKPELLNKF---QITTSFGSTQKILTAMIGLNKK 417
QY 154 ELDLQARHYLHGKFLYNSDSFG----- 177
Db 418 TLDDKTSYKIDGK-GWQKDKSGGVNTRVEVVGNGIDLKQAISSDNIFPARVALELGS 476
QY 178 -KVQRLIVFHSSEGSTVSYDLFDAQ-----GO-----YPTLLRIY- 213
Db 477 KKEFGMKKLGVGEDIPSYFFYNAQISNKNLNEILLADSGYGQGEILINPVQILSIYS 536
QY 214 --RDNKTINSEN 224
Db 537 ALENGNGINAPHL 549

Search completed: August 12, 2004, 13:33:13
Job time : 11.3708 secs

ETXE STAAU STANDARD; PRT; 257 AA.
 ID ETXE STAAU STANDARD; PRT; 257 AA.
 AC P12993;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Enterotoxin type E precursor (SEE).
 GN ENTE.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.
 RC STRAIN=MJB285;
 RX MEDLINE=88257005; PubMed=3384800;
 RA Couch J.L., Soltis M.T., Betley M.J.;
 RT "Cloning and nucleotide sequence of the type E staphylococcal
 enterotoxin gene";
 RL J. Bacteriol. 170:2954-2960(1988).
 RN [2]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=96022987; PubMed=7552730;
 RA Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
 RT "Residues defining V beta specificity in staphylococcal
 enterotoxins";
 RL Nat. Struct. Biol. 2:680-686(1995).
 CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
 CC staphylococcal food poisoning syndrome. The illness characterized
 CC by high fever, hypotension, diarrhea, shock, and in some cases
 CC death.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
 CC for the toxin interaction with MHC class II (By similarity).
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
 CC family.
 CC
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 CC
 CC EMBL; M21319; AAA26617.1; -.
 CC PIR; A28179; A28179.
 CC PDB; 1SEE; 15-OCT-95.
 CC InterPro; IPR008992; Bact_endotox.
 CC InterPro; IPR006177; Bctrl_tox.
 CC InterPro; IPR006123; Staph_Strep_toxin.
 CC InterPro; IPR006126; Staph/Strep_tox.
 CC InterPro; IPR006173; Staph_tox_OB.
 CC Pfam; PF02876; Staph_Strep_tox_C; 1.
 CC Pfam; PF01123; Staph_Strep_toxin; 1.
 CC PRINTS; PR02279; BACTRLOXIN.
 CC PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 CC PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 CC Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
 CC 3D-structure.
 CC
 CC SIGNAL 1 27
 CC CHAIN 28 257 ENTEROTOXIN TYPE E.
 CC METAL 211 211 ZINC (BY SIMILARITY).
 CC METAL 249 249 ZINC (BY SIMILARITY).
 CC METAL 251 251 ZINC (BY SIMILARITY).
 CC METAL 33 35 ZINC (BY SIMILARITY).
 CC HELIX 39 41
 CC STRAND 42 42
 CC TURN 46 47
 CC HELIX 48 51
 CC HELIX 52 54
 CC STRAND 59 64
 CC TURN 66 67
 CC STRAND 69 69

FT TURN 73 74
 FT STRAND 75 79
 FT TURN 83 84
 FT STRAND 90 94
 FT HELIX 98 104
 FT TURN 105 106
 FT STRAND 109 113
 FT STRAND 115 116
 FT TURN 118 119
 FT STRAND 128 132
 FT STRAND 135 137
 FT TURN 139 140
 FT STRAND 142 142
 FT STRAND 152 152
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 FT TURN 156 157
 FT STRAND 163 163
 FT STRAND 171 171
 FT STRAND 173 175
 FT HELIX 176 190
 FT TURN 191 191
 FT STRAND 203 211
 FT STRAND 219 221
 FT STRAND 227 227
 FT HELIX 234 239
 FT STRAND 242 244
 FT TURN 245 247
 FT STRAND 249 257
 SQ SEQUENCE 257 AA; 29358 MW; 27EDA94B97770CE3 CRC64;

Query Match 97.7%; Score 1210; DB 1; Length 257;
 Best Local Similarity 97.9%; Pred. No. 7.4e-95;
 Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SEKFEINEXDLRKKSLOGTALGNLKOIYYNEKATTENKESDDQDLENTLLFKGFFTG 60
 DB 25 SEKFEINEXDLRKKSLOGTALGNLKOIYYNEKATTENKESDDQDLENTLLFKGFFTG 84
 QY 61 HPWYNLLVLDLGSKDATNKYKKVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
 DB 85 HPWYNLLVLDLGSKDATNKYKKVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
 QY 121 BEKVPINLMDGKQTTVPIDKVKTSKEVTQVELDLQARHYLHGKFGLYNSDSFGKQV 180
 DB 145 BEKVPINLMDGKQTTVPIDKVKTSKEVTQVELDLQARHYLHGKFGLYNSDSFGKQV 204
 QY 181 RGLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNKTINSENHLALYLYTT 233
 DB 205 RGLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNKTINSENHLALYLYTT 257

RESULT 2

ETXA STAAU STANDARD; PRT; 257 AA.
 ID ETXA STAAU STANDARD; PRT; 257 AA.
 AC P13153;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Enterotoxin type A precursor (SEA).
 GN ENTA OR MW1889.
 OS Staphylococcus aureus (strain MW2), and
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=196620, 1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MW2;
 RX MEDLINE=22040717; PubMed=12044378;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA.";

RL Lancet 359:1819-1827(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-FRI337;
 RX MEDLINE=88086892; PubMed=3335483;
 RA Betley M.J., Mekalanos J.J.;
 RT "Nucleotide sequence of the type A staphylococcal enterotoxin gene."
 RL J. Bacteriol. 170:34-41(1988).
 RN [3]
 RP SEQUENCE OF 25-257.
 RX MEDLINE=87222293; PubMed=3584106;
 RA Huang I.-Y., Hughes J.L., Bergdoll M.S., Schantz E.J.;
 RT "Complete amino acid sequence of staphylococcal enterotoxin A."
 RL J. Biol. Chem. 262:7006-7013(1987).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
 RX MEDLINE=95354648; PubMed=7628431;
 RA Schad E.M., Zaitsev V.N., Dohlstien M., Kalland T.,
 RA Schlievert P.M., Ohlendorf D.H., Svensson L.A.;
 RT "Crystal structure of the superantigen staphylococcal enterotoxin
 type A."
 RL EMBO J. 14:3292-3301(1995).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=97113025; PubMed=8943278;
 RA Sundstroem M., Hallen D., Svensson A., Schad E., Dohlstien M.,
 RA Abrahamson L.;
 RT "The Co-crystal structure of staphylococcal enterotoxin type A with
 Zn²⁺ at 2.7-A resolution. Implications for major histocompatibility
 complex class II binding."
 RL J. Biol. Chem. 271:32212-32216(1996).
 RN [6]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=96022987; PubMed=7552730;
 RA Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
 RT "Residues defining V beta specificity in staphylococcal
 enterotoxins."
 RL Nat. Struct. Biol. 2:680-686(1995).
 RN [7]
 RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
 RX MEDLINE=97334373; PubMed=9191070;
 RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
 RT "A structural and functional comparison of staphylococcal
 enterotoxins A and C2 reveals remarkable similarity and
 dissimilarity."
 RL J. Mol. Biol. 269:270-280(1997).
 CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
 staphylococcal food poisoning syndrome. The illness characterized
 by high fever, hypotension, diarrhea, shock, and in some cases
 death.
 CC -!- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
 for the toxin interaction with MHC class II.
 CC -!- SUBUNIT: Monomer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
 CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
 family.
 CC
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 CC
 CC
 DR EMBL; AP004828; BAB95754.1; -;
 DR EMBL; M18970; AAZ26881.1; -;
 DR FIR; A28664; A28664.
 DR PDB; 1BSF; 11-JUL-96.
 DR PDB; 1SXT; 19-NOV-97.
 DR PDB; 1DQ; 21-FEB-02.
 DR PDB; 1I4G; 21-MAR-01.

DR PDB; 1I4H; 21-MAR-01.
 DR PDB; 1LOS; 18-DEC-02.
 DR PDB; 1SEA; 15-OCT-95.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bct1_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006136; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_05.
 DR Pfam; PF02876; Staph_strep_tox_C; 1.
 DR Pfam; PF01123; Staph_strep_toxin; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Enterotoxin; Toxin; signal; Superantigen; Metal-binding; Zinc;
 KW 3D-structure; Complete proteome.
 FT SIGNAL 1 24
 FT CHAIN 25 257 ENTEROTOXIN TYPE A.
 FT DISULFID 120 130
 FT METAL 211 211 ZINC.
 FT METAL 249 249 ZINC.
 FT METAL 251 251 ZINC.
 FT CONFLICT 242 242 T -> S (IN REF. 3).
 FT HELIX 28 31
 FT TURN 32 33
 FT HELIX 39 41
 FT TURN 44 45
 FT HELIX 46 55
 FT TURN 56 56
 FT STRAND 59 65
 FT STRAND 69 69
 FT TURN 73 74
 FT STRAND 75 78
 FT TURN 79 80
 FT TURN 90 94
 FT HELIX 98 104
 FT TURN 105 106
 FT STRAND 108 116
 FT TURN 118 119
 FT TURN 125 126
 FT STRAND 128 132
 FT STRAND 135 137
 FT TURN 139 140
 FT STRAND 142 149
 FT STRAND 151 155
 FT TURN 156 157
 FT STRAND 158 160
 FT HELIX 164 166
 FT STRAND 167 171
 FT STRAND 173 175
 FT HELIX 176 191
 FT TURN 193 194
 FT HELIX 197 199
 FT TURN 200 200
 FT STRAND 205 212
 FT STRAND 218 221
 FT TURN 222 223
 FT HELIX 230 233
 FT HELIX 234 237
 FT TURN 238 239
 FT STRAND 242 244
 FT STRAND 248 255
 SQ SEQUENCE 257 AA; ADEBF5BCALP14677 CRC64;

Query Match 83.8%; Score 1037; DB 1; Length 257;
 Best Local Similarity 83.3%; Pred. No. 2.8e-80;
 Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELOGTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFTG 60
 DB 25 SEKSEINEKDLRKKSSELOGTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFTG 84
 QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYCYQCAGTGNKTCMYGGVTLHDNNRLT 120


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CC CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC -----
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CC -----
DR EMBL; U11702; AAA19777.1; -.
DR EMBL; AP004822; BAB93916.1; -.
DR PDB; 1ENF; 10-JAN-01.
DR PDB; 1EMC; 10-JAN-01.
DR PDB; 1E77; 10-JAN-01.
DR PDB; 1E8Y; 27-JUN-01.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph_strep_toxin.
DR Pfam; PF01123; Staph_strep_toxin_1.
DR Pfam; PF02876; Staph_strep_toxin_2.
DR PRINIS; PR00279; BACTLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
KW 3D-structure; Complete proteome.
FT SIGNAL 1 24
FT CHAIN 25 241 ENTEROTOXIN TYPE H.
FT METAL 230 230 ZINC.
FT METAL 232 232 ZINC.
FT DISULFID 106 116
FT SEQUENCE 241 AA; 27858 MW; 70F77985877616CE CRC64;
Query Match 29.1%; Score 360; DB 1; Length 241;
Best Local Similarity 37.5%; Fred. No. 2.9e-23;
Matches 84; Conservative 45; Mismatches 83; Indels 12; Gaps 7;
QY 10 KDLRRKSELOGTALGNLQIYYVNEKAITENKESDQDFLENTLFGFFFTGHPWYNDLV 69
D 25 EDLHDKSELTDALAN--AYQYNHPFIKENIKSDEISGEKDLIFRN--QGDSG-NDLRV 79
QY 70 DLGSKDATNKYGGKVDLYGAYGYQACGTPNTACMYGVTVLHDNNRLTEKKVPINL 129
D 80 KFATDLAQKFNKNDVITYGASFPYKCEKISINISECLYGGTTL-NSEKLAQERVIGANV 138
QY 130 WIDGKQITVPIDKVKTSKKEVTVQELDLQARHYLHGKGLNDSFGKVGQGVIVFHS 189
D 139 WVDGIQKETEL--IRTNKNVTLQELDKIRKILSKDKIYKDKS---EISKGLIEFD 193
QY 190 EGSTVSVDLFDPAQGYFDTLRIYRDNKTINSNL-HIALYLT 232
D 194 TPDYSFDIYDLKGENDYEIDKIVEDNKNLTKSDSDISHIDVNLVT 237
RESULT 5
ETXB STAAU
ID ETXB STAAU STANDARD; PRT; 266 AA.
AC P01552;
DT 21-JUL-1986 (Rel. 01, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Enterotoxin type B precursor (SEB).
GN ENTB.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=86168029; PubMed=3957869;
RA Jones C.L., Khan S.A.;
RT "Nucleotide sequence of the enterotoxin B gene from Staphylococcus

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RT aureus.";
RL J. Bacteriol. 166:29-33(1986).
RN [2]
RP SEQUENCE OF 40-91 FROM N.A.
RX MEDLINE=85298255; PubMed=3898073;
RA Ranelli D.M., Jones C.L., Johns M.B., Mussey G.J., Khan S.A.;
RT "Molecular cloning of staphylococcal enterotoxin B gene in
RT Escherichia coli and staphylococcus aureus.";
RL Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854(1985).
RN [3]
RP SEQUENCE OF 28-266 (S-6).
RX MEDLINE=71007902; PubMed=5470821;
RA Huang I.-Y., Bergdoll M.S.;
RT "The primary structure of staphylococcal enterotoxin B. 3. The
RT cyanogen bromide peptides of reduced and aminoethylated enterotoxin
RT B, and the complete amino acid sequence.";
RL J. Biol. Chem. 245:3518-3525(1970).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
RX MEDLINE=93063291; PubMed=1436058;
RA Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
RT "Crystal structure of staphylococcal enterotoxin B, a superantigen.";
RL Nature 359:801-806(1992).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.
RX MEDLINE=94203282; PubMed=8152483;
RA Jardtaky T.S., Brown J.H., Gorga J.C., Stern L.J., Urban R.G.,
RA Chi Y.I., Stauffacher C., Strominger J.L., Wiley D.C.;
RT "Three-dimensional structure of a human class II histocompatibility
RT molecule complexed with superantigen.";
RL Nature 368:711-718(1994).
RN [6]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH TCR.
RX MEDLINE=99096298; PubMed=9881971;
RA Li H., Llera A., Tsuchiya D., Leder L., Ysern X., Schlievert P.M.,
RA Karjalainen K., Mariuzza R.A.;
RT "Three-dimensional structure of the complex between a T cell receptor
RT beta chain and the superantigen staphylococcal enterotoxin B.";
RL Immunity 9:807-816(1998).
RN [7]
RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
RX MEDLINE=98181012; PubMed=9514739;
RA Papageorgiou A.C., Tranter H.S., Acharya K.R.;
RT "Crystal structure of microbial superantigen staphylococcal
RT enterotoxin B at 1.5-A resolution: implications for superantigen
RT recognition by MHC class II molecules and T-cell receptors.";
RL J. Mol. Biol. 277:61-79(1998).
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases
CC death.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC -----
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CC -----
DR EMBL; M11118; AAA88550.1; -.
DR PIR; S27360; ENSAB6.
DR PDB; 1SEB; 20-JUN-96.
DR PDB; 2SEB; 28-JAN-98.
DR PDB; 3SEB; 27-MAY-98.
DR PDB; 1SE3; 16-JUN-97.
DR PDB; 1SE4; 15-OCT-97.
DR PDB; 1SEB; 04-MAR-99.
DR PDB; 1DSM; 14-MAR-01.
DR PDB; 1DSX; 28-JUN-00.

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Query Match      24.6%; Score 304.5; DB 1; Length 266;
Best Local Similarity 34.4%; Pred. No. 1.5e-18;
Matches      84; Conservative 45; Mismatches 96; Indels 19; Gaps 8;

QY      1 SEKSEINEKDLRKKSLOGTALCNLQIYYNEKAITENKESDQOFLNTLLKXGFTG 60
      : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      27 AESQPPKPEDEHKSSKFTG-LMENMKVLDDNHVSAI-NVKSIDOLFYFDIYIISIKTK 84
      : : : : : : : : : : : : : : : : : : : : : : : : : :
QY      61 HPWYNDLLVDLGSKDANKYKGGKVDLYGAYGYQC-----AGTGNPKTKACMYGG 110
      : : : : : : : : : : : : : : : : : : : : : : : : : :

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CC -----
CC EMBL; AF003364; BAB58171.1; -
CC EMBL; AF003135; BAB43097.1; -
CC EMBL; X51661; CAA35972.1; -
CC PIR; S11885; S11885
CC PDB; 1JCK; 12-NOV-97.
CC PDB; 1JLG; 02-AUG-02.
CC PDB; 1KLU; 14-AUG-02.
CC InterPro; IPR008992; Bact_endotox.
CC InterPro; IPR006177; Bctrl tox.
CC InterPro; IPR006123; Staph/Strep toxin.
CC InterPro; IPR006126; Staph/Strep tox.
CC InterPro; IPR006173; Staph tox OB.
CC Pfam; PF02876; Staph_strep_tox_C; 1.
CC Pfam; PF01123; Staph_strep_toxin; 1.
CC PRINTS; PR00279; BACTRLTOXIN.
CC PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
CC PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
CC Enterotoxin; Toxin; Signal; Superantigen; 3D-structure;
KW Complete proteome. 27
FT SIGNAL 1
FT CHAIN 28 266 ENTEROTOXIN TYPE C-3.
FT DISULFID 120 137
SQ SEQUENCE 266 AA; 30671 MW; 5ED8A32D11FFCA59 CRC64;

Query Match 24.4%; Score 302.5; DB 1; Length 266;
Best Local Similarity 33.8%; Pred. No. 2.3e-18;
Matches 79; Conservative 47; Mismatches 89; Indels 19; Gaps 9;

Qy 11 DLKKSELOQTALGNLQIYYNEKAITENK-ESDDQFLENTLIFKGFTHGHPWYNDLV 69
Db 37 DLKSSSEFTGI-MGNMK--YLYDDHYVSATKVKSVDFLAHLDIYNSDKKLNKYDKVKT 93

Qy 70 DLGSKDATNKYKKVDLYGAYGYQC-----AGTTPNKATAGYGGVTLHNNRLTEE 122
Db 94 ELLNEDLAKYKDVVDVYSGNYVYFCSSKDVNGVGTGKTCMYGGITKHEGNHFDNG 153

Qy 123 --KKVPLNLWDGKQTTVPIDKVTSKKEVTQVQLDQARHLHGKFLYNSPSFGKVKQ 180
Db 154 NLQNVLRVY-ENKRNITSE-VDTKKSVTAQELDIKRNFLINKNLKLTFFNS--SPYE 209

Qy 181 RGLIVFHSSEGSTVSYDLFDAQGYPP--TLRLIYRDNKTNGSENHLIALYLT 232
Db 210 TGYIKFIENNGTWFYDMPAPGDKFQSKYLMYNDNKTVDKSVKIEVHLIT 263

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RESULT 7

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ID ETC2 STAAU STANDARD; PRT; 266 AA.
AC P34071;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Enterotoxin type C-2 precursor (SEC2).
GN ETC2.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CC NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.
RX MEDLINE=89277549; PubMed=2543637;
RA Bohach G.A., Schlievert P.M.;
RT "Conservation of the biologically active portions of staphylococcal
enterotoxins C1 and C2."
RL Infect. Immun. 57:2249-2252(1989).
RN [2]
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
RX MEDLINE=96027099; PubMed=7582894;
RA Papageorgiou A.C., Acharya K.R., Shapiro R., Passalacqua E.F.,
RA Brehm R.D., Tranter H.S.;
RT "Crystal structure of the superantigen enterotoxin C2 from
Staphylococcus aureus reveals a zinc-binding site."

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RL Structure 3:769-779(1995).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=96022987; PubMed=7552730;
RA Swaminathan S., Furey W.F. Jr., Fletcher J., Sax M.;
RT "Residues defining V beta specificity in staphylococcal
enterotoxins."
RL Nat. Struct. Biol. 2:680-686(1995).
RN [4]
RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
RX MEDLINE=97334373; PubMed=9131070;
RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
RT "A structural and functional comparison of staphylococcal
enterotoxins A and C2 reveals remarkable similarity and
dissimilarity."
RL J. Mol. Biol. 269:270-280(1997).
CC -1- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases
CC death.
CC -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
CC for the toxin interaction with MHC class II.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
DR PIR; A80114; A60114.
DR PDB; 1STE; 23-DEC-96.
DR PDB; 1SE2; 08-MAR-96.
DR PDB; 1CQV; 19-SEP-01.
DR PDB; 1I4P; 19-SEP-01.
DR PDB; 1I4Q; 19-SEP-01.
DR PDB; 1I4R; 19-SEP-01.
DR PDB; 1I4X; 19-SEP-01.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen; Metal-binding; Zinc;
KW 3D-structure.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN TYPE C-2.
FT DISULFID 120 137
FT METAL 36 36 ZINC.
FT METAL 110 110 ZINC.
FT METAL 145 145 ZINC.
FT METAL 149 149 ZINC.
FT HELIX 35 37
FT HELIX 41 43
FT STRAND 44 44
FT TURN 48 48
FT TURN 49 55
FT STRAND 60 65
FT STRAND 69 69
FT TURN 73 74
FT STRAND 75 79
FT TURN 83 86
FT STRAND 90 94
FT HELIX 98 104
FT TURN 105 106
FT STRAND 109 113
FT STRAND 116 116
FT TURN 118 119
FT TURN 128 129
FT STRAND 136 139
FT STRAND 142 144
FT TURN 146 147
FT STRAND 149 149

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FT HELIX 151 153
FT STRAND 156 164
FT TURN 165 166
FT STRAND 167 176
FT STRAND 178 178
FT STRAND 180 182
FT HELIX 183 198
FT STRAND 208 216
FT TURN 218 219
FT STRAND 222 232
FT STRAND 232 232
FT STRAND 237 241
FT HELIX 242 246
FT STRAND 249 251
FT TURN 252 254
FT STRAND 256 263
SQ SEQUENCE 266 AA; 30604 MW; 8407FBI8536FAC08 CRC64;

Query Match 24.1%; Score 298.5; DB 1; Length 266;
Best Local Similarity 32.8%; Pred. No. 4.9e-18;
Matches 80; Conservative 48; Mismatches 97; Indels 19; Gaps 9;

QY 1 SKSBEINEKDKRKSELOGTALGNLKOIYYNEKAITENK-ESDDOLENTLLFKGFFT 59
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
27 AESQDPDTPDELHKSSEFTGT-MGNMK--YLYDDHYVSATKVMVDKFLADHLIYNSDK 83
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 60 GHFWYNDLLVGLSGDATNKYKGGKVDLYGAYGYQC-----AGGTFNKTCMYGGVT 112
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 84 KLVKDYKVKVTELLNEDLAKYKDEVDVYGSNYVYCNFYSSKDNKGVKVTGGKTCYGGIT 143
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 113 LHDNRLTSE--KKVPINLWIDGKQTTPIDIKVTSKEVTVOEQLDQARVHLHGKFLY 170
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 144 KHEGNHFDGNLQNLVIRY-ENKRNITSE-VQTDKKSVAQAEIDIKARNFLINKNLY 201
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 171 NSDSFGKVGQGLVPHSSEGSTVSVDLFDAGQVDP--TLIRYRDKNTINSENHLAL 228
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 202 EFNS--SPYETGVIKFIENNGNTFWDDMPAPGDFDQSKYLMYNDKNTVDSKSVKIEV 259
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 229 YLYT 232
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 260 HLTT 263
: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 8
SPEA_STRPY STANDARD; PRT; 251 AA.
AC P08025;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin)
DE (SPE A).
GN SPEA OR SPYM18_0393.
OS Streptococcus pyogenes, and
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314, 186103;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86166804; PubMed=3514452;
RA Weeks C.R., Ferretti J.J.;
RT "Nucleotide sequence of the type A streptococcal exotoxin
RT (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
RT T12."
RL Infect. Immun. 52:144-150(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=86284313; PubMed=3526093;
RA Johnson L.P., L'Italien J.J., Schlievert P.M.;
RA "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is
RT related to Staphylococcus aureus enterotoxin B."
RL Mol. Gen. Genet. 203:354-356(1986).

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RN RP SEQUENCE FROM N.A.
RC STRAIN=MGAS232 / Serotype M18;
RX MEDLINE=21927593; PubMed=11917108;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Rickielfs S.M., Porcella S.F.,
RA Parks L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A Streptococcus strains associated with acute rheumatic fever
RT outbreaks."
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
RN [4]
RX X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).
RX MEDLINE=99094887; PubMed=9878045;
RA Papageorgiou A.C., Collins C.M., Gutman D.M., Kline J.B.,
RA O'Brien S.M., Tranter H.S., Acharya K.R.;
RT "Structural basis for the recognition of superantigen streptococcal
RT pyrogenic exotoxin A (SpeA) by MHC class II molecules and T-cell
RT receptors."
RL EMBO J. 18:9-21(1999).
CC -!- FUNCTION: Causative agent of the symptoms associated with scarlet
CC fever, have been associated with streptococcal toxic shock-like
CC disease and may play a role in the early events of rheumatic
CC fever.
CC -!- SUBUNIT: Binds to major histocompatibility complex class II beta
CC chain.
CC -!- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY BACTERIOPHAGE T12.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC -----
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CC -----
CC EMBL; U0453; AAC48868.1; -
CC EMBL; X03929; CAA27568.1; -
CC EMBL; AE009882; AAL97141.1; -
CC PIR; A26152; A26152.
CC PDB; 1B12; 24-NOV-99.
CC PDB; 1FNU; 17-NOV-00.
CC PDB; 1FNW; 17-NOV-00.
CC PDB; 1FNW; 17-NOV-00.
CC PDB; 1HAS; 03-APR-02.
CC PDB; 1LOX; 03-APR-02.
CC InterPro; IPR008992; Bact_endotox.
CC InterPro; IPR006177; Bctrl_tox.
CC InterPro; IPR006123; Stap/Strep_toxin.
CC InterPro; IPR006126; Stap/Strep_tox.
CC InterPro; IPR006173; Staph_tox_Ob.
CC Pfam; PF02876; Stap_Strep_tox_C; 1.
CC Pfam; PF01123; Stap_Strep_toxin; 1.
CC PRINTS; PR00279; BACTRLTOXIN.
CC PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
CC PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
CC Toxin; Signal; 3D-structure; Complete proteome.
FT SIGNAL 1 30
FT CHAIN 31 251 EXOTOXIN TYPE A.
FT DISULFID 117 128 K -> E (IN REF. 2).
FT CONFLICT 6 6 VT -> MK (IN REF. 2).
FT CONFLICT 17 18 SQEWFACQDD -> LPKGICSTRPK (IN REF. 2).
FT CONFLICT 25 35 H -> Q (IN REF. 2).
FT CONFLICT 40 40 S -> N (IN REF. 2).
FT CONFLICT 43 43 NLQNIYFLYEGDP -> TFKIYIFFMRVTL (IN
FT CONFLICT 47 59 REF. 2).
FT CONFLICT 129 129 I -> L (IN REF. 2).
FT CONFLICT 165 178 TNKQWTAQELDYK -> QIKNGNCRISYT (IN
FT REF. 2).

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FT HELIX 36 38
FT HELIX 42 44
FT TURN 48 48
FT HELIX 49 56
FT STRAND 60 66
FT STRAND 69 69
FT TURN 73 74
FT STRAND 75 78
FT STRAND 82 82
FT TURN 83 84
FT STRAND 85 85
FT STRAND 87 91
FT HELIX 95 101
FT TURN 102 103
FT STRAND 105 110
FT STRAND 113 113
FT TURN 115 116
FT STRAND 126 130
FT STRAND 133 135
FT TURN 137 138
FT STRAND 140 153
FT TURN 154 155
FT STRAND 156 167
FT STRAND 169 171
FT HELIX 172 187
FT STRAND 199 205
FT STRAND 212 215
FT HELIX 224 227
FT HELIX 228 231
FT TURN 232 233
FT STRAND 236 238
FT TURN 239 241
FT STRAND 243 249
SQ SEQUENCE 251 AA; 29246 MW; 54001FE4CCBFC3 CRC64;

Query Match 22.9%; Score 283.5; DB 1; Length 251;
Best Local Similarity 33.8%; Pred. No. 8.4e-17;
Matches 80; Conservative 44; Mismatches 94; Indels 19; Gaps 10;

QY 4 SEINEKDLRKSELOGTAL-GNLKQIYY-YNEKAIT-ENKESDDOPLENTLLFKGFTG 60
Db 25 SQEFAQDDPPSQHRSLLVKNLQNIYFLYEGDPVTHENVKSDLLSHDLIYN--VS 81
QY 61 HPVNDLLVDLGSKDQATKYGKGVLDLYGAYGYQC-AGGTPNKACMYGGVTLHDNNRL 119
Db 82 GPNYDKLTELKNQEMATLPKDKNDIVGVYHYHLCVLCNAESACIYGGVTHNENHNL 141
QY 120 TEEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGVNSDSFGKV 179
Db 142 BIPKIVVKSIGDIQ-SLSFD-IETNKMVTAQELDYKVRKYLTDNKLTYNGP--SKY 197
QY 180 QRGIVVHSSSEGSTVSYDLFD-AGQGYPTLLRIYRDNKTNSENLHIALVLT 232
Db 198 ETGIKFIKPKNESFWDFPEPEFTQSKY----LMYKDNELSDNTSQTIEVYLT 250

RESULT 9
ETC1 STAAU STANDARD; PRT; 266 AA.
AC P01553;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Enterotoxin type C-1 precursor (SEC1).
GN ETC1.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_taxid=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88038352; PubMed=2823067;
RA Bohach G.A., Schlievert P.M.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C1 gene and

relatedness to other pyrogenic toxins."; Mol. Gen. Genet. 209:15-20(1987).
[2]
RP SEQUENCE OF 28-266.
RX MEDLINE=83213327; PubMed=6189824;
RA Schmidt J.J., Spero L.;
RT "The complete amino acid sequence of staphylococcal enterotoxin C1."; J. Biol. Chem. 258:6300-6306(1983).
CC -!- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases death.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.
CC
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CC
CC EMBL: X05815; CAA329260.1; --
CC PIR: S06356; ENSACL.
CC HSP: P34071; ISE2.
CC InterPro: IPR008992; Bact_endotox.
CC InterPro: IPR006177; Bct1_tox.
CC InterPro: IPR006123; Staph/Strep_toxin.
CC InterPro: IPR006126; Staph/Strep_tox.
CC InterPro: IPR006173; Staph_tox_OB.
CC Pfam: PF02876; Staph_strep_tox_C; 1.
CC Pfam: PF01123; Staph_strep_toxin; 1.
CC PRINTS: PR00279; BACTRTOXIN.
CC PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
CC PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Enterotoxin; Toxin; Signal; Superantigen.
FT SIGNAL 1 27
FT CHAIN 28 266 ENTEROTOXIN TYPE C-1.
FT DISULFID 120 137
FT CONFLICT 177 177 D -> N (IN REF. 2).
SQ SEQUENCE 266 AA; 30546 MW; 3A7AB59A896853B CRC64;

Query Match 21.8%; Score 270.5; DB 1; Length 266;
Best Local Similarity 31.3%; Pred. No. 1.1e-15;
Matches 76; Conservative 49; Mismatches 101; Indels 17; Gaps 8;

QY 1 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDOPLENTLLFKGFTG 60
Db 27 AESQDPPTDELHKASKFTG-LMENKVIYDDHYVSATKVK-SVDKFLAHLIYNISDKK 84
QY 61 HPVNDLLVDLGSKDQATKYGKGVLDLYGAYGYQC-----AGTPTNKACMYGGVTL 113
Db 85 LKNYDKVKTTELLNEGLAKYKDEVDVYGSNYVNCYFSSKDNVGVTKTGKTCMYGITK 144
QY 114 HDNNRLTEE--KKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGV 171
Db 145 HEGNHFNGNLQNLIRVY-ENKRTISFE-VQTKSVTAQELDIKARFLINKQLVE 202
QY 172 SDSFGKVGQRLIVFHSSEGSTVSYDLFDQAQGYPD--TLRIYRDNKTNSENLHIALY 229
Db 203 FNS--SPYETGVTKFIENNGNTFWYDMPAPGDKFDQSKYLMWYNDNKTVDKSKVIEVH 260
QY 230 LVT 232
Db 261 LTT 263

RESULT 10
ETXG STAAU STANDARD; PRT; 258 AA.
ID ETXG STAAU
AC G85382;

Query Match	20.7%;	Score 256;	DB 1;	Length 258;
Best Local Similarity	29.6%;	Pred. No. 1.8e-14;		
Matches 74;	Conservative 50;	Mismatches 84;	Indels 42;	Gaps 12;

DR InterPro: IPR006173; Staph tox OB.
DR Pfam: PF02876; Staph_strep_tox_C7_1.
DR Pfam: PF01123; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Toxin; Signal; Complete proteome.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 234 EXOTOXIN TYPE G.
FT SEQUENCE 234 AA; 27262 MW; 49525C49E4BA2052 CRC64;
Query Match 16.9%; Score 209; DB 1; Length 234;
Best Local Similarity 32.6%; Pred. No. 1.5e-10;
Matches 56; Conservative 31; Mismatches 71; Indels 14; Gaps 6;
QY 64 YNDLLVDLGSKDATNKKYKGVLDLYGAYGYOCAGGTENKTCACMGVTLHNNRLTEEK 123
DB 73 YVDSIVSLGITD--QFIRKDKVDFGLPNF-----SPYVDNIYGGIVKHSNQGNKQLQ 125
QY 124 KVPINLWIDGKQTTPIDKVTSKKEVTQVQELDLQARHVLHGKFLYNSDSFGGKVQVQGL 183
DB 126 FVGI-LNQGKETYLPSEAVRIKKQFTLQEFDFKIRKELMEKYNIDSES---RYTSGS 181
QY 184 IVFHSSEGSTVSYDLPDAQGY--PDTLLRIYRDNKTINSENL-HIALYLYT 232
DB 182 LFLATKDSKHVEYDLFNKDKLLSRDSFFRYKDKNFENSEIISHFDIYLT 233
RESULT 12
SPEC_STRPY
ID SPEC_STRPY STANDARD; PRT; 236 AA.
AC Q9X5C8;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Exotoxin type H precursor (SPE H).
GN SPEH OR SPY1008.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
[1] _
RN SEQUENCE FROM N.A.
RC STRAIN=M15;
RX MEDLINE=99093428; PubMed=9874566;
RA Proft T., Moffatt S.L., Berkahn C.J., Fraser J.D.;
RT "Identification and characterization of novel superantigens from
Streptococcus pyogenes.";
RL J. Exp. Med. 189:89-102(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
CC -!- FUNCTION: Mitogenic for human peripheral blood lymphocytes.
CC -!- SUBUNIT: Binds to major histocompatibility complex class II beta
chain.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
family.

CC EMBL; AF124500; AAD30989.1; -
DR EMBL; AB006546; AAK33907.1; -
DR PDB; 1ET9; 24-MAY-00.
DR PDB; 1EU4; 24-MAY-00.
DR InterPro: IPR008992; Bact endotox.
DR InterPro: IPR006123; Staph7Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Staph_strep_tox_C7_1.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Toxin; Signal; Complete proteome; 3D-structure.
FT SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 236 EXOTOXIN TYPE H.
FT SEQUENCE 236 AA; 27485 MW; 16352923907AD40D CRC64;
Query Match 15.4%; Score 191; DB 1; Length 236;
Best Local Similarity 26.1%; Pred. No. 4.9e-09;
Matches 55; Conservative 44; Mismatches 82; Indels 30; Gaps 9;
QY 25 NLKQIYYNKAITEN--KSSDDQFLENTLLFK-----GFTTGHWPYNDLLVDLGSKDA 76
DB 42 NLESLYKXHSNLIADSIKNSPDIVTSHMLKYSVKDKNLSVFFEKDW-----I 89
QY 77 TNKYKGGKVDLYGAYGYOCAGGTENKTCACMGVTLHNNRLTEEKVPIINLWIDGKQT 136
DB 90 SQEFKDEVDIYALSQEVCE--CPGKRYEAFGGITLTNSEK--KEIKVFNVDLNSGKDIVF 145
QY 137 TVPIDKVTSKKEVTQVQELDLQARHVLHGKFLYNSDSFGGKVQVQGLIVFHSSEGSTVSY 196
DB 146 --PEMFITVANKPKVTAQEVDIKVKLLIKYDIYNNRE--QKYSKGTVTLDLNSGKDIVF 201
QY 197 DL-FDAQGYDPTLLRIYRDNKTINSENLHI 226
DB 202 DLYYFGNGDF-NSMLKIYSNNERIDSTQPHV 231
RESULT 13
SPEC_STRPY
ID SPEC_STRPY STANDARD; PRT; 235 AA.
AC P13380;
DT 01-JAN-1990 (Rel. 13, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Exotoxin type C precursor (SPE C).
GN SPEC OR SPY0711.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
[1] _
RN SEQUENCE FROM N.A. AND SEQUENCE OF 28-52.
RC STRAIN=T18P / MGAS 1585;
RX MEDLINE=88314303; PubMed=3045005;
RA Goshorn S.C., Schlievert P.M.;
RT "Nucleotide sequence of streptococcal pyrogenic exotoxin type C.";
RL Infect. Immun. 56:2518-2520(1988).
RN [2]
RP REVISIONS TO 21-26.
RC STRAIN=T18P / MGAS 1585;
RX MEDLINE=92363541; PubMed=1500157;
RA Kapur V., Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
RT "Molecular population genetic evidence of horizontal spread of two
alleles of the pyrogenic exotoxin C gene (speC) among pathogenic
clones of Streptococcus pyogenes.";
RL Infect. Immun. 60:3513-3517(1992).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,

RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
 RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
 RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.,
 RT "Complete genome sequence of an M1 strain of Streptococcus
 RT Pyogenes.";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
 RN [4]
 RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 30-235.
 RX MEDLINE=97397352; PubMed=9253413;
 RA Roussel A., Anderson B.F., Baker H.M., Fraser J.D., Baker E.N.;
 RT "Crystal structure of the streptococcal superantigen SPE-C:
 RT dimerization and zinc binding suggest a novel mode of interaction
 RT with MHC class II molecules.";
 RL Nat. Struct. Biol. 4:635-643(1997).
 CC -1- FUNCTION: Causative agent of the symptoms associated with scarlet
 CC fever, have been associated with streptococcal toxic shock-like
 CC disease and may play a role in the early events of rheumatic
 CC fever.
 CC -1- SUBUNIT: Binds to major histocompatibility complex class II beta
 CC chain.
 CC -1- MISCELLANEOUS: THIS TOXIN SEEMS TO BE CODED BY A BACTERIOPHAGE.
 CC -1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
 CC family.
 CC -----
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 CC -----
 DR EMBL; M35514; AAA27017.1; ALT_SEQ.
 DR EMBL; M97156; AAB59091.1; -.
 DR EMBL; M97157; AAB59092.1; -.
 DR EMBL; AE006523; AAK33664.1; -.
 DR PIR; A30509; A30509.
 DR PIR; A44799; A44799.
 DR PDB; 1AN8; 29-APR-98.
 DR PDB; 1KTK; 07-JUN-02.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bctrl_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF02876; Stab_Strep_tox_C; 1.
 DR Pfam; PF01123; Stab_Strep_toxin; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Toxin; Signal; 3D-structure; Complete proteome.
 FT SIGNAL 1 27
 FT CHAIN 28 235 EXOTOXIN TYPE C.
 FT CONFLICT 53 53 N -> D (IN REF. 1).
 FT HELIX 33 44
 FT STRAND 49 59
 FT STRAND 63 67
 FT STRAND 69 72
 FT TURN 74 75
 FT STRAND 77 81
 FT HELIX 84 87
 FT TURN 88 89
 FT TURN 92 93
 FT STRAND 95 100
 FT TURN 108 109
 FT STRAND 110 114
 FT STRAND 117 119
 FT STRAND 127 128
 FT STRAND 131 135
 FT TURN 136 137
 FT STRAND 141 142
 FT TURN 144 145
 FT STRAND 148 149

FT STRAND 153 155
 FT HELIX 156 171
 FT TURN 173 174
 FT TURN 176 177
 FT STRAND 182 189
 FT TURN 190 191
 FT TURN 194 198
 FT TURN 204 205
 FT HELIX 208 212
 FT HELIX 213 217
 FT STRAND 220 222
 FT HELIX 223 225
 FT STRAND 226 235
 SQ SEQUENCE 235 AA; 27371 MW; 070534ABB952C1E0 CRC64;
 Query Match 13.98; Score 171.5; DB 1; Length 235;
 Best Local Similarity 26.3%; Pred. No. 2.1e-07;
 Matches 59; Conservative 42; Mismatches 78; Indels 45; Gaps 11;
 QY 37 ITENKESDDQFLENTLIFKGFFTGHPW-VNDLLVLDLGSKDA-----TNKYKGK----- 83
 DB 25 IKSDSKDINVKSDLLYA--YITPVDYKNCRVNFTHTLNDITOKYRGKDYISSEM 82
 QY 84 -----KVDLYGAYGYQCAGGTGPNKTCACMGVGTLDHNNELTEKKVPINLWI 131
 DB 83 SYEASQKFKRDDHVDVDFGLFVILNSHTG-----EYIYGITPAQNNKVNH--KLLGNLFI 135
 QY 132 DGKQTTVPIDKVKTSKKEVTQVELDQARHLGKFGLYNSDS--FGKQVQRLVHFSS 189
 DB 136 SGESQQLNNKILIEKDIVTFQELDFKIRKLYMDNYKIYDATSPYVSGRIEIG-----TK 190
 QY 190 EGSTVSYDLFDA--QGYQPTLLRIYEDNKTIINSENL-HIALYL 230
 DB 191 DGKEQIDLFDSPEGTRSDIFAK-YKDNRIINMKNFSDIYL 233
 RESULT 14
 ID TSST STAAU STANDARD; PRT; 234 AA.
 AC P06886;
 DT 01-JAN-1988 (Rel. 06, Created)
 DT 01-JAN-1988 (Rel. 06, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Toxic shock syndrome toxin-1 precursor (TSST-1).
 GN TSST.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RN SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RX MEDLINE=87057222; PubMed=3782090;
 RA Blomster-Hautamaa D.A., Kreiswirth B.N., Kornblum J.S., Novick R.P.,
 RA Schlievert P.M.;
 RT "The nucleotide and partial amino acid sequence of toxic shock
 RT syndrome toxin-1.";
 RL J. Biol. Chem. 261:15783-15786(1986).
 RN [2]
 RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=94150598; PubMed=8107781;
 RA Acharya K.R., Passalacqua E.F., Jones E.Y., Harlos K., Stuart D.I.,
 RA Brehm R.D., Tranter H.S.;
 RT "Structural basis of superantigen action inferred from crystal
 RT structure of toxic-shock syndrome toxin-1.";
 RL Nature 367:94-97(1994).
 RN [3]
 RN X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=94092653; PubMed=8268150;
 RA Prasad G.S., Earhart C.A., Murray D.L., Novick R.P., Schlievert P.M.,
 RA Ohlendorf D.H.;
 RT "Structure of toxic shock syndrome toxin 1.";
 RL Biochemistry 32:13761-13766(1993).
 RN [4]
 RN X-RAY CRYSTALLOGRAPHY (2.07 ANGSTROMS).

RX MEDLINE=96319751; PubMed=8759320;
RA Papegeorgiou A.C., Brehm R.D., Leonidas D.D., Tranter H.S.,
RT Acharya K.R.;
RT "The refined crystal structure of toxic shock syndrome toxin-1 at
RT 2.07-A resolution.";
RL J. Mol. Biol. 260:553-569(1996).
[5]
RP X-RAY CRYSTALLOGRAPHY (2.05 ANGSTROMS).
RX MEDLINE=97337442; PubMed=9194182;
RA Prasad G.S., Radhakrishnan R., Mitchell D.T., Earhart C.A.,
RA Dingus M.N., Cook W.J., Schlvert P.M., Ohlendorf D.H.;
RT "Refined structures of three crystal forms of toxic shock syndrome
RT toxin-1 and of a tetramutant with reduced activity.";
RL Protein Sci. 6:1220-1227(1997).
[6]
RP X-RAY CRYSTALLOGRAPHY (1.95 ANGSTROMS) OF MUTANTS.
RX MEDLINE=98254504; PubMed=9585531;
RA Earhart C.A., Mitchell D.T., Murray D.L., Pinheiro D.M., Matsumura M.,
RA Schlvert P.M., Ohlendorf D.H.;
RT "Structures of five mutants of toxic shock syndrome toxin-1 with
RT reduced biological activity.";
RL Biochemistry 37:7194-7202(1998).
CC -!- FUNCTION: Responsible for the symptoms of toxic shock syndrome.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC -----
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CC -----
CC EMBL; J02615; AAA26682.1; -;
DR PIR; A24606; XCSAS1.
DR PDB; 2TSS; 24-DEC-97.
DR PDB; 3TSS; 24-DEC-97.
DR PDB; 4TSS; 24-DEC-97.
DR PDB; 5TSS; 24-DEC-97.
DR PDB; 1QIL; 12-AUG-97.
DR PDB; 2QIL; 12-AUG-97.
DR PDB; 1AW7; 18-NOV-98.
DR PDB; 1TS2; 16-DEC-98.
DR PDB; 1TS3; 16-DEC-98.
DR PDB; 1TS4; 16-DEC-98.
DR PDB; 1TS5; 16-DEC-98.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR008375; Staph_exotoxin.
DR InterPro; IPR006173; Staph_toxin.
DR InterPro; IPR006125; Staph_tox OB.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR PRINTS; PR01600; STAPHSTREP_TOXIN.
DR PRINTS; PR01501; TOXICSHOCKTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Toxin; Superantigen; Signal; 3D-structure.
FT SIGNAL 1 40
FT CHAIN 41 234 TOXIC SHOCK SYNDROME TOXIN-1.
FT HELIX 46 54
FT STRAND 58 69
FT TURN 70 71
FT STRAND 72 76
FT TURN 78 79
FT STRAND 82 86
FT TURN 90 91
FT TURN 98 99
FT STRAND 101 108
FT STRAND 113 114

FT TURN 116 117
FT STRAND 120 125
FT STRAND 128 129
FT STRAND 133 138
FT STRAND 142 146
FT TURN 147 148
FT STRAND 149 151
FT STRAND 159 161
FT STRAND 163 164
FT HELIX 166 181
FT TURN 183 185
FT TURN 187 188
FT STRAND 192 198
FT TURN 199 200
FT STRAND 203 207
FT TURN 208 209
FT HELIX 214 226
FT STRAND 221 222
FT HELIX 223 225
FT STRAND 226 234
SQ SEQUENCE 234 AA; 26306 MW; E95789FF9A1D7AB4 CRC64;
Query Match 8.5%; Score 105.5; DB 1; Length 234;
Best Local Similarity 22.6%; Pred. No. 0.077;
Matches 52; Conservative 36; Mismatches 69; Indels 73; Gaps 12;
QY 11 DLRLKSELQGTALGNLQIYYNKAITENKESDDQFLENTLLFKGFFTHGFWYNDLLVD 70
DB 58 DFTNSEVLDSLSGVR-----IKNTDGI--SLIIFPS-----EYSPAFY- 97
QY 71 LGSKDATNYKKGKVDL-----YGAYGYQCAGTPTNKATCMYGGVTLHNNR 118
DB 98 -----KGEKVDLNTKRTKKSQHTSEGYTHFQISGVT-----NTEK 133
QY 119 LTBEKKVPINLMDGKOTTPIDIKVTSKKEVTVOELDQARHYLHGKFLY-NSDSFG 177
DB 134 LPTPIELPKVKGKDSPLKYGP-KFDKKQLAISTLDFEIRHQLTQHLVRSSDKTGG 192
QY 178 --KVORGLIVFHSSEGSTVSYDL---FDAQGYPTLLFIYRDNKNTINSE 222
DB 193 YWKIT-----MNDGSTYQSLSKKFEYNTKPPINI---DEIKTIEAE 232
RESULT 15
DPOL_METUA STANDARD; PRT; 1634 AA.
AC Q58295;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE DNA polymerase (EC 2.7.7.7) [Contains: Mja pol-1 intein; Mja pol-2
DE intein].
DE GN POL OR M70885.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OC NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrman J.L., Nguyen D.,
RA Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073 (1996).
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate

```

CC + {DNA} (N).
CC -!- PTM: This protein undergoes a protein self splicing that involves
CC a post-translational excision of the intervening region (intron)
CC followed by peptide ligation (Potential).
CC -!- SIMILARITY: Belongs to the DNA polymerase type-B family.
CC -----
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CC -----
CC EMBL; U67532; AAB98889.1; -.
CC DR HSP; P56689; ITGO.
CC DR TIGR; MJ0885; -.
CC DR InterPro; IPR006172; DNA_pol_B.
CC DR InterPro; IPR006134; DNA_pol_B_dom.
CC DR InterPro; IPR006133; DNA_pol_B_exo.
CC DR InterPro; IPR003587; Hedgehog_hint_N.
CC DR InterPro; IPR003586; Hedgehog_hint_C.
CC DR InterPro; IPR006142; INTIN.
CC DR InterPro; IPR004042; Intein_endonuc.
CC DR InterPro; IPR006141; Intein_S.
CC DR InterPro; IPR004578; Pol2.
CC DR Pfam; PF00136; DNA_pol_B_3.
CC DR Pfam; PF03104; DNA_pol_B_exo; 1.
CC DR PRINTS; PR00379; INTEIN.
CC DR SMART; SM00305; HintC; 2.
CC DR SMART; SM00306; HintN; 2.
CC DR SMART; SM00486; POLBc; 1.
CC DR TIGRams; TIGR01443; intein_Cterm; 2.
CC DR TIGRams; TIGR01445; intein_Nterm; 2.
CC DR TIGRams; TIGR00592; pol2; 1.
CC DR PROSITE; PS00116; DNA_POLYMERASE_B; 1.
CC DR PROSITE; PS00818; INTEIN_CTER; 2.
CC DR PROSITE; PS00819; INTEIN_ENDONUCLEASE; 2.
CC DR PROSITE; PS00817; INTEIN_NTER; 2.
CC DR Transferrase; DNA-directed DNA polymerase; DNA replication;
CC DNA-binding; Autocatalytic cleavage; Protein splicing;
CC Complete proteome.
CC CHAIN 1 425 POL, 1ST PART (POTENTIAL).
CC FT CHAIN 426 794 MJA POL-1 INTEIN (POTENTIAL).
CC FT CHAIN 795 882 POL, 2ND PART (POTENTIAL).
CC FT CHAIN 883 1358 MJA POL-2 INTEIN (POTENTIAL).
CC FT CHAIN 1359 1634 POL, 3RD PART (POTENTIAL).
CC SQ SEQUENCE 1634 AA; 191708 MW; 84A1FAFAB1F97DDD CRC64;

Query Match 8.2%; Score 101; DB 1; Length 1634;
Best Local Similarity 22.9%; Pred. No. 1.9;
Matches 53; Conservative 33; Mismatches 79; Indels 66; Gaps 10;

QY 12 LRKSELOGTALGNLQIYVYNEKATENKESDDQFLENTLIFKGFTHCPHYNDLLVDL 71
DB 614 VREKTKTAITLCAKADKDYLYKTEELKNK---KYLPAAIL-RGFEGDGVNTRRAV 669
QY 72 GSKDANKYKGGK-----VDLYGAYGYCAGGTENKTKACMYGGVTLHDNNRLTEKKVP 126
DB 670 VVNGGINNVYDKIFIASLDRDLGKISF-----YTVSEERGGKLRKV 713
QY 127 INWIGKQTTVPIDKVTES-----KKEVTVQELDQARHYLHGKFLGNSD----- 173
DB 714 IEIFSKG-----DLIKFSILSIFSRKNNLLNEIRQKTLXIGDYGFDLDDVCVS 766
QY 174 --SFGGKV-----QRGLIVFHSSEGS-TVSYDLFDAQGYPDTL 209
DB 767 LESYKGEVDLTLEGRPYFANGILHNSLYSIISVNI-----SPDTL 811

RESULT 16
R19E_THEVO STANDARD; PRT; 150 AA.
ID_R19E_THEVO

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AC Q97CU4;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S19E.
GN RPS19E OR TV0007 OR TVG0008143.
OS Thermoplasma volcanium.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=50339;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GSS1 / DSM 4299 / JCM 9571;
RX MEDLINE=20570466; PubMed=1121031;
RA Kawashima T., Amano N., Koike H., Makino S.-I., Higuchi S.,
RA Kawashima-Ohya Y., Watanabe K., Yamazaki M., Kanehori K., Kawamoto T.,
RA Nunoshiba T., Yamamoto Y., Aramaki H., Makino K., Suzuki M.;
RT "Archaeal adaptation to higher temperatures revealed by genomic
RT sequence of Thermoplasma volcanium";
RL Proc. Natl. Acad. Sci. U.S.A. 97:14257-14262(2000).
CC -!- SIMILARITY: Belongs to the S19E family of ribosomal proteins.
CC -----
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CC -----
CC EMBL; AP000991; BAB59149.1; -.
CC DR InterPro; IPR001266; Ribosomal_S19E.
CC DR Pfam; PF01090; Ribosomal_S19e_1.
CC DR ProDom; PD003854; Ribosomal_S19E; 1.
CC DR PROSITE; PS00628; RIBOSOMAL_S19E; FALSE_NEG.
CC KW Ribosomal protein; Complete proteome.
CC SQ SEQUENCE 150 AA; 17063 MW; FD5881CF684EB415 CRC64;

Query Match 7.7%; Score 95.5; DB 1; Length 150;
Best Local Similarity 29.5%; Pred. No. 0.31;
Matches 23; Conservative 17; Mismatches 37; Indels 1; Gaps 1;

QY 116 NNRLETEKKVPINLWIDGKQTTVPIDKVTESKEVTVQELDQARHYLHGKFLGYN-SDS 174
DB 17 SGKLKEEKIKEPNVKFKVTGSKPKPLQDDWIYVRAASMLRKLKLYINGYLGRMSSE 76
QY 175 FGGKVQEGGLIVFHSSEGS 192
DB 77 YGGKVDGRGSKRYHAAGS 94

RESULT 17
R19E_THEAC STANDARD; PRT; 150 AA.
ID_R19E_THEAC
AC Q9EHZ1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 30S ribosomal protein S19E.
GN RPS19E OR TA0050.
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=2303;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 1728;
RX MEDLINE=20479972; PubMed=11029001;
RA Ruepp A., Graml W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermoacidophilic scavenger Thermoplasma
RT acidophilum";
RL Nature 407:508-513(2000).

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DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical zinc protease ymxG (EC 3.4.99.-) (ORFP).
GN ymxG OR BSU16710
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RC STRAIN=168 / 8G5;
RA Bolhuis A., Vehmancpera J., Venema G., Bron S., van Dijk J.M.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Boursier R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denzot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Chim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holtsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karimata D., Kashara Y., Kiehr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardiniois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portecelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tossato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis".
RL Nature 390:249-256(1997).
RN [3]
RP SEQUENCE OF 30-409 FROM N.A.
RC STRAIN=168;
RX MEDLINE=93352813; PubMed=8098035;
RA Chen N.-Y., Jiang S.-Q., Klein D.A., Paulus H.;
RT "Organization and nucleotide sequence of the Bacillus subtilis
RT diaminopimelate operon, a cluster of genes encoding the first three
RT enzymes of diaminopimelate synthesis and dipicolinate synthase".
RL J. Biol. Chem. 268:9448-9465(1993).
CC -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
CC -!- SIMILARITY: Belongs to peptidase family M16.
CC
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CC
CC EMBL; U27560; AAA73485.1; -
DR EMBL; Z99112; CAB13544.1; -
DR EMBL; L08471; AAA22379.1; -
DR PIR; E69886; E69886.
DR MEROPS; M16.UPS; -

DR Subtilist; BG10779; ymxG.
DR InterPro; IPR001431; Peptidase_M16.
DR InterPro; IPR007863; Peptidase_M16_C.
DR Pfam; PF00675; Peptidase_M16; 1.
DR Pfam; PF05193; Peptidase_M16_C; 1.
DR PROSITE; PS00143; INSULINASE; 1.
KM Hypothetical protein; Hydrolase; Metalloprotease; Zinc;
KW Complete Proteome.
FT METAL 46 46 ZINC (BY SIMILARITY).
FT ACT_SITE 49 49 BY SIMILARITY.
FT METAL 50 50 ZINC (BY SIMILARITY).
FT METAL 126 126 ZINC (BY SIMILARITY).
FT CONFLICT 270 271 FO -> LE (IN REF. 3).
FT CONFLICT 360 360 E -> Q (IN REF. 3).
SQ SEQUENCE 409 AA; 45963 MW; EA9CF00EBD57563 CRC64;

Query Match 7.1%; Score 87.5; DB 1; Length 409;
Best Local Similarity 22.7%; Pred. No. 5;
Matches 55; Conservative 43; Mismatches 79; Indels 65; Gaps 15;

QY 10 KDLRK---XSELGQTALGNLKQIYYNKAITENKESDDQPLENTLLPKGFTGHWYND 66
DB 198 KDKVWFGSYEAKGKATG-LERPEFTEK-LTRKKEIQAH--CLGFKGLEVGHERIYD 253
QY 67 LLV---DLGSKDQATNKY-----KGRKVDLYGAYGYQCAGTTPNKTCMYGCVTLHDNN 117
DB 254 LIVLNNVLGGSSRLFDVREDKGLAYSIVSYHSSYEDSG-----MLTIYGGTGANQLQ 308
QY 118 RLTEKKVPINLWDGQTVTDIKVTSKKE-VTVQELDLQARHVLHGKFGYKNSDSFG 176
DB 309 QLSE-----TIQ-ETLATLRGDTISKELE-NSKEQMKGSL-MLSLESTN 350
QY 177 GKVORG-----LIVFHSSEGSTVSYDLFPAQGYPTLRIYRDNKNKTINSENLH-IALYL 230
DB 351 SKMSRNGKELLGKHK-----TLDEIINELNVLNLRVNGLARGL 391
QY 231 YT 232
DB 392 FT 393

RESULT 20
MDR_PLAFF STANDARD; PRT; 1419 AA.
AC P13568;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Multidrug resistance protein (Chloroquine resistance protein).
GN MDR1.
OS Plasmodium falciparum (isolate FC27 / Papua New Guinea).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5837;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89288297; PubMed=2701941;
RA Foote S.J., Thompson J.K., Cowman A.F., Kemp D.J.;
RT "Amplification of the multidrug resistance gene in some chloroquine-
RT resistant isolates of P. falciparum".
RL Cell 57:921-930(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92017800; PubMed=1922044;
RA Triglia T., Foote S.J., Kemp D.J., Cowman A.F.;
RT "Amplification of the multidrug resistance gene pfmdr1 in Plasmodium
RT falciparum has arisen as multiple independent events".
RL Mol. Cell. Biol. 11:5244-5250(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93149200; PubMed=8426608;
RA Wilson C.M., Volkman S.K., Thaitong S., Martin R.K., Kyle D.E.,
RA Milhous W.K., Wirth D.F.;
RT "Amplification of pfmdr1 associated with mefloquine and halofantrine

resistance in Plasmodium falciparum from Thailand.";
RL Mol. Biochem. Parasitol. 57:151-160(1993).
CC -!- FUNCTION: Energy-dependent efflux pump responsible for decreased
CC drug accumulation in multidrug-resistant cells.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- MISCELLANEOUS: P.falciparum resistant to the drug chloroquine
CC have multiple copies of the gene coding for MDR.
CC -!- SIMILARITY: Belongs to the ABC transporter family. MDR subfamily.
CC -----
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CC -----
DR EMBL; M29154; AAA29646.1; -;
DR EMBL; X56851; CAA40180.1; -;
DR EMBL; S53996; AAD13870.1; -;
DR PIR; S18204; DVZQF.
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR001140; ABC_TM_transpt.
DR InterPro; IPR003439; ABC_Transporter.
DR Pfam; PF00664; ABC_membrane; 2.
DR Pfam; PF00005; ABC_tran; 2.
DR ProDom; PD000006; ABC_transporter; 2.
DR SMART; SM00382; AAA; 2.
DR PROSITE; PS00929; ABC_TM1F; 2.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; 2.
DR PROSITE; PS00893; ABC_TRANSPORTER_2; 2.
KW ATP-binding; Glycoprotein; Transmembrane; Transport; Repeat.
FT DOMAIN 1 55
FT TRANSMEM 56 82
FT TRANSMEM 91 116
FT TRANSMEM 160 188
FT TRANSMEM 194 212
FT TRANSMEM 279 298
FT TRANSMEM 314 338
FT TRANSMEM 339 788
FT DOMAIN 789 807
FT TRANSMEM 825 846
FT TRANSMEM 908 928
FT TRANSMEM 1028 1048
FT TRANSMEM 1063 1083
FT DOMAIN 1084 1419
FT DOMAIN 1419 1619
FT NP_BIND 413 420
FT NP_BIND 1161 1168
FT REPEAT 1 721
FT REPEAT 722 1419
FT CARBOHYD 228 228
FT CARBOHYD 258 258
FT CARBOHYD 964 964
SQ SEQUENCE 1419 AA; 162251 MW; 0F96C7C1850B33D0 CRC64;

Query Match 7.0%; Score 87; DB 1; Length 1419;
Best Local Similarity 21.8%; Pred. No. 24;
Matches 65; Conservative 37; Mismatches 112; Indels 84; Gaps 15;

QY 3 KSEINERKDD-----LRKSELOQTALGNLKOI-----YYYN--EKAIT 38
DB 955 KSKIEKENSSGVFAFSSDDEMFKDPFLIQEAFYNMHTVINYGLDYFCNLIEKAID 1014

QY 39 -ENKESDDQFLENTLLFKGFTGHP-----WYNLLVDLGS-----KCA-----T 77
DB 1015 YKNGQKRIIVNAALW-GFQSQAQLFINSFAYWFGSLIKRGFTLLVDPMKSLFTFTFT 1073

QY 78 NKYGGKVDLYG-----AYGYQCA-----GGTPNKTCMYGGVTLHD--NN 117
DB 1074 GSYAGKLSLKGSDENAKLSPEKYPLMIRKSNIDVRDGDGIRINKNLKGVKIDVNF 1133

QY 118 RLTEKKVPI-----NLWIDGQTTVPIDKVKTSKK---EVTVQLDLQARHYL-----HGK 166

Db 1134 RVISRENVPIYKNSLPTCDSKKTAIVGTSGKSTFVNLRLRFDLKNHILKNDMTN 1193
QY 167 FGLYNSDSFGGKVGQRLIVFHSSEGSTVSYDLDFAQGGYFDLLIYRNKNTINSEN 224
DB 1194 FQDYQNNNNNSLVKNNVFNFSQSGSAEDYTVFNNGE-----ILLDDINICDYNL 1244

RESULT 21
YCX9 CHLRE STANDARD; PRT; 2971 AA.
AC Q32065; Q95635;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical 341.7 kDa protein in psbd-psbC intergenic region
DE (ORF2971) (ORF).
OS Chlamydomonas reinhardtii.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
OC Chlamydomonadaceae; Chlamydomonas.
OX NCBI_TaxID=3055;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=137C / CC-125;
RA Watson A.T., Purton S.;
RT "Unidentified open reading frame ORF2971 (ORF) from the chloroplast
RT genome of Chlamydomonas reinhardtii.";
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 2635-2971 FROM N.A.
RC STRAIN=137C / CC-125;
RX MEDLINE=89305500; PubMed=2663467;
RA Rochaix J.D., Kuchka M., Mayfield S., Schirmer Rahire M.,
RA Girard Bascou J., Bennis P.;
RT "Nuclear and chloroplast mutations affect the synthesis or stability
RT of the chloroplast psbc gene product in chlamydomonas reinhardtii.";
RL EMBL J. 8:1013-1021(1989).
RN [3]
RP COMPLETE PLASTID GENOME.
RX MEDLINE=22305394; PubMed=12417694;
RA Maul J.E., Lilly J.W., Cui L., dePamphilis C.W., Miller W.,
RA Harris E.H., Stern D.B.;
RT "The Chlamydomonas reinhardtii plastid chromosome: islands of genes in
RT a sea of repeats.";
RL Plant Cell 14:2659-2679(2002).
CC -----
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CC -----
DR EMBL; U62943; AAB05800.1; -;
DR EMBL; X13879; CAA32083.1; -;
DR EMBL; BX000554; DAA00965.1; -;
DR InterPro; IPR003959; AAA_ATPase_cent.
DR Pfam; PF00004; AAA; 1.
KW Chloroplast; Hypothetical protein.
SQ SEQUENCE 2971 AA; 341663 MW; 3BE294AF2248348A CRC64;

Query Match 7.0%; Score 86.5; DB 1; Length 2971;
Best Local Similarity 21.5%; Pred. No. 66;
Matches 47; Conservative 34; Mismatches 65; Indels 73; Gaps 9;

QY 4 SEINEKDLRKSELOQT-ALGNLKOIYYYNKAITENKESDDQFLENTLLFKGFTGHP 62
DB 2453 SKKLKELNVLKSLGNGTVSQGNVQLGVFAQIVNKQKSLQQLPNS-----2501

QY 63 WYNLLVDLGSKDANKYKGVKVDLYGAYGYGCCAGGTENKTCMYGGVTLHD--NNRLT 120

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Db 2502 -----KKSFKKXKDKALIYEV-----GKFLVNYFLNNQLT 2533
Qy 121 EKKVPINLWIDGKQTTVPIDKVKTSKEVTV---QELDLQARHYLHGKFGLYNSDS--- 174
Db 2534 QSSIIDKPSVNTKQT-----NDITFGNDLFLNLTINYL-----SLYNSKNKIL 2578
Qy 175 -----FGKQVORGL-----IVFHSBEGSVSVSYDLFDAQG 203
Db 2579 LQMLIFGGKISQLSSKNLVKSLKQASINSYWEESG 2617

RESULT 22
LACB_STAEP STANDARD; PRT; 171 AA.
AC Q8CRJ3;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DE Galactose-6-phosphate isomerase lacB subunit (EC 5.3.1.26).
GN LACB OR SE1786.
OS Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12228;
RA Zhang Y.-Q., Ren S.-X., Li H.-L., Wang Y.-X., Fu G., Yang J.,
  Qian Z.-O., Miao Y.-G., Wang W.-Y., Chen R.-S., Shen Y., Chen Z.,
  Yuan Z.-H., Zhao G.-P., Qu D., Danchin A., Wen Y.-M.;
  Genome-based analysis of virulence genes in a non-biofilm-forming
  RT Staphylococcus epidermidis strain (ATCC 12228).;
  RL Mol. Microbiol. 49:1577-1593 (2003).
CC -!- CATALYTIC ACTIVITY: D-galactose 6-phosphate = D-tagatose 6-
  phosphate.
CC -!- PATHWAY: Tagatose 6-phosphate pathway of lactose catabolism.
CC -!- SUBUNIT: Heteromultimeric protein consisting of lacA and lacB.
CC
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CC
CC EMBL; AEO16750; AAC05427.1; -.
CC InterPro; IPR003500; Rib/Gal isomerase.
CC Pfam; PF02502; LacAB rp18; 1.
CC TIGRfam; TIGR00689; rp18 lacA lacB; 1.
CC Lactose metabolism; isomerase; Complete proteome.
CC SQ SEQUENCE 171 AA; 18903 MW; 0CF3B0A59420B477 CRC64;

Query Match 6.9%; Score 86; DB 1; Length 171;
Best Local Similarity 23.1%; Pred. No. 2.3;
Matches 45; Conservative 28; Mismatches 56; Indels 66; Gaps 11;

Qy 37 ITENKESDQFLNTLLFKGFTGHPWYNDLLVDLGSKDATNKYKGVKVDLYGAYGYQC 96
Db 11 VTDTKMEVSQHLKS-----QGHE-----VIDGVTYDFTTH-----YPIYKGVKGVSKV 53
Qy 97 AGGTENKTKCMYV-GVTLHNNRLTBEKVPINLWIDGKQTTVPIDKVKTSKEVTVQ 153
Db 54 ASGEADLVGVCIGTGVGISN-----AANKVP-----GVRTALVRDMTSALYSKEELNA- 101
Qy 154 ELDLQARHYLHGKFGLYNSDSFGKQVORGLIVFHSBEGSVSYDLFDA--QQQYPTDLR 211
Db 102 -----NVVSFGKGVAGELFTF-----DIVDAFIEAEYKPT--- 131
Qy 212 IYRDNKNTINSENLIH 226
Db 132 --EENKLIAKINHL 144

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RESULT 23
PFPA_RICCO STANDARD; PRT; 617 AA.
AC Q41140;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Pyrophosphate-fructose 6-phosphate 1-phosphotransferase alpha subunit
  (EC 2.7.1.90) (PFP) (6-phosphofructokinase, pyrophosphate dependent)
DE (Pyrophosphate-dependent 6-phosphofructose-1-kinase) (PPI-PFK).
GN PFP-ALPHA.
OS Ricinus communis (Castor bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
  OC eurosids I; Malpighiales; Euphorbiales; Acalyphoideae; Acalyphaceae;
  OC Ricinus.
OX NCBI_TaxID=3988;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=95137384; PubMed=7835697;
RA Todd J.F., Blakeley S.D., Dennis D.T.;
  "Structure of the genes encoding the alpha- and beta-subunits of
  RT castor pyrophosphate-dependent phosphofructokinase.";
  RL Gene 152:181-186 (1995).
CC -!- FUNCTION: The alpha subunit may be involved in the regulation of
  PFP by Fru-2,6-P (By similarity).
CC -!- CATALYTIC ACTIVITY: Diphosphate + D-fructose 6-phosphate =
  phosphate + D-fructose 1,6-bisphosphate.
CC -!- SUBUNIT: Tetramer of two alpha and two beta chains (By
  similarity).
CC -!- MISCELLANEOUS: The active site might be on the beta subunit.
CC -!- SIMILARITY: HIGH, TO POTATO PYROPHOSPHATE--FRUCTOSE 6-PHOSPHATE 1-
  PHOSPHOTRANSFERASE ALPHA SUBUNIT.
CC -!- SIMILARITY: TO OTHER PLANT ALPHA SUBUNITS AND ALSO, TO THE
  BETA SUBUNITS.
CC
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CC
CC EMBL; Z32849; CAA83682.1; -.
CC PIR; T10102; T10102.
CC InterPro; IPR000023; Ppfruckinase.
CC Pfam; PF00365; PFK; 1.
CC ProDom; PD000707; Ppfruckinase; 1.
CC Transferase; Kinase; Allosteric enzyme.
CC SQ SEQUENCE 617 AA; 67360 MW; 1C9B2A0AF11FF3F0 CRC64;

Query Match 6.9%; Score 85; DB 1; Length 617;
Best Local Similarity 30.2%; Pred. No. 13;
Matches 26; Conservative 9; Mismatches 35; Indels 16; Gaps 3;

Qy 74 KDATNKYKGVKVDLYGAYGYQCAGGTENKTKCMYGVTV-----LHNNRLTEE 122
Db 412 REGT--YKGRKFNALCHFFGQARGSLPSKFDGCDYAYVLGHICHYHVAAGLNGYMATATN 469
Qy 123 KKVPINLWIDGKQTTVPIDKVKTSKK 148
Db 470 LKQPVNKRRCG---AAPIAAMTVKR 492

RESULT 24
TYCC_BREPA STANDARD; PRT; 6486 AA.
AC O30409;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)

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Tyrosine synthase III [Includes: ATP-dependent asparagine adenylase (AsnA) (Asparagine activase); ATP-dependent glutamine adenylase (GlnA) (Glutamine activase); ATP-dependent tyrosine adenylase (TyrA) (Tyrosine activase); ATP-dependent valine adenylase (ValA) (Valine activase); ATP-dependent ornithine adenylase (OrnA) (Ornithine activase); ATP-dependent leucine adenylase (LeuA) (Leucine activase)].

GN TYCC.

OS Brevibacillus parabravis.

OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Brevibacillus.

OX NCBI_TaxID=54914;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 8185 / IAM 1031 / IFO 3331 / NCD0 717 / NCIB 8598;

RX MEDLINE=98012987; PubMed=9352938;

RA Mootz H.D., Marahiel M.A.;

RT "The tyrosine biosynthesis operon of Bacillus brevis: complete nucleotide sequence and biochemical characterization of functional internal adenylation domains".

RI J. Bacteriol. 179:6843-6850(1997).

CC -!- FUNCTION: INCORPORATES SIX AMINO ACIDS. (FOR TYROCIDINE A, ASN, GLN, TYR, VAL, ORN, AND LEU) IN THEIR L-CONFIGURATION INTO THE PEPTIDE PRODUCT.

CC -!- COFACTOR: Contains 6 covalently bound phosphopantetheines (By similarity).

CC -!- PATHWAY: Cyclic peptide antibiotic tyrocidine biosynthesis.

CC -!- SUBUNIT: LARGE MULTIMERIC COMPLEX OF TYCA, TYCB AND TYCC.

CC -!- DOMAIN: CONSISTS OF SIX MODULES, AND HARBOURS A PUTATIVE THIOESTERASE DOMAIN AT ITS C-TERMINAL END. EACH MODULE INCORPORATES ONE AMINO ACID INTO THE PEPTIDE PRODUCT AND CAN BE FURTHER SUBDIVIDED INTO DOMAINS RESPONSIBLE FOR SUBSTRATE ADENYLATION, THIOLEATION, CONDENSATION (NOT FOR THE INITIATION MODULE), AND EPIMERIZATION (OPTIONAL), AND N METHYLATION (OPTIONAL).

CC -!- MISCELLANEOUS: TYROCIDINE IS A MIXTURE OF FOUR CYCLIC DECAPEPTIDES, TYROCIDINE A (D-PHE-PRO-PHE-D-PHE-ASN-GLN-TYR-VAL-ORN-LEU), B, C, AND D, IN WHICH PHE, AT POSITIONS 3, 4, AND TYR RESIDUES ARE GRADUALLY REPLACED BY TRP, DEPENDING ON THE RELATIVE CONCENTRATIONS OF THESE AMINO ACIDS IN THE GROWTH MEDIUM.

CC -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme family.

CC -!- SIMILARITY: Contains 6 acyl carrier domains.

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EMBL; AF004835; AAC45930.1; --

PDB; 1DNY; 17-MAY-00.

DR InterPro; IPR000873; AMP-bind.

DR InterPro; IPR001242; Condensatn.

DR InterPro; IPR006163; PP bind.

DR InterPro; IPR006162; Ppanine S.

DR InterPro; IPR000379; Ser setrs.

DR InterPro; IPR001031; Thioesterase.

DR Pfam; PF00501; AMP-binding; 6.

DR Pfam; PF00668; Condensation; 6.

DR Pfam; PF00550; pp-binding; 6.

DR Pfam; PF00975; Thioesterase; 1.

DR PRINTS; PR00154; AMPBINDING.

DR PROSITE; PS00012; PHOSPHOPANTHETHEINE; 6.

DR PROSITE; PS00455; AMP BINDING; 6.

DR PROSITE; PS00075; ACP_DOMAIN; 6.

KW Ligase; Antibiotic biosynthesis; Phosphopantetheine; Multifunctional enzyme; Repeat; 3D-structure.

KW REPEAT 466 1038 DOMAIN 1 (ASPARAGINE-ACTIVATING).

FT REPEAT 1521 2070 DOMAIN 2 (GLUTAMINE-ACTIVATING).

FT REPEAT 2536 3113 DOMAIN 3 (TYROSINE-ACTIVATING).

FT REPEAT 3590 4149 DOMAIN 4 (VALINE-ACTIVATING).

FT REPEAT 4606 5203 DOMAIN 5 (ORNITHINE-ACTIVATING).

FT REPEAT 5658 6245 DOMAIN 6 (LEUCINE-ACTIVATING).

FT DOMAIN 970 1037 ACYL CARRIER (ACP) 1.

FT DOMAIN 2007 2074 ACYL CARRIER (ACP) 2.

FT DOMAIN 3045 3112 ACYL CARRIER (ACP) 3.

FT DOMAIN 4080 4147 ACYL CARRIER (ACP) 4.

FT DOMAIN 5124 5191 ACYL CARRIER (ACP) 5.

FT DOMAIN 6167 6234 ACYL CARRIER (ACP) 6.

FT BINDING 1000 1000 PHOSPHOPANTHETHEINE (BY SIMILARITY).

FT BINDING 2037 2037 PHOSPHOPANTHETHEINE (BY SIMILARITY).

FT BINDING 3075 3075 PHOSPHOPANTHETHEINE (BY SIMILARITY).

FT BINDING 4110 4110 PHOSPHOPANTHETHEINE (BY SIMILARITY).

FT BINDING 5154 5154 PHOSPHOPANTHETHEINE (BY SIMILARITY).

FT BINDING 6197 6197 PHOSPHOPANTHETHEINE (BY SIMILARITY).

SQ SEQUENCE 6486 AA; 724011 MW; 4934900AF07DF786 CRC64;

Query Match 6.9%; Score 85; DB 1; Length 6486;

Best Local Similarity 20.5%; Pred. No. 2,2e-02;

Matches 50; Conservative 42; Mismatches 76; Indels 76; Gaps 12;

QY 16 SEIQGTALGNLKOIY-----YNEKAITENKESDDQFLENTLLFKGFTGH--PMY 64

DB 789 ASMQPVPVSGSLGEMVIAGDVGKVFNRPELTKEKFDINPFPGTKMVR---TGDLAKWL 845

QY 65 NDLLVD-LGSKDATNKYKGGKVDLYGAYGYOCAGTGNKTCMYGVTLDHNNRLTEEK 123

DB 846 PDGNEYAGRMVYQVKIRHRIEM-----GEI-----ETRLTQHE 880

QY 124 KVPINLWIDGKQTTVIDKVKT-----SKKEVTQVELDQARHYLHGKFGLYNSD 173

DB 881 AV-----KEAVIVKDESGQNVLYAYLVSERELTVAEL-----REFLGRTLPSYMP 928

QY 174 SP-----GGKVGRLIVFHSSEGSTVSYSYDLFDA-QCQYPTDLLRIYRDKNKTS 221

DB 929 SFPIRLAEIPLTANGKVERKKL--PKPAGAVVTGTAYAAPONEIEAKLAEIQVVLGISQ 986

QY 222 ENLH 225

DB 987 VGIIH 990

RESULT 25

PEXA_PICPA STANDARD; PRT; 419 AA.

AC Q32265;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Peroxisome assembly protein PAS7 (Peroxin-10).

GN PEX10 OR PAS7.

OS Pichia pastoris (Yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Pichia.

OX NCBI_TaxID=4922;

RN [1]

RN SEQUENCE FROM N.A.

RP MEDLINE=96026021; PubMed=7565793;

RX Kalish J.E., Theda C., Mortell J.C., Berg J.M., Gould S.J.;

RA "Formation of the peroxisome lumen is abolished by loss of Pichia pastoris Pas7p, a zinc-binding integral membrane protein of the peroxisome."

RT Peroxisome."

RT Mol. Cell. Biol. 15:6406-6419(1995).

CC -!- FUNCTION: Necessary for peroxisome assembly, essential for import of both PTS1 and PTS2 proteins, and required for the establishment of the peroxisome lumen.

CC -!- SUBCELLULAR LOCATION: Peroxisomal; membrane-associated.

CC -!- SIMILARITY: Contains 1 RING-type zinc finger.

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RC STRAIN=UAB CTIP;
 RX MEDLINE=21267165; PubMed=11353084;
 RA Chabaud I., Heilig R., Ferris S., Barbe V., Samson D., Galisson F.,
 RA Moszer I., Dybvig K., Wroblewski K., Viari A., Rocha E.P.C.,
 RA Blanchard A.;
 RT "The complete genome sequence of the murine respiratory pathogen
 RT Mycoplasma pulmonis";
 RL Nucleic Acids Res. 29:2145-2153(2001).
 CC !- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
 CC of DNA into RNA using the four ribonucleoside triphosphates as
 CC substrates.
 CC !- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC {RNA}(N).
 CC !- SUBUNIT: Homodimer. The RNAP catalytic core consists of 2 alpha, 1
 CC beta, 1 beta', and 1 omega subunit (by similarity).
 CC !- DOMAIN: The N-terminal domain is essential for RNAP assembly and
 CC basal transcription, whereas the C-terminal domain is involved in
 CC interaction with transcriptional regulators and with upstream
 CC promoter elements (by similarity).
 CC !- SIMILARITY: Belongs to the RNA polymerase alpha chain family.
 CC -----
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 CC -----
 DR EMBL; AL445565; CAC13734.1; -
 DR PIR; A99582; A99582; -
 DR MYPULIST; MYPU 5610; -
 DR HAKAP; MF_00059; -; 1.
 DR InterPro; IPR009025; Rapi1-like RNAPo.
 DR InterPro; IPR001700; RNA polA_bac_org.
 DR Pfam; PF01000; RNA pol A bac; 1.
 DR Pfam; PF03118; RNA pol A_CTD; 1.
 DR ProDom; PD001179; RNA_PoLA_bac_org; 1.
 DR SMART; SM00682; RPOD; 1.
 KW Transference; Transcription; DNA-directed RNA polymerase;
 KW Complete proteome.
 FT DOMAIN 1 246 ALPHA N-TERMINAL DOMAIN (ALPHA-NTD)
 FT (BY SIMILARITY).
 FT DOMAIN 262 333 ALPHA C-TERMINAL DOMAIN (ALPHA-CTD)
 FT (BY SIMILARITY).
 FT SEQUENCE 333 AA; 37907 MW; 7C23D7D86409604A CRC64;
 Query Match 6.8%; Score 84; DB 1; Length 333;
 Best Local Similarity 23.5%; Pred. No. 7.6;
 Matches 38; Conservative 24; Mismatches 38; Indels 62; Gaps 9;
 QY 25 NLKQIY-YNKEATENK-----ESDDQFLENTLLFKGFFTGHPWYNDLLV 69
 DB 82 NVKNIHLYDENIFEDNKIVRGVIETKNEKITSSDLKPPEN-----EI 125
 QY 70 DLGSKD---ATNKYGGKVDLYGAYY---GYQCAGGTENKACMGVTLHDNRLEET 122
 DB 126 EIVNKLEIATN--NGQKPFVWEYVPHVGRGY-----ISFDENKLLIEZ 167
 QY 123 KKVPIINWID-GKQTTV-----PIDKVTSKKEVTVOELDLQ 158
 DB 168 KVALLNSTIKRGKFLAIDSDSPVEKVKVQVEINSSSLNIE 209
 RESULT 28
 ID AMY2_DICTH STANDARD; PRT; 562 AA.
 AC P14898;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Alpha-amylase 2 (EC 3.2.1.1) (1,4-alpha-D-glucan glucanohydrolase).
 GN AMYB.

OS Dictyoglomus thermophilum.
 OC Bacteria; Dictyoglomi; Dictyoglomales; Dictyoglomaceae; Dictyoglomus.
 OX NCBI_TaxID=14;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-8.
 RC STRAIN=H-6-12; PubMed=2458257;
 RX MEDLINE=88329076; Fukusumi S., Ohshima T., Beppu T.;
 RA Horinouchi S.;
 RT "Cloning and expression in Escherichia coli of two additional amylase
 RT genes of a strictly anaerobic thermophile, Dictyoglomus thermophilum,
 RT and their nucleotide sequences with extremely low
 RT guanine-plus-cytosine contents.";
 RL Eur. J. Biochem. 176:243-253(1988).
 CC !- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
 CC linkages in oligosaccharides and polysaccharides.
 CC !- COFACTOR: Binds 1 calcium ion per subunit (Potential).
 CC !- PATHWAY: Polysaccharide degradation.
 CC !- SUBUNIT: Monomer (By similarity).
 CC !- SUBCELLULAR LOCATION: Cytoplasmic.
 CC !- MISCELLANEOUS: WHEN COMPARED TO AMYA, AMYB PRODUCED LARGER AMOUNTS
 CC OF REDUCING SUGAR.
 CC !- SIMILARITY: Belongs to family 13 of glycosyl hydrolases.
 CC -----
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 CC -----
 DR EMBL; X13199; CAA31586.1; -
 DR PIR; S01312; S01312; -
 DR InterPro; IPR006589; Alp amyl_cat_sub.
 DR InterPro; IPR006047; Alpha amyl_cat.
 DR Pfam; PF00128; alpha-amylase; 1.
 DR SMART; SM00642; Amy; 1.
 KW Carbohydrate metabolism; Hydrolase; Glycosidase; Calcium-binding;
 KW Multigene family.
 FT ACT SITE 309 309 BY SIMILARITY.
 FT ACT SITE 338 338 BY SIMILARITY.
 FT ACT SITE 404 404 BY SIMILARITY.
 FT METAL 236 236 CALCIUM (POTENTIAL).
 FT SEQUENCE 562 AA; 66999 MW; 9583342CFB7A369F CRC64;
 Query Match 6.8%; Score 84; DB 1; Length 562;
 Best Local Similarity 23.0%; Pred. No. 14;
 Matches 60; Conservative 31; Mismatches 94; Indels 76; Gaps 15;
 QY 25 NLKQIYYNEKA-----ITENKESDDQFL---ENTL---LFK---GFTGHPWN 65
 DB 317 NFWSIYYNKRSEFPETFYGEIVETPKTKYGVKFGDTLDFYLFKIRDPFGKRWS 376
 QY 66 D---LLVDLGGSKDATNKY-----KGGKVDLYGAYYGYQCAGGTENK 104
 DB 377 KEFVKMIDLEERFYGNKPKRISFLENHDSNRLFWAKDKLLRLASIFQFSI----NAI 431
 QY 105 ACMYGV-----TLHDNRLEETKKVPINLMDGKQTTVPID----KVTSSKEVT 151
 DB 432 PIYYNGQEMGCSQYRDILEGNRTLHEARLPIP-WSDDKQDKXELDFYRQLVKRSHPA 490
 QY 152 VOELDLQARHYLHGKFGLYNSD--SFGGKVQ-RGSIIVFHSSSGSVSYVDLPDAQOYDPT 208
 DB 491 LYK-----GTFIPFSDMISFIKETQESILVLINEDEK---EIFNLNGTYRDL 537
 QY 209 LL-RYRDNKNKTINSENHLIAL 228
 DB 538 FSGNIYTNLSKLGPMASALL 558
 RESULT 29
 ID RFAL_HUMAN STANDARD; PRT; 616 AA.
 RFAL_HUMAN

AC DT 01-AUG-1992 (Rel. 23, Created)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Replication protein A 70 kDa DNA-binding subunit (RP-A) (RP-A)
DE (Replication factor-A protein 1) (Single-stranded DNA-binding protein)
GN RPA1 OR RPA70 OR RPA1.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX MEDLINE=91268092; PubMed=2050703;
RA Erdlie L.F., Heyer W.-D., Kolodner R., Kelly T.J.;
RT "Type I human complement C2 deficiency. A 28-base pair gene deletion causes skipping of exon 6 during RNA splicing."
RN J. Biol. Chem. 268:2268-2268(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Uterus;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences."
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 183-420.
RX MEDLINE=97144356; PubMed=8990123;
RA Bochkarev A., Pfuetzner R.A., Edwards A.M., Frappier L.;
RT "Structure of the single-stranded-DNA-binding domain of replication protein A bound to DNA."
RN Nature 385:176-181(1997).
CC -!- FUNCTION: Absolutely required for simian virus 40 DNA replication in vitro. It participates in a very early step in initiation. RP-A is a single-stranded DNA-binding protein.
CC -!- SUBUNIT: Heterotrimer of 70, 32/30, and 14 kDa chains. The DNA-binding activity may reside exclusively on the 70 kDa subunit.
CC -!- SUBCELLULAR LOCATION: Nuclear.
CC -!- SIMILARITY: TO OTHER SPECIES RPA2/RPA2.
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CC

CC DR EMBL; M63488; AAA36584.1; --
DR EMBL; BC018126; AAH18126.1; --
DR PIR; A40457; A40457.
DR PDB; 1JMC; 15-OCT-97.
DR PDB; LEW1; 10-MAY-00.
DR PDB; IFGU; 14-FEB-01.
DR PDB; 1L10; 05-JUN-02.
DR Genew; HGNC:10289; RPA1.
DR GK; P27694; --
DR MIM; 179835; --
DR GO; GO:0005662; C:DNA replication factor A complex; TAS.
DR GO; GO:0003697; F:single-stranded DNA replication; TAS.
DR GO; GO:0006261; P:DNA dependent DNA replication; TAS.
DR GO; GO:0006310; P:DNA recombination; TAS.
DR GO; GO:0006281; P:DNA repair; TAS.
DR InterPro; IPR008994; Nucleic_acid_OB.
DR InterPro; IPR007199; Rep-A_N.
DR InterPro; IPR004591; Rpa1.
DR InterPro; IPR004385; trna_anti.
DR Pfam; PF04057; Rep-A_N; 1.
DR TIGR; TIGR00617; rpa1; 1.
DR TIGR; TIGR00617; rpa1; 1.
KW DNA replication; DNA-binding; Zinc-finger; Nuclear protein;
FT 3D-structure. 481 503 C4-TYPE (POTENTIAL).
FT ZN_FING 184 184
FT STRAND 187 189
FT HELIX 192 193
FT TURN 198 206
FT STRAND 210 213
FT STRAND 218 227
FT STRAND 232 238
FT STRAND 239 245
FT HELIX 246 248
FT TURN 251 252
FT STRAND 254 258
FT STRAND 261 264
FT STRAND 267 269
FT STRAND 276 279
FT TURN 282 283
FT STRAND 285 288
FT STRAND 302 302
FT STRAND 305 310
FT TURN 313 314
FT STRAND 316 326
FT STRAND 330 334
FT TURN 335 338
FT STRAND 339 349
FT TURN 351 352
FT STRAND 355 361
FT STRAND 362 367
FT TURN 371 372
FT STRAND 375 384
FT TURN 386 387
FT STRAND 390 392
FT STRAND 398 400
FT HELIX 406 417
FT TURN 418 419
SQ SEQUENCE 616 AA; 68138 MW; FE038F40F5886CD1 CRC64;
Query Match 6.8%; Score 84; DB 1; Length 616;
Best Local Similarity 26.5%; Pred. No. 16;
Matches 59; Conservative 28; Mismatches 66; Indels 70; Gaps 15;
QY 6 EINE-----VDLRKSKELQGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 250 EVNKVYFSGTKLKIANKQFTAVNDYEMTFNNTSVMPC--DDHLP-TVQFD--FTG 304
QY 61 HPWYNDLLVDLGSKDAFNKYKKVDLYGAYGYQCAGGTGNTACMGVGLHDNNRLT 120
DB 305 -----ID-----DLENKSKSLVDIIIGICKSYEDA-----TKITVRSNNREV 341


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CC -----
DR EMBL: AL591983; CAD00639.1; -.
DR PIR: A11394; A11394.
DR LiliList: LMO02561; -.
DR HAMAP: MF_00123; -.
DR InterPro: IPR001278; Arg tRNA-synt_1c.
DR InterPro: IPR005148; N.
DR InterPro: IPR008909; tRNA-synt_1d_C.
DR InterPro: IPR001412; tRNA-synt_1.
DR Pfam: PF03485; N-Arg, 1.
DR Pfam: PF00750; tRNA-synt_1d, 1.
DR Pfam: PF05746; tRNA-synt_1d_C, 1.
DR PRINTS: PRO1038; TRNASYNTHARG.
DR TIGRFAMs: TIGR00456; args, 1.
DR PROSITE: PS00178; AA tRNA LIGASE I, 1.
KW Aminocacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
FT SITE 134 "HIGH" REGION.
SQ SEQUENCE 556 AA; 62836 MW; A9B8C425B3997820 CRC64;

Query Match 6.7%; Score 83; DB 1; Length 556;
Best Local Similarity 20.6%; Pred. No. 17;
Matches 62; Conservative 47; Mismatches 80; Indels 112; Gaps 16;

QY 5 EBINKDKRKSELOQTALGNLKOI-YYNEKAITENKESDDQFLENTLLFKGFTHGPW 63
Db 259 EWFSETSYEENKVL-PALERLRENGTYEQDGTWLRITTFEDDKDRVLKSDGS---- 313
QY 64 YNDLLVDLGSKDATNKYK--GKKVDLGA-YGY-----OCAGGTENKTCMYGGV 111
Db 314 YYYFDPDIAYH--LNKLERGFVLIDWGADHGVIPMRRAIEALGVSP----- 361
QY 112 TLHDNNRLTEKKVPINLWDGKQTTVPIDKVTSK--KEVT-----VOELDLQARHYLH 164
Db 362 -----NQLVEIILQLVHLFEDGVQ-----VEMSKRTGKSTVMDLIEEVGLDTRYF- 408
QY 165 GKFGLYNSDF-----GKVGORGLIVFHSSEGS 192
Db 409 --FAMRSSDTHMFMDSIAKSTNDNPVYQYAHARISSILRSK-EGGLEVTKQADMS 465
QY 193 TV-----SYDLFDAQGYPTLL-----RIVRDNKNKTINSENLH 225
Db 466 LQTEAEYDLLKVLGEFADVVAEAAKRAPHRIVRYLNDLASAPHRFVNSKNVLDMDNLE 525
QY 226 I 226
Db 526 V 526

RESULT 34
RPOA_LACPL STANDARD; PRT; 314 AA.
AC Q88XW0;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE DNA-directed RNA polymerase alpha chain (EC 2.7.7.6) (RNAP alpha subunit) (transcriptase alpha chain) (RNA polymerase alpha subunit).
GN RPOA OR LP_1062.
OS Lactobacillus plantarum.
OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1590;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCIMB 8826 / WCFS1;
RX MEDLINE=22480296; PubMed=12566566;
RA Kleerebezem M., Boekhorst J., van Kranenburg R., Molenaar D.,
RA Kuipers O.P., Leer R., Turchini R., Peters S.A., Sandbrink H.M.,
RA Fiers M.W.E.J., Silekema W., Klein Lankhorst R.M., Bron P.A.,
RA Hoffer S.M., Nierop Groot M.N., Kerkhoven R., De Vries M., Ursing B.,
RA De Vos W.M., Siezen R.J.;

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RT "Complete genome sequence of Lactobacillus plantarum WCFS1.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:1990-1995(2003).
CC -!- FUNCTION: DNA-dependent RNA polymerase catalyzes the transcription
CC of DNA into RNA using the four ribonucleoside triphosphates as
CC substrates.
CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC [RNA](N).
CC -!- SUBUNIT: Homodimer. The RNAP catalytic core consists of 2 alpha, 1
CC beta, 1 beta', and 1 omega subunit (By similarity).
CC -!- DOMAIN: The N-terminal domain is essential for RNAP assembly and
CC basal transcription, whereas the C-terminal domain is involved in
CC interaction with transcriptional regulators and with upstream
CC promoter elements (By similarity).
CC -!- SIMILARITY: Belongs to the RNA polymerase alpha chain family.
CC -----
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CC -----
DR EMBL: AL935254; CAD63597.1; -.
DR HAMAP: MF_00059; -.
DR InterPro: IPR009025; RBP1-like RNapo.
DR InterPro: IPR001700; RNA_polA_bac_org.
DR Pfam: PF01000; RNA_pol_A_bac, 1.
DR Pfam: PF03118; RNA_pol_A_CTD, 1.
DR Transferase; Transcription; DNA-directed RNA polymerase;
KW Complete proteome. 1 228 ALPHA N-TERMINAL DOMAIN (ALPHA-NTD) (BY
DOMAIN SIMILARITY).
FT DOMAIN 245 314 ALPHA C-TERMINAL DOMAIN (ALPHA-CTD) (BY
FT SIMILARITY).
SQ SEQUENCE 314 AA; 34842 MW; 573B3160D42DE7DF CRC64;

Query Match 6.7%; Score 82.5; DB 1; Length 314;
Best Local Similarity 38.3%; Pred. No. 9.5;
Matches 18; Conservative 11; Mismatches 15; Indels 3; Gaps 1;

QY 119 LTBKKVPINLWDGKQTTVPIDKVTSKK---EVTVQELDLQARHY 162
Db 217 LTDLHSIFVNLTDKAKNTDWWVEKEETHKEKMLEMIEELDLVRSY 263

RESULT 35
YB70_HAEIN STANDARD; PRT; 328 AA.
AC Q57527; O05047;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical paba-like protein H1170.
GN H1170.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae

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RT Rn; Science 269:496-512 (1995).
 CC -1- SIMILARITY: TO THE C-TERMINAL OF PARA-AMINOBENZOATE SYNTHASE
 CC COMPONENT 1.
 CC -----
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 CC -----
 CC EMBL; U32797; AAC22834.1; --
 DR PIR; F64187; F64187.
 DR TIGR; H1170; --
 DR InterPro; IPR005801; Anth synth_chor.
 DR Pfam; PF00425; chorismate_bind; 1.
 DR PRINTS; PD00095; ANTSYNTHASE1.
 DR ProDom; PD00079; Anth synth_chor; 1.
 DR Hypothetical protein; Complete proteome.
 KW SEQUENCE 328 AA; 37734 MW; 1C02BCD008957B0 CRC64;
 SQ -----
 Query Match 6.7%; Score 82.5; DB 1; Length 328;
 Best Local Similarity 27.3%; Pred. No. 10; Indels 13; Gaps 3;
 Matches 24; Conservative 16; Mismatches 35; Indels 13; Gaps 3;
 QY 136 TTVPIDKVKTSKEVT---VQELDQARHYLHGKFLGNSDSFGGKVGQGLI-----V 185
 Db 237 TLLPAGSISGAPKEKTTQIIQAQKQKGYTGFIFGFDGKTLQSAVAIRFISQVDEKRY 296
 QY 186 FHSSEGSTVSVDLFDAGQYPTDILRIY 213
 Db 297 FHSGGGITH---SNAQDEVEELLEKRY 321
 RESULT 36
 BFP_STAAU STANDARD; PRT; 670 AA.
 AC P07944;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 01-NOV-1990 (Rel. 16, Last annotation update)
 DE Beta-lactam-inducible penicillin-binding protein.
 GN BFP.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87304805; PubMed=3305073;
 RA Song M.D., Wachi M., Doi M., Ishino F., Matsushashi M.;
 RT "Evolution of an inducible penicillin-target protein in methicillin-
 RL resistant Staphylococcus aureus by gene fusion."
 RL FEBS Lett. 221:167-171 (1987).
 CC -1- INDUCTION: IN THE PRESENCE OF BETA-LACTAM ANTIBIOTICS, MRSA
 CC CELLS PRODUCE THIS UNIQUE PBP IN EXCESSIVELY LARGE AMOUNTS AND
 CC CAN STILL PROLIFERATE, WHILE ALL THE NORMAL PBPS ARE INACTIVATED
 CC (REVERSIBLE SWITCHING ABILITY OF PBP FORMATION).
 CC -1- MISCELLANEOUS: PBP HAS EXTREMELY LOW AFFINITY TO PENICILLIN AND
 CC MOST OTHER BETA-LACTAM ANTIBIOTICS.
 CC -1- SIMILARITY: TWO DIFFERENT SETS OF CONSERVED SEQUENCES CONTAINING
 CC S-X-X-K FOR PENICILLIN-BINDING WERE FOUND IN MRSA PBP, THE FIRST
 CC BEING LOCATED AROUND SER-25 (HOMOLOGY WITH THE PENICILLIN-BINDING
 CC DOMAIN OF THE PENICILLINASE) AND THE SECOND AROUND SER-405 (HIGH
 CC HOMOLOGY WITH BOTH THE PUTATIVE TRANSGLYCOSYLASE (N-TERMINAL) AND
 CC TRANSPEPTIDASE (C-TERMINAL) PENICILLIN-BINDING DOMAIN OF E.COLI
 CC PBPS 2 AND 3). THE AUTHORS SUGGEST THE SER-405 RESIDUE TO BE THE
 CC PENICILLIN-BINDING SITE AND THE SEQUENCE AROUND SER-25 TO BE A
 CC RELIC OF THE EVOLUTION OF THIS DOMAIN FROM A PENICILLINASE GENE.
 CC -----
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 CC -----
 CC EMBL; Y00688; CAA68684.1; --
 DR MEROPS; S12.UNW; --
 DR InterPro; IPR007887; Meca_N.
 DR InterPro; IPR006311; PBP_dimer.
 DR InterPro; IPR001460; Transpeptidase.
 DR Pfam; PF05223; Meca_N; 1.
 DR Pfam; PF03717; PBP_dimer; 1.
 DR Pfam; PF00905; Transpeptidase; 1.
 KW Peptidoglycan synthesis; Cell division; Antibiotic resistance;
 KW Cell wall.
 FT BINDING 25 25 PENICILLIN (PROBABLE).
 FT BINDING 405 405 PENICILLIN (PROBABLE).
 SQ SEQUENCE 670 AA; 76463 MW; 2DAA414D35DA993A CRC64;
 Query Match 6.7%; Score 82.5; DB 1; Length 670;
 Best Local Similarity 20.3%; Pred. No. 24;
 Matches 64; Conservative 44; Mismatches 88; Indels 119; Gaps 15;
 QY 7 INEKDLRKKSELOG-----TALGNLKOIYYNEK-----AITE 39
 Db 259 INSELKQK-EYKGYKDDAVIGKKGLEKLYKGLQHEGGRVTVIRVDNSNTIAHTLIE 317
 QY 40 NKESDDQPLENTLFGKFFTHGHPWYNDLLVDLGSKDATNKYKGGKVDL-----YGAYGY 94
 Db 318 KKKDKGDIQITDAK---VQKSIYNNKNDYSGSTAIHQTGELLALVSTPSVDVY--- 371
 QY 95 QCAGTNPNTACTMGVYVLDHNNELTEKKVP-INLWIDGKQTVP--IDKVTSKKEVT 151
 Db 372 -----PFMY-GMSNEEYKLTEDKKEPLNKF---QITTPSGTQKILTAMIGLN 417
 QY 152 VOELDQARHYLHGKFLGNSDSFG-----177
 Db 418 NKTLDKTSYKIDGK-GWQDKKSGGYNVTRYEVVNGNIDLKQAISSDNIFARVALEL 476
 QY 178 ---KVQRGLIVFHSSEGSTVSVDLFDAG-----GQ-----YPTDILRI 212
 Db 477 GSKKFEKGMKGLGVGEDIPSDYPYNAQISKNLDBEILLADSGYGGGEILINPVQILSI 536
 QY 213 Y---RDNKTINSENI 224
 Db 537 YSALENNGNINAPHL 551
 RESULT 37
 TOP2_CAEEL
 ID TOP2_CAEEL STANDARD; PRT; 1520 AA.
 AC Q23670; Q27509;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Probable DNA topoisomerase II (EC 5.99.1.3).
 GN K12D12.1.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
 OC Rhabditidae; Peloderae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Swinburne J.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Coles L.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Control of topological states of DNA by transient

DE Hypothetical protein MPN042 (B01_orf672) .
 GN MEN042 OR MP112.
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2104;
 [i]
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29342 / M129;
 RX MEDLINE=97105895; PubMed=8948633;
 RA Hammeleirich R., Halbert H., Flagens H., Pirkel E., Li B.-C.,
 RT Herrmann R.;
 RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
 RL pneumoniae";
 RL Nucleic Acids Res. 24:4420-4449(1996).
 CC -!- SIMILARITY: BELONGS TO THE MG032 / MG096 / MG288 FAMILY.

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CC EMBL; AE000013; AAB95760.1; -.
CC PIR; S73438; S73438.
CC InterPro; IPR004306; MG032/096/288_1.
CC InterPro; IPR004319; MG032/096/288_2.
CC Pfam; PF03072; DUF237; 1.
CC Pfam; PF03086; DUF240; 1.
CC ProDom; PD004834; MG032/096/288_2; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 672 AA; 77588 MW; 1A7A593003ADB866 CRC64;

```

387 TN-----NDLRRLKLGTYTKEDNVTBTRAGLFPALFVSGFNYPAWFYITLLGWKOTTEKIFKK 442
      QY      82 GKXVDL-----YGAY-----YGYQCAGGTPNKTCAMYGQVTLHDNN 117
      Db      443 AKWQDIRDDEKFRKAFGLSPKATEKDVGKVTNPGYGY--GIYIKDS-LRDLGIAKYS 498
      QY      118 RLTEKKVPINL-----WIDGKQTTVPIDKVKTS---KKE 149
      Db      499 TVSEPKNVKVSPLGVGDNECKIWIASHNFRQNHWGAG-----EAFKYSAYRFKFD 551
      QY      150 VTVOQ-ELDLQAR-----HYLHGKFLG-YNSD-----SFGGK 178
      Db      552 VTVDYDVEVSARKWWTAFRGSIPGYWRGKFVTSYFDGVVPSWKYGHIOVRTPOYSFNKQ 611
      QY      179 VORGILIVHSSSGSVSYVDLFDACGYDPDLLRIYRDNKTINSENLH-----IAY 229
      Db      612 EQKILFVPHAIQ-----KIAAEGSNLDLINFPLDKQKDLDEFEHVHPDLTPDLVLVYL 664
      QY      230 LY 231
      Db      665 LY 666

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RESULT 39	
GLPK AQAUE	STANDARD;
ID GLPK AQAUE	PRT; 492 AA.
AC C66746;	
DT 30-MAY-2000	(Rel. 39, Created)
DT 30-MAY-2000	(Rel. 39, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glycyl kinase (EC 2.7.1.30) (ATP:glycerol 3-phosphotransferase)
DE (Glycerokinase) (GK)
GN GLPK OR AQ 434
OS Aquifex aeolicus.
OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
OX NCBI_TaxID=63363;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VF5;
RX MEDLINE=98196666; PubMed=9537320;
RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,
RA Graham D.E., Overbeek R., Shead M.A., Keller M., Aujay M., Huber R.,
RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
RA "The complete genome of the hyperthermophilic bacterium Aquifex
RT aeolicus.";
RL Nature 392:353-358(1998).
CC -1- FUNCTION: Key enzyme in the regulation of glycerol uptake and
CC metabolism.
CC -1- CATALYTIC ACTIVITY: ATP + glycerol = ADP + glycerol 3-phosphate.
CC -1- PATHWAY: Glycerol utilization; rate-limiting step.
CC -1- SIMILARITY: Belongs to the fucokinase / gluconokinase /
CC glycerokinase / xylulokinase family.
CC -----
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CC -----
CC EMBL; AB000690; AAC0670.1; -;
CC PIR; F70339; F70339.
CC HSP; P08859; IGLC.
CC HAMAP; MF 00186; -; 1.
CC InterPro; IPR000577; FGGY_kin.
CC InterPro; IPR005999; Glycerol_kin.
CC Pfam; PF00370; FGGY; 1.
CC Pfam; PF02782; FGGY_C; 1.
CC TIGRfam; TIGR01311; glycerol_kin; 1.
CC PROSITE; PS00445; FGGY_KINASES_2; 1.
CC PROSITE; PS00933; FGGY_KINASES_1; 1.
CC GlycoLip metabolism; Transferase; Kinase; ATP-binding;
CC Complete proteome.
CC NP BIND 148
CC SITE 160 ATP (PROBABLE).
CC SEQUENCE 492 AA; 55297 MW; CE9F0E8FF593B37 CRC64;
Query Match 6.5%; Score 81; DB 1; Length 492;
Best Local Similarity 26.3%; Pred. No. 22;
Matches 57; Conservative 27; Mismatches 61; Indels 72; Gaps 15;
Qy 26 LKQIYYNEKAIENKESDDQLENTLLFKGFTGHPWYNDLL-VDLGSKDANKYKGGK 84
Db 67 LKEI---NSTGNTQRE-----TVLLWDEKTRPVNAILWQDLRHDIC-----RK 110
Qy 85 VDLGAYGYQCAGGTGPNKTCACMGVYGLHDNNRLTEKKVPINLWIDGKQTTPIDKYK 144
Db 111 LSEYSEYIKENT-----GLLHPYFSASK-----VN-WI-----IENVN 143
Qy 145 TSKEVTVQELDLQARHYLHGK--FGLYNS-----DSFGKGVQKGLIVFHSSEGSTSYD- 197
Db 144 GKVKDIE-----RKVFIFGVTDVTLWNLTLGKGV-----HKTEPSNASRTL 184
Qy 198 LFDQAQ-QYDPTLLRIVRDKNKTINSE-NLHIALYLYT 232
Db 185 LFNKRLKYDELLKIFRIPKNIPLPEVNESSLEFGYT 221
RESULT 40
SYN LISIN STANDARD; PRT; 556 AA.
AC Q927T2;

DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Arginyl-tRNA synthetase (EC 6.1.1.19) (Arginine--tRNA ligase) (ARGRS).
GN ARGS OR LIN2706.
OS Listeria innocua.
OC Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
OX NCBI_TaxID=1642;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CLIP 11262 / Serovar 6a;
RX MEDLINE=21537279; PubMed=11679669;
RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
RA Baquero F., Berche P., Bloecker H., Brandt P., Chakraborty T.,
RA Charbit A., Chetouani F., Couve E., de Darvar A., Dehoux P.,
RA Domann E., Dominguez-Bernal G., Duchaud E., Durant L., Dussurget O.,
RA Entian K.-D., Feihi H., Garcia-del Portillo F., Garrido P.,
RA Gautier L., Goebel W., Gomez-Lopez N., Hain T., Hauf J., Jackson D.,
RA Jones L.-M., Kaerst U., Krest J., Kuhn M., Kunst F., Kurapkat G.,
RA Madueno E., Maitournam A., Mata Vicente J., Ng E., Medjari H.,
RA Nordsiek B., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
RA Remmel G., Rose M., Schlueter T., Simoes N., Tierrez A.,
RA Vazquez-Boland J.-A., Voss H., Wehland J., Cossart P.;
RA "Comparative genomics of Listeria species.";
RL Science 294:849-852(2001).
CC -1- CATALYTIC ACTIVITY: ATP + L-arginine + tRNA(Arg) = AMP +
CC diphosphate + L-arginyl-tRNA(Arg).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
CC -----
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CC -----
CC EMBL; AL596173; CAC97932.1; -;
CC PIR; AD1770; AD1770.
CC ListList; LIN02706; -;
CC HAMAP; MF_00123; -; 1.
CC InterPro; IPR001278; Arg_tRNA-synt_1c.
CC InterPro; IPR005148; N.
CC InterPro; IPR008909; tRNA-synt_1d_C.
CC InterPro; IPR001412; tRNA-synt_1.
CC Pfam; PF03485; N-Arg; 1.
CC Pfam; PF00750; tRNA-synt_1d; 1.
CC Pfam; PF05746; tRNA-synt_1d_C; 1.
CC PRINTS; PR01038; TRNASYNTHARG.
CC TIGRfam; TIGR00456; argS; 1.
CC PROSITE; PS00178; AA tRNA LIGASE I; 1.
CC Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
CC Complete proteome.
CC SITE 134 142 "HIGH" REGION.
CC SEQUENCE 556 AA; 62784 MW; 54CCEP31B6567056 CRC64;
Query Match 6.5%; Score 81; DB 1; Length 556;
Best Local Similarity 20.6%; Pred. No. 25;
Matches 62; Conservative 46; Mismatches 81; Indels 112; Gaps 16;
Qy 5 REINEKDLRKSEJOGTALGNLKOI-YYNEKATENKESDDQLENTLLFKGFTGHPW 63
Db 259 EWFSETSLYEENKVL-PALERLENGYIYODGATWLTTFDDDKRVLKSDGS----- 313
Qy 64 YNDLLVLDLGSKDANKYK--GKKVLYGA-YYGY-----QCAGTPTNKTCMGV 111
Db 314 YTYFLPDIAVH--LNKLERGFDVLIDIWGDHGVIPMRRAIEALGVSP----- 361
Qy 112 TLHDNNRLTEKKVPINLWIDGKQTTPIDKYKSK---KEVT---VOELDLQARHYLH 164
Db 362 -----NQLVEIILQVHLFEDGVQ-----VKMSKRTGKSVTRDLIEEVLGDLATRYF- 408

QY 165 GKFGLYNSDSF-----GKQVGRGLVPHSSEGS 192
 Db 409 --FAMRSSDTHMVPMSLAKSTSDNPNVYQYAHARSSILRSK-EGGLEVSKDANMS 465
 QY 193 TV-----SYDLFDAQQYPTLL-----RYRDNKNTINSENLH 225
 Db 466 LLETEABYDLKLVLGEFADVAEAAVKRAPHRIYRVLYNLDLATAFHFRFVNSKNVLDMDNLE 525
 QY 226 I 226
 Db 526 V 526

RESULT 41
 PFPA SOLTU
 ID PFPA SOLTU STANDARD; PRT; 616 AA.
 AC P21342;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Pyrophosphate--fructose 6-phosphate 1-phosphotransferase alpha subunit
 DE (EC 2.7.1.90) (PPP) (6-phosphofructokinase, pyrophosphate-dependent)
 DE (Pyrophosphate-dependent 6-phosphofructose-1-kinase) (Pp1-PFK).
 OS Solanum tuberosum (Potato)
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 277-295.
 RC STRAIN=cv. Kennebec;
 RX MEDLINE=91009330; PubMed=2170409;
 RA Carlisle S.M., Blakeley S.D., Hemmingsen S.M., Trevanion S.J.,
 RA Hiroyoshi T., Kruger N.J., Dennis D.T.;
 RT "Pyrophosphate-dependent phosphofructokinase. Conservation of protein
 RT sequence between the alpha- and beta-subunits and with the ATP-
 RT dependent phosphofructokinase";
 RL J. Biol. Chem. 265:18366-18371(1990).
 CC -!- FUNCTION: The alpha subunit may be involved in the regulation of
 CC FPP by Fru-2,6-P.
 CC -!- CATALYTIC ACTIVITY: Diphosphate + D-fructose 6-phosphate =
 CC phosphate + D-fructose 1,6-bisphosphate.
 CC -!- ENZYME REGULATION: Fru-2,6-P is an activator of the plant enzyme.
 CC -!- SUBUNIT: Tetramer of two alpha and two beta chains.
 CC -!- MISCELLANEOUS: The active site might be on the beta subunit.
 CC -!- SIMILARITY: TO OTHER PLANT ALPHA SUBUNITS AND ALSO, STRONG, TO THE
 CC BETA SUBUNITS.

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 EMBL; M55190; AAA63451.1; -
 DR PIR; A36094; A36094.
 DR InterPro; IPR000023; Pfruckinase.
 DR Pfam; PF00365; PFK; 1.
 DR ProDom; PD000707; Pfruckinase; 1.
 DR Transferase; Kinase; Allosteric enzyme.
 SQ SEQUENCE 616 AA; 67157 MW; 2D33EP2ADF3AA0AF CRC64;
 Query Match 6.5%; Score 81; DB 1; Length 616;
 Best Local Similarity 30.2%; Pred. No. 29;
 Matches 26; Conservative 8; Mismatches 36; Indels 16; Gaps 3;
 QY 74 KDATNKYKGVLDLYGAYGYQCAGGTPNKACMGVYT-----LHNNRUTE 122
 Db 412 KEGT--YKGFNAICHFFGQAGSPLSKFDCDYAVLVGVCHVLAAGLNGYMATITN 469

QY 123 KKVPINLWIDGKQTTVPIDKVKTSKK 148
 Db 470 LKNPANKWHCGAS---PISAMTVKR 492

RESULT 42
 MPGP PYRHO
 ID MPGP PYRHO STANDARD; PRT; 243 AA.
 AC OS6690;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mannosyl-3-phosphoglycerate phosphatase (EC 3.1.3.70) (MPGP).
 GN MNGB OR PH0926.
 OS Pyrococcus horikoshii.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus
 OX NCBI_TaxID=53953;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=OT3;
 RX MEDLINE=98344137; PubMed=9679194;
 RA Karabavayi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
 RA Yamanoto S., Sekine M., Baba S.-I., Kosugi H., Hosoyama A., Nagai Y.,
 RA Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
 RA Funahashi T., Tanaka T., Kudo Y., Yamazaki J., Kushida N., Oguchi A.,
 RA Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
 RA Masuchi Y., Shizuya H., Kikuchi H.;
 RT "Complete sequence and gene organization of the genome of a hyper-
 RT thermophilic archaeobacterium, Pyrococcus horikoshii OT3";
 RL DNA Res. 5:55-76(1998).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=21570230; PubMed=11562374;
 RA Empadinhas N., Marugg J.D., Borges N., Santos H., da Costa M.S.;
 RT "Pathway for the synthesis of mannosylglycerate in the
 RT hyperthermophilic archaeon Pyrococcus horikoshii. Biochemical and
 RT genetic characterization of key enzymes";
 RL J. Biol. Chem. 276:43580-43588(2001).
 CC -!- FUNCTION: Hydrolyzes mannosyl-3-phosphoglycerate (MPG) to form the
 CC osmolyte mannosylglycerate (MG). The enzyme is absolutely specific
 CC for MPG.
 CC -!- CATALYTIC ACTIVITY: 2(alpha-D-mannosyl)-3-phosphoglycerate + H(2)O
 CC = 2(alpha-D-mannosyl)-D-glycerate + phosphate.
 CC -!- COFACTOR: Magnesium.
 CC -!- PATHWAY: Biosynthesis of alpha-mannosylglycerate from GDP-mannose;
 CC second step.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the HAD superfamily. MPGP family.

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 EMBL; AF000004; BAA30022.1; -
 DR PIR; H71082; H71082.
 DR HAMAP; MF_00617; -; 1.
 DR InterPro; IPR006379; HAD_SF_IIB.
 DR InterPro; IPR006381; HAD_SF_Yedp.
 DR TIGRFAMs; TIGR01486; HAD-SF-IIB-Yedp; 1.
 DR TIGRFAMs; TIGR01484; HAD-SF-IIB; 1.
 KW Hydrolyase; Magnesium; Complete proteome.
 SQ SEQUENCE 243 AA; 27959 MW; FE5EE94DCAAD3636 CRC64;
 Query Match 6.5%; Score 80.5; DB 1; Length 243;
 Best Local Similarity 22.2%; Pred. No. 10;
 Matches 43; Conservative 37; Mismatches 71; Indels 43; Gaps 9;
 QY 27 KQIYYNE-----KAITENKESDDQFLENTLLFKGFF-----TGHWPYNDLLVLGSKDAT 77

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Db 46 EQEYRKELEVEVTPFISNGSA-----IPKGVFPDVKGKGVNVIIVELGIRVEK 98
QY 78 NKYKGGKVD-LYGAYGYOCAGGTNKTACMTGGVTLHNNRLTEBKVPINLWDGKQT 136
Db 99 IREELKLENIYGLKY-----YGNSTKEIEKFTGMPPELVPLAVEREYS 143
QY 137 TVPIDKVKTSKEVTYQ---ELDQARHY-LAGKGLVNSDFGKGKVGORGLIVFHSSEGS 192
Db 144 EEIFEWSRGWEVLVEGFKVTMGSRFTVHG-----NSDK--GKAAILLDFYKRLGQ 196
QY 193 TVSYDLFDAQQGYV 206
Db 197 IESYAVGDSYNDPP 210

RESULT 43
ITAL HUMAN STANDARD; PRT; 1151 AA.
AC P56139;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Integrin alpha-1 (laminin and collagen receptor) (VLA-1) (CD49a).
GN ITGAL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9315124; PubMed=8428973;
RA Briesewitz R.; Epstein M.R.; Marcantonio E.E.;
RT "Expression of native and truncated forms of the human integrin alpha
RT 1 subunit."
RL J. Biol. Chem. 268:2989-2996(1993).
CC -!- FUNCTION: INTEGRIN ALPHA-1/BETA-1 IS A RECEPTOR FOR LAMININ AND
CC COLLAGEN. IT RECOGNIZES THE PROLINE-HYDROXYLATED SEQUENCE G-F-P-G-
CC E-R IN COLLAGEN.
CC -!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. ALPHA-1
CC ASSOCIATES WITH BETA-1.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- DOMAIN: THE INTEGRIN I-DOMAIN (INSERT) IS A VWFA DOMAIN. INTEGRINS
CC WITH I-DOMAINS DO NOT UNDERGO PROTEASE CLEAVAGE.
CC -!- SIMILARITY: Belongs to the integrin alpha chain family.
CC -!- SIMILARITY: Contains 1 VWFA domain.
CC -!- SIMILARITY: Contains 7 FG-GAP repeats.
CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD49a entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd49a.htm".
DR PIR; A45226; A45226.
DR PDB; 1QC5; 17-MAY-00.
DR Genew; HGNC:6134; ITGAL.
DR MIM; 192368; -.
DR GO; GO:0008305; C:integrin complex; TAS.
DR GO; GO:0004895; F:cell adhesion receptor activity; NAS.
DR GO; GO:0005518; F:collagen binding; TAS.
DR GO; GO:0007160; P:cell-matrix adhesion; NAS.
DR InterPro; IPR000413; integrin_alpha.
DR InterPro; IPR002035; VWF_A.
DR Pfam; PF01839; FG-GAP; 3.
DR Pfam; PF00357; integrin_A; 1.
DR Pfam; PF00092; vwa; 1.
DR SMART; SM00191; Int_alpha; 5.
DR SMART; SM00327; VWF; 1.
DR PROSITE; PS00242; INTEGRIN_ALPHA; 1.
DR PROSITE; PS50234; VWFA; 1.
KW Integrin; Cell adhesion; Receptor; Glycoprotein; Transmembrane;
Repeat; Calcium; Magnesium; 3D-structure.
FT DOMAIN 1 1113 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1114 1136 POTENTIAL.
FT DOMAIN 1137 1151 CYTOPLASMIC (POTENTIAL).
FT REPEAT 16 75 FG-GAP 1.
FT REPEAT ? ? FG-GAP 2.

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DOMAIN 147 360
REPEAT 349 404
FG-GAP 3.
REPEAT 405 457
FG-GAP 4.
REPEAT 459 520
FG-GAP 5.
REPEAT 540 599
FG-GAP 6.
REPEAT 602 654
FG-GAP 7.
REPEAT 654 678
POTENTIAL.
FT CA_BIND 552 560
CA_BIND 560 570
POTENTIAL.
FT CA_BIND 622 622
GPFKR MOTIF.
FT SITE 1139 1142
BY SIMILARITY.
FT DISULFID 54 64
BY SIMILARITY.
FT DISULFID 660 669
BY SIMILARITY.
FT DISULFID 675 728
BY SIMILARITY.
FT DISULFID 780 786
BY SIMILARITY.
FT DISULFID 850 858
BY SIMILARITY.
FT DISULFID 1002 1034
BY SIMILARITY.
FT DISULFID 1037 1044
BY SIMILARITY.
FT CARBOHYD 46 46
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 72 72
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 77 77
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 84 84
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 189 189
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 289 289
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 313 313
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 374 374
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 390 390
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 432 432
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 504 504
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 671 671
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 720 720
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 752 752
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 812 812
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 855 855
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 880 880
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 887 887
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 911 911
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 938 938
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 946 946
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 980 980
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1045 1045
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1055 1055
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1074 1074
N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 1085 1085
N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 1151 AA; 127837 MW; 6B3F3C1AAAF52808 CRC64;

Query March 6.58; Score 80.5; DB 1; Length 1151;
Best Local Similarity 27.94; Pred. No. 67;
Matches 50; Conservative 23; Mismatches 63; Indels 43; Gaps 11;

QY 72 GSKDATNKYKGV---DLYGAYGYQCAGGTNKTACMYGVTL----- 113
Db 596 GGDGKTLKFTGSHGEMDLG-----DLGTDVTIGLGAALFWSRDVAWVVTWN 647
QY 114 HNNRLTEKKVPINLWDGKQT-----TVPIDKVKTSKEVTVOELDQARHYLHKFG 168
Db 648 FEPNKNVIQKK---NCHMEGKETVCINATVCFE-VKLKSKEDTIEADLOYRVTLDLRQ 703
QY 169 LYNDSDFGG---KVQRGLIVFHSSEGSTVSYDLFDAQQGYVPTLLRIYRDNKTINSEN 223
Db 704 ISRS-FFSGTQERKVRQNIIV-RKSECTKHSFYMLD-KHDFQDS-VRIITLDFNLDPEN 758

RESULT 44
DPOL PYRSD STANDARD; PRT; 1312 AA.
AC Q51334; Q51335; Q51336;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-NOV-2003 (Rel. 41, Last annotation update)
DE DNA polymerase (EC 2.7.7) (Deep vent DNA polymerase) [Contains:
DE Endonuclease PI-PspI (EC 3.1.-.-) (Psp-GDB pol intein)].
GN POL.
OS Pyrococcus sp. (strain GB-D).

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OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=69013;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 493-517.
 RX MEDLINE=94094330; PubMed=8269515;
 RA XU M.-Q., Southworth M.W., Merisha F.B., Hornstra L.J., Perler F.B.;
 RT "in vitro protein splicing of purified precursor and the
 RT identification of a branched intermediate.";
 RL Cell 75:1371-1377(1993).
 CC -!- FUNCTION: In addition to polymerase activity, this DNA polymerase
 CC exhibits 3' to 5' exonuclease activity.
 CC -!- FUNCTION: INTEIN ENCODED ENDONUCLEASES ARE THOUGHT TO MEDIATE
 CC INTEIN MOBILITY BY SITE-SPECIFIC RECOMBINATION INITIATED BY
 CC ENDONUCLEASE CLEAVAGE AT THE "HOMING SITE" IN GENE THAT LACK THE
 CC INTEIN.
 CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
 CC + [DNA] (N).
 CC -!- PTM: This protein undergoes a protein self splicing that involves
 CC a post-translational excision of the intervening region (intein)
 CC followed by peptide ligation.
 CC -!- BIOTECHNOLOGY: used in the PCR method because of its high
 CC thermostability and low error rate. Sold by New England Biolabs.
 CC -!- SIMILARITY: Belongs to the DNA polymerase type-B family.
 CC -!- SIMILARITY: In the intein section, belongs to the homing
 CC endonuclease family.
 CC -----
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 CC -----
 DR EMBL; U00707; AAA67130.1; -;
 DR EMBL; U00707; AAA67131.1; -;
 DR EMBL; U00707; AAA67132.1; -;
 DR PIR; S68593; S68593.
 DR HSP; P56689; 1TGO.
 DR REBASE; 2819; PI-Pspt.
 DR InterPro; IPR006172; DNA_pol_B.
 DR InterPro; IPR006134; DNA_pol_B_dom.
 DR InterPro; IPR006133; DNA_pol_B_exo.
 DR InterPro; IPR003587; Hedgehog_hint_N.
 DR InterPro; IPR003586; Hedgehog_hint_C.
 DR InterPro; IPR006142; INTEIN.
 DR InterPro; IPR004442; INTEIN_endonuc.
 DR InterPro; IPR006141; INTEIN_S.
 DR InterPro; IPR004578; Pol2.
 DR Pfam; PF00136; DNA_pol_B; 2.
 DR Pfam; PF03104; DNA_pol_B_exo; 1.
 DR PRINTS; PR00106; DNAPOL2.
 DR PRINTS; PR00379; INTEIN.
 DR SMART; SM00305; HintC; 1.
 DR SMART; SM00306; HintN; 1.
 DR SMART; SM00486; POLBc; 1.
 DR TIGRFAMs; TIGR01443; intein_Cterm; 1.
 DR TIGRFAMs; TIGR01445; intein_Nterm; 1.
 DR TIGRFAMs; TIGR00592; pol2; 1.
 DR PROSITE; PS00116; DNA_POLYMERASE_B; 1.
 DR PROSITE; PS00818; INTEIN_C_TER; 1.
 DR PROSITE; PS00819; INTEIN_ENDONUCLEASE; 1.
 DR PROSITE; PS00817; INTEIN_N_TER; 1.
 KW DNA-binding; Hydroxylase; Endonuclease; DNA replication;
 KW protein splicing; Intron homing
 FT CHAIN 1 492 DNA POLYMERASE, 1ST PART.
 FT CHAIN 493 1029 ENDONUCLEASE P1-PSPI.
 FT CHAIN 1030 1312 DNA POLYMERASE, 2ND PART.
 SQ SEQUENCE 1312 AA; 152852 MW; B62518905641D26A CRC64;

Query Match

6.5%; Score 80.5; DB 1; Length 1312;

Best Local Similarity 23.9%; Pred. No. 78;
 Matches 62; Conservative 33; Mismatches 85; Indels 79; Gaps 16;
 QY 4 SERINEXDLRKK-----SELQGTALGNL--KQIYYNEKAITENKESD-----44
 DB 923 NEEDKFTYRKKNVHSHVVPKDILKETGKVFQKNISYKKFRELVENGLDREKAKRI 982
 QY 45 -----DQFLENTILFK-GFTGHPWYNDLLVD-----LGSKDATNKYKGGKVDLYG 89
 DB 983 EWLINGDIVLDRVVVEIKREYDGVV--DLSVDEDENFLAGFGLYAHNSYVG-----1033
 QY 90 AYGYG-----QCAGTGNKTCACMYGGVTLHDNRLTEEK---KVPINLWI--DOKQT 136
 DB 1034 -YGVAKARWYKCECA-----ESVTANGREYIFVRKELEKEKFGKV---LYIDTDLGYA 1084
 QY 137 TVPIDKVKTSKKEVTQELDQARHYLHGKF-GLYNSDSFGKVGQGLIVFHSSEGSTVS 195
 DB 1085 TIFGAPKEEIKKKA-----LEFVDVINAKLPGLLELE-YEGFYVRGFFV-----TKKK 1131
 QY 196 YDLFDAQGQYPTDLLRIYR 214
 DB 1132 YALIDEEGKIITRGLTIVR 1150
 RESULT 45
 PGK_GLOMO STANDARD; PRT; 416 AA.
 ID PGK_GLOMO
 AC 074233;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Phosphoglycerate kinase (EC 2.7.2.3).
 GN PGK.
 OS Glomus mosseae.
 OC Eukaryota; Fungi; Glomeromycota; Glomeromycetes; Glomerales;
 OC Glomeraceae; Glomus.
 OX NCBI_TaxID=27381;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BEG 12;
 RA Harrier L.A., Hooker J.E.;
 RT "Isolation of the 3-phosphoglycerate kinase gene of the arbuscular
 RT mycorrhizal fungus Glomus mosseae Gerdemann & Trappe.";
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -!- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-
 CC phospho-D-glyceroyl phosphate.
 CC -!- PATHWAY: Second phase of glycolysis; second step.
 CC -!- SUBUNIT: Monomer (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the phosphoglycerate kinase family.
 CC -----
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 CC -----
 DR EMBL; AF072893; AAD09406.1; -;
 DR EMBL; AF074394; AAC26131.1; -;
 DR HSP; P00560; 1QPG.
 DR InterPro; IPR001576; PGK.
 DR Pfam; PF00162; PGK; 1.
 DR PRINTS; PR00477; PHGLYCKINASE.
 DR PROSITE; PS00111; PGLYCERATE_KINASB; 1.
 KW transferase; Kinase; Glycolysis.
 SQ SEQUENCE 416 AA; 44764 MW; 53179DF32BEFEC48 CRC64;

Query Match

6.5%; Score 80; DB 1; Length 416;

Best Local Similarity 22.5%; Pred. No. 22;
 Matches 53; Conservative 24; Mismatches 59; Indels 100; Gaps 12;

QY 4 SEINEKDLRKKSE-----LOGTALGNLKOI-----YYNEKAITENKESD 44
 Db 4 SNKLSIRDLNVKDKRVLRVDFNVLPGTITTNQRIIVAALEFQAKTV-----58
 QY 45 DQFLENTLLFKGFTGHPWYNLLVDLGSKDATNKYKGVLDY-----89
 Db 59 -----VLMSHLGRPD-----GKVDKYSILAPVAKEVERLLGKK 91
 QY 90 AYYGYOCAG-GTGN--KTACMYGGVTLHDNNRLTEK-----KVPINLWIDGKQTTVPIDK 142
 Db 92 VTFLDCVGEVENVYKNAC-DGEVILLLENLAFHAEEGSSGKP-----DGKKVADLEK 145
 QY 143 VKTSKEVTVQELDLQARHYLHGKFLGYNLSDSGFGKVQRLVPHSSEGSTVSVDL 198
 Db 146 VKFEFRSLTALG-----DVIINDAFG-----TAHRAHSSVMGVVEL 180

RESULT 46
 LEC_PAPC STANDARD; PRT; 447 AA.
 AC P83304;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Mannose/glucose-specific lectin.
 OS Parkia platycephala.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Mimosoideae; Parkieae; Parkia.
 OC NCBI_TaxID=185447;
 RN [1]
 RP SEQUENCE, SUBUNIT, MASS SPECTROMETRY, AND VARIANTS VAL-70; ARG-227 AND
 RP ASN-296.
 RC TISSUE=Seed;
 RX MEDLINE=21393945; PubMed=11502201;
 RA Mann K., Farias C.M.S.A., Del Sol F.G., Santos C.F., Grangeiro T.B.,
 RA Ngano C.S., Cavada B.S., Calveite J.J.,
 RA "The amino-acid sequence of the glucose/mannose-specific lectin
 RT isolated from Parkia platycephala seeds reveals three tandemly
 RT arranged jacinin-related domains.";
 RN Eur. J. Biochem. 268:4414-4422(2001).
 RL [2]
 RP FUNCTION.

RA Ramos M.V., Cavada B.S., Bomfim L.R., Debray H., Mazard A.-M.,
 RA Calveite J.J., Grangeiro T.B., Rouge P.,
 RA "Interaction of the seed lectin from Parkia platycephala (Mimosoideae)
 RT with carbohydrates and complex glycans.";
 RL Protein Pept. Lett. 6:215-222(1999).
 CC -1- FUNCTION: Mannose/glucose specific lectin. Shows agglutinating
 CC activity against rabbit erythrocytes.
 CC -1- SUBUNIT: Homodimer.
 CC -1- MASS SPECTROMETRY: MW=47946; MW_ERR=6; METHOD=Electrospray.
 CC -1- MASS SPECTROMETRY: MW=47951; MW_ERR=9; METHOD=MALDI.
 CC -1- SIMILARITY: Belongs to the Jacalin lectin family.
 DR GO; GO:0005536; F:glucose binding; IDA.
 DR GO; GO:0005537; F:mannose binding; IDA.
 DR GO; GO:0000721; P:agglutination; IDA.
 DR InterPro; IPR001229; Jacalin_Lectin.
 DR Pfam; PF01419; Jacalin; 3.
 DR Lentin; Mannose-binding; Repeat.
 FT MOD_RES 1 1
 FT DOMAIN 1 447 3 X APPROXIMATE TANDEM REPEATS.
 FT REPEAT 1 149 1.
 FT REPEAT 150 295 2.
 FT REPEAT 296 447 3.
 FT REPEAT 70 227 I -> V.
 FT VARIANT 227 K -> R.
 FT VARIANT 296 D -> N.
 SQ SEQUENCE 447 AA; 47521 MW; 8F14ED460874BBB2 CRC64;

Query Match 6.5%; Score 80; DB 1; Length 447;
 Best Local Similarity 23.6%; Pred. No. 24;
 Matches 38; Conservative 20; Mismatches 65; Indels 38; Gaps 8;

QY 60 GHPW-----VNDLLVDLGSKDATNKYKGVLDYGAIVGYOCAGGTNNKTCMYGGVT 112
 Db 311 GDFWSTYANEGINQIIYAGSNIKSVAFK-----DTSGLDSATFGGVN 353
 QY 113 LHDNNRLTEKKVPINLWIDGKQTTVPIDKVTSKKEV--TVQELDLQARHYLHGKFLY 170
 Db 354 PKDTG--EKNTVSIN-WPSEYLTISGTYGQYKFKDVFTTITSLTFTTNLATYGPFGKA 409
 QY 171 NSDSFGGKVQGLIV-PHSSEGSTVSVDLFDQAQGY--PDT 208
 Db 410 SATSFSPIHNNMVGVGHGAG-----DYLDALGIFVKPDT 445

RESULT 47
 YF08_MYCPN STANDARD; PRT; 509 AA.
 ID P75278;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein MPN508 (P02_orf509).
 GN MPN508 OR MP334.
 OS Mycoplasma pneumoniae.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OC NCBI_TaxID=2104;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 29342 / M129;
 RX MEDLINE=97105885; PubMed=8948633;
 RA Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
 RA Hermann R.;
 RA "Complete sequence analysis of the genome of the bacterium Mycoplasma
 RT pneumoniae.";
 RL Nucleic Acids Res. 24:4420-4449(1996).
 CC -1- SIMILARITY: BELONGS TO THE MG032 / MG096 / MG288 FAMILY.
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 CC -----
 CC EMBL; AF000031; AAB95982.1; --
 DR PIR; S73660; S73660.
 DR InterPro; IPR004306; MG032/096/288_1.
 DR InterPro; IPR004319; MG032/096/288_2.
 DR Pfam; PF03072; DUF237; 1.
 DR Pfam; PF03086; DUF240; 1.
 DR ProDom; PD004834; MG032/096/288_2; 1.
 KW Hypothetical protein: Complete proteome.
 SQ SEQUENCE 509 AA; 57825 MW; 8CDC95BB941A6987 CRC64;

Query Match 6.5%; Score 80; DB 1; Length 509;
 Best Local Similarity 22.0%; Pred. No. 28;
 Matches 56; Conservative 39; Mismatches 106; Indels 54; Gaps 13;

QY 3 KSERINEKDLRKKSELQ--TALGNLKOIYYNEKAITENKE-----SDDOFLENTL 52
 Db 234 KAEVKKLEAREAFNKSLSLTAASEFKQWSKKNKDVTDKKQLAEALKISLEADNRFTSF 293
 QY 53 LFKGFTGHPWYNLLVDLGSKDATNKYKGV-----KVDLYGAYYGYOCAGGPNNTAC 106
 Db 294 LIAGFRTAIDWYNNAKKE--NNDAKQKAFSGQIQFPKDGNGIYMPDWLRGELTSKS-- 349
 QY 107 MYGGVTLDHNNRLTEKKV-----PINLWIDGKQTTVPIDKVTSKKEVTVQELDLQAR 160
 Db 350 -----NINLTKELKVQNKIESPTINWIDG---VGKQDKANPFRFV-DIKYTG 398
 QY 161 HYLHGK---GLYNS--DSFGKVQRLVPHSSEGSTVSVDLFDQAQGYEDTLLRYRD 215

Query Match 6.5%; Score 80; DB 1; Length 447;
 Best Local Similarity 23.6%; Pred. No. 24;
 Matches 38; Conservative 20; Mismatches 65; Indels 38; Gaps 8;


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Db 399 YQLYGFYFAALFTKPPSSNCSGEMMLKFTV-----DGSIPVYTV--AKKDYPGSLQFQFN-- 450
QY 216 NKTINSNHNHIALYL 230
Db 451 -----DKDELLFTLYV 461

RESULT 48
YB64_PASMU
ID YB64_PASMU STANDARD; PRT; 324 AA.
AC Q9CKY16;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Hypothetical paba-like protein PM1464.
GN PM1464.
OS Pasteurella multocida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Pasteurella.
OX NCBI_TaxID=747;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN:PM70;
RA MEDLINE=21145866; PubMed=11248100;
RA May B.J., Zhang Q., Li L.L., Paustian M.L., Whittam T.S., Kapur V.;
RT "Complete genomic sequence of Pasteurella multocida PM70.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465 (2001).
CC -!- SIMILARITY: TO THE C-TERMINAL OF PARA-AMINOBENZOATE SYNTHASE
CC COMPONENT 1.
CC -----
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CC -----
CC EMBL; AE006183; AAK03548.1;
CC InterPro; IPR005801; Anth synth chor.
CC Pfam; PF00425; chorismate_bind; 1.
CC PRINTS; PR00095; ANTSNTHASE1.
CC ProDom; PD000779; Anth synth chor; 1.
CC Hypothetical protein; Complete proteome.
KW SEQUENCE 324 AA; 37309 MW; E9336FF3890A32AE CRC64;
Query Match 6.4%; Score 79.5; DB 1; Length 324;
Best Local Similarity 27.3%; Pred. No. 19;
Matches 24; Conservative 17; Mismatches 34; Indels 13; Gaps 3;

QY 136 TTVPIDKVKTSKKEVTVOEL---DLQARHYLHGKFLYNSDSFGKVGQRLI-----V 185
Db 236 TLLPAGSISGAPKKTQVQIIHAAEQRPGRYTGIFGLDGSLSQSAVAIRFIEQVDEKLI 295

QY 186 FHSSSGTSVSDLPDAQQYPTLLRIY 213
Db 236 FRSGGGITILSELED---EYQELQKVY 320

RESULT 49
DP3A_HELPY
ID DP3A_HELPY STANDARD; PRT; 1211 AA.
AC P56157;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE DNA polymerase III alpha subunit (EC 2.7.7.7).
GN DNAE OR HPI460.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=26695 / ATCC 700392;
RA MEDLINE=97394467; PubMed=9252185;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S., Dougherty B.A.,
RA Nelson K., Quackenbush J., Zhou L., Kirkness E.F., Peterson S.,
RA Loftus B., Richardson D., Dodson R., Khalak H.G., Glodek A.,
RA McKenney K., Fitzgerald L.M., Lee N., Adams M.D., Hickey E.K.,
RA Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D., Kelley J.M.,
RA Cotton M.D., Weidman J.M., Fujii C., Bowman C., Matthey L., Wallin E.,
RA Hayes W.S., Borodovsky M., Karp P.D., Smith H.O., Fraser C.M.,
RA Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori.";
RL Nature 388:539-547 (1997).
CC -!- FUNCTION: DNA polymerase III is a complex, multichain enzyme
CC responsible for most of the replicative synthesis in bacteria.
CC This DNA polymerase also exhibits 3' to 5' exonuclease activity.
CC The alpha chain is the DNA polymerase (By similarity).
CC -!- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
CC + {DNA}(N).
CC -!- SUBUNIT: DNA polymerase III contains a core (composed of alpha,
CC epsilon and theta chains) that associates with a tau subunit. This
CC core dimerizes to form the POLIII' complex. PolIII' associates
CC with the gamma complex (composed of gamma, delta, delta', psi and
CC chi chains) and with the beta chain to form the complete DNA
CC polymerase III complex (By similarity).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -!- SIMILARITY: Belongs to the DNA polymerase type-C family. DnaE
CC subfamily.
CC -----
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CC -----
CC EMBL; AE000646; AAD08502.1;
CC F1R; D64702; D64702.
CC TIGR; HPI460;
CC InterPro; IPR004013; PHP_C.
CC InterPro; IPR003141; PHP_N.
CC InterPro; IPR004805; PolC_alpha.
CC Pfam; PF02811; PHP_C; 1.
CC Pfam; PF02231; PHP_N; 1.
CC SMART; SM00481; POLIIC; 1.
CC TIGRfams; TIGR00594; polc; 1.
CC Transferase; DNA-directed DNA polymerase; DNA replication;
KW Complete proteome.
SQ SEQUENCE 1211 AA; 138052 MW; FB248DD47E4CBB0C CRC64;
Query Match 6.4%; Score 79.5; DB 1; Length 1211;
Best Local Similarity 25.7%; Pred. No. 87;
Matches 28; Conservative 19; Mismatches 45; Indels 17; Gaps 4;

QY 66 DLLVDLIG-SKDATNKYKGGKVDLYGAYGYQCAGGTPTKTACMYGVTLLHNNRLTEEEK 124
Db 936 DLICDAGRAKDKANEMWQGNLSFGA-----MEGTTKEQVLDMLDGEHDAKTLLECEY 990

QY 125 VPINLWIDGKQTTVPIDKVKTS-----KKEVTVOELDLQARHYLHGK 166
Db 991 ETIGIHVSGN-----PLDFEKEIKGFNVLKSIDIEELIGSQAYLLGK 1035

RESULT 50
PHYB_SOYBN
ID PHYB_SOYBN STANDARD; PRT; 1156 AA.
AC P42499;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)

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DR PROSITE; PS00847; GRAM_POS ANCHORING; 1.
DR PROSITE; PS00136; SUBTILASE ASP; 1.
DR PROSITE; PS00137; SUBTILASE HIS; 1.
DR PROSITE; PS00138; SUBTILASE SER; 1.
KW Hydrolase; Serine protease; Cell wall; Peptidoglycan-anchored; Zymogen;
FT SIGNAL; 1 33
FT PROPEP 34 187
FT CHAIN 188 1870
FT ACT_SITE 1871 1902
FT ACT_SITE 217 217
FT ACT_SITE 281 281
FT ACT_SITE 620 620
FT SITE 1867 1871
FT MOD_RES 1870 1870
FT SEQUENCE 1902 AA; 200139 MW; 4B8DB84D98CDF7 CRC64;
Query Match 6.4%; Score 79; DB 1; Length 1902;
Best Local Similarity 24.8%; Pred. No. 1.6e+02;
Matches 51; Conservative 9; Mismatches 64; Indels 82; Gaps 9;
QY 46 OFLENTLLFK-----GFTGHPWYNDLLVDLGSXDATNKKYKGVLDYGYG 93
DB 805 QFVEGFLNFKSGDGLNLPYMGFGD---WND-----GKIVDSLNG-IT 845
QY 94 YOCAGG-----TPNKTACHYGVVTLHDNRLTEKKVPINLWIDKQTTVIDKVK 145
DB 846 YSPAGGNFGTVPLTNKNTGYGGWYTD-----ADGNQF----- 881
QY 146 SKKEVTVCGLDQARHLYLHGLNGLNDFSGKVGQVGLVHFSSEGSFVSYDLFDAQQY 205
DB 882 -----VDDQATFSSDKNALYNDISMKYLLRNI-----SNVQVILDGQGNK 924
QY 206 PTLRLIRVNDKNTKNSNHLIALYLY 231
DB 925 VTTLSSTNRKTY--YNAHSQQYTY 948
RESULT 52
YJEA_BACSU STANDARD; PRT; 467 AA.
AC O34798;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical protein yJea precursor.
GN YJEA OR BSU12100.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]_BACSU
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98240225; PubMed=9579062;
RA Rivolta C., Soldo B., Lazarevic V., Joris B., Maue C., Karamata D.;
RT "A 35.7 kb DNA fragment from the Bacillus subtilis chromosome
containing a putative 12.3 kb operon involved in hexuronate catabolism
and a perfectly symmetrical hypothetical catabolite-responsive
element.";
RL Microbiology 144:877-884 (1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogawara N., Moszer I., Albertini A.M., Alloni G.,
Azevedo V., Betero M.G., Bessieres P., Solotkin A., Borchert S.,
Boriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
Brouillet S., Bruch C.V., Caldwell B., Capuano V., Carter N.M.,
Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
Denizot F., Devine K.M., Duxterhof A., Ehrlich S.D., Emmerson P.T.,
Entian K.D., Ewing J., Fabret C., Ferrari E., Foulger D.,
Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,

Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
Joris B., Karamata D., Kasahara Y., Klaier-Blanchard M., Klein C.,
Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
Lee S.M., Levine A., Liu H., Masuda S., Maue C., Medigue C.,
Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
Parro V., Pohl T.M., Portetelle D., Rapoport G., Rey M., Reynolds S.,
Prescan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
Sekiguchi J., Sekowska A., Seror S.J., Serror P., Shin B.S., Soldo B.,
Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
subtilis.";
RL Nature 390:249-256 (1997).
CC -1- SIMILARITY: Belongs to the polysaccharide deacetylase family.
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CC
EMBL; AF015825; AAC46306.1; -
DR EMBL; Z99110; CAB13067.1; -
DR PIR; G69849; G69849.
DR Subtilist; BG13184; yJea.
DR InterPro; IPR002509; Polysacc deacet.
DR Pfam; PF01522; Polysacc deacet; 1.
KW Hypothetical protein; Hydrolase; Signal; Complete proteome.
FT SIGNAL 1 26 POTENTIAL.
FT CHAIN 27 467 HYPOTHETICAL PROTEIN YJEA.
SQ SEQUENCE 467 AA; 53838 MW; 95D2B1245968F804 CRC64;
Query Match 6.3%; Score 78.5; DB 1; Length 467;
Best Local Similarity 25.2%; Pred. No. 33;
Matches 36; Conservative 20; Mismatches 54; Indels 33; Gaps 8;
QY 11 DLKKSELOQT--ALGNLKIYVYNEKAITENKESDDQFLENTLLFKGFTGHPWYNDLL 68
DB 298 DSLKKYKGHTFFVLGS--RVQYYPETLIRMLKEGNE-----VGNHSHPL 343
QY 69 VDLGSKDATNKYKGVLDYGYGYQCAGGTENKTACMYGGVTLHDNRLTEKKVPIN 128
DB 344 TRLSVKALKQINDTQ-DITEKISGYR-----FTLVPPYGGI-----NDELRSQMKMDVA 393
QY 129 LW-IDGKQTTPIDKVKTSKEV 150
DB 394 LWDVD-----PSDWKDRNKTTI 410
RESULT 53
CLSI_BACAA STANDARD; PRT; 509 AA.
AC Q81V75;
DT 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Cardiolipin synthetase 1 (EC 2.7.8.-) (Cardiolipin synthase 1) (CL
synthase 1).
GN CLSI OR CLS-1 OR BA0625.
OS Bacillus anthracis (strain Ames).
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=198094;

RESULT 54
ETF1_YABAM
ID ETF1_Y
AC Q9QB97
DT 16-OCT
DT 16-OCT

```

[1]
SEQUENCE FROM N.A.
RC STRAIN=E8775;
RA Wolf M.K., de Haan L.A.M., Cassels F.C., Willshaw G.A.,
RA Gestel E.C.M., Gaastra W., Warren R., Boedeker E.C.;
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF C6 FIMBRIAL
CC SUBUNITS ACROSS THE OUTER MEMBRANE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
CC (by similarity).
CC -!- SIMILARITY: Belongs to the fimbrial export usher family.
CC -----
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CC or send an email to license@sb-sib.ch).
CC -----
DR EMBL: U04846; AAB51364.1; -
DR InterPro: IPR000015; FimB_usher.
DR Pfam: PF00577; Usher; 1.
DR PROSITE; PS01151; FIMBRIAL USHER; FALSE NEG.
KW Outer membrane; Transmembrane; Fimbria; Transport; Signal.
FT SIGNAL 1 ? POTENTIAL.
FT CHAIN ? 802 OUTER MEMBRANE USHER PROTEIN CSSD.
SQ SEQUENCE 802 AA; 90393 MW; 5EFD0B6F17F5B5E0 CRC64;

Query Match 6.3%; Score 78.5; DB 1; Length 802;
Best Local Similarity 20.0%; Pred.No.64;
Matches 49; Conservative 36; Mismatches 97; Indels 61; Gaps 10;

QY 26 LKQIYYNKAIAITENKESDDQFLE-----NTLLFKGFFTGHPWYNDLLVLGSKDAT 77
DB 192 LRLNLFNFQNDKTBWNTYITLLEKSPYDKLLNLVVGESVTNSGVNMYNYSFTGISVSTDT 251
QY 78 NKYKXGKVDLYGAYGYQCAGGTFNKTACMYGGVTLHDNNRLTEKKVP-----INL 129
DB 252 DMVTPSEIDVTPSEIHG-----VADSDSQIIVRQGNITLINESVPAGPFSFPTNL 301
QY 130 WIDGKQTTVPIDKVKYSKKEVTV-----QELDLQARHYLHGK----- 166
DB 302 MYTGGQLNVEITDIYGNKKQYTVNNSGLPYVRKAGLVMYNFIQGLTKNSEDDGDFFTQG 361
QY 167 ---FGL-YNSDSGGGKVQORGLIVFHSESGSTVSVDLFDAGQYVPTLLRIYRDN-KTINS 221
DB 362 DINVGTHYNSTLFGG-YQFSKNYFNLSGT--IGTDL---GFSGAWLLHVSRSFNKXNG 414
QY 222 ENLHI 226
DB 415 YNNIL 419

RESULT 56
FNEA STAAU STANDARD; PRT; 1018 AA.
ID FNEA STAAU
AC F14738;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Fibronectin-binding protein precursor (FNEP).
GN FNEA
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NCTC 8325-4;
RX MEDLINE=89098998; PubMed=2521391;
RA Signaes C., Raucci G., Joensen K., Lindgren P.-E.,
RA Arancharamatiah G.M., Hoeoek M., Lindberg M.;
RT "Nucleotide sequence of the gene for a fibronectin-binding protein

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RT from Staphylococcus aureus: use of this peptide sequence in the
RT synthesis of biologically active peptides.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:699-703(1989).
CC -I- FUNCTION: THE ABILITY OF BACTERIA TO BIND FIBRONECTIN HAS BEEN
CC PROPOSED AS A VIRULENCE FACTOR ENABLING BACTERIA TO COLONIZE
CC WOUND TISSUES AND BLOOD CLOTS. BINDING OF PLASMA FIBRONECTIN TO
CC THE BACTERIAL SURFACE MIGHT BLOCK ADHESION RECEPTORS ON S.AUREUS,
CC THUS REPRESENTING AN IMPORTANT DEFENSE MECHANISM AGAINST TISSUE
CC INVASION.
CC -I- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
CC an amide bond (Potential).
CC -----
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CC -----
DR EMBL; J04151; AAA26632.1; -.
DR InterPro; IPR004237; Fn bind.
DR InterPro; IPR005877; Gpos_YSIK.
DR InterPro; IPR001899; Gram_pos_anchor.
DR Pfam; PF02986; Fn_bind_1;
DR Pfam; PF00746; Gram_pos_anchor; 1.
DR Pfam; PF04650; YSIK_signal; 1.
DR TIGRFAMS; TIGR01167; LPXTG_signal; 1.
DR TIGRFAMS; TIGR01168; YSIK_signal; 1.
DR PROSITE; PS50847; GRAM_POS_ANCHORING; 1.
DR Cell wall; Peptidoglycan-anchor; Repeat; Signal.
FT SIGNAL 1 36
FT CHAIN 37 985 FIBRONECTIN-BINDING PROTEIN.
FT PROPEP 986 1018 REMOVED BY SORTASE (POTENTIAL).
FT REPEAT 545 574 B-1.
FT REPEAT 575 604 B-2.
FT DOMAIN 745 878 4 X APPROXIMATE TANDEM REPEATS,
FT FIBRONECTIN-BINDING DOMAIN.
FT REPEAT 745 782 D-1.
FT REPEAT 783 820 D-2.
FT REPEAT 821 859 D-3.
FT REPEAT 860 878 D-4 (INCOMPLETE).
FT DOMAIN 879 948 5 X TANDEM REPEATS, PRO-RICH (WR).
FT REPEAT 879 892 WR1.
FT REPEAT 893 906 WR2.
FT REPEAT 907 920 WR3.
FT REPEAT 921 934 WR4.
FT REPEAT 935 948 WR5.
FT SITE 982 986 LPXTG SORTING SIGNAL (POTENTIAL).
FT MOD_RES 985 985 AMIDE-LINKED TO CELL WALL (POTENTIAL).
SQ SEQUENCE 1018 AA; 111780 MW; 58175E0020E81FIF CRC64;

Query Match 6.3%; Score 78.5; DB 1; Length 1018;
Best Local Similarity 21.8%; Pred. No.85;
Matches 55; Conservative 25; Mismatches 85; Indels 87; Gaps 12;

QY 3 KSEINEKDLRKSLEQGTALGNLQKLYYYNNEKAITENKES-----DDQFLENT-- 51
Db 411 KSVYANTDTTSKFKEVTSNNMNLN---LQNNGSYSLNIENLDKTVVHYHDEYGLNGTDE 467
QY 52 LLFKGFTTGHPWYNDLLDGLSGDATNKYKGKVDLYGAY--GYQCAGGTENKTACWYG 109
Db 468 VDFRTQMVGHP-----EQLYKYVDGY-----TLTWDN 496
QY 110 GVTLDHNNRLTEBEKKVPI--NLWDGKQTV-----PIDK--VKTSKKEVTVQVELDLOA 159
Db 497 GLVLYSNKANGNEKNGPFIQNNKFYEKDTIKETLTGYDKNLVTVVEEYDSLTLDID- 555
QY 160 RYHLHGKFGLYNS--DSFGGKVGRLGVLFVHSSEGSTVSYDLFDAGQYPTDLLIRYDNK 217
Db 556 -----YHTADGGGGYVDGYETIEETEDSSAIDYHTA----- 589
QY 218 TINSENLHIALY 229

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Db 590 -VDSEAGHGGY 600
::||| |. |
RESULT 57
COBQ_METMA STANDARD; PRT; 485 AA.
AC Q800P3;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable cobyrric acid synthase.
GN COBQ OR MM0093.
OS Methanosarcina mazei (Methanosarcina frisia).
OC Archaea; Euryarchaeota; Methanomicrobia; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2209;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Goel / Go1 / ATCC BAA-199 / DSM 3647 / OCM 88;
RX MEDLINE=22120827; PubMed=12125824;
RA Deppenmeier U., Johann A., Hartsch T., Merkl R., Schmitz R.A.,
RA Martinez-Arias R., Henne A., Wierzer A., Baeumer S., Jacobi C.,
RA Brueggemann H., Lienard T., Christmann A., Boemcke M., Steckel S.,
RA Bhattacharyya A., Lykidis A., Overbeek R., Klenk H.-P., Gunsalus R.P.,
RA Fritz H.-J., Gottschalk G.;
RT "The genome of Methanosarcina mazei: evidence for lateral gene
transfer between Bacteria and Archaea.";
RL J. Mol. Microbiol. Biotechnol. 4:453-461(2002).
CC -!- FUNCTION: Catalyzes amidations at positions B, D, E, and G on
adenosylcobyrrinic A,C-diamide. NH(2) groups are provided by
glutamine, and one molecule of ATP is hydrolyzed for each
amidation (By similarity).
CC -!- PATHWAY: Cobalamin biosynthesis.
CC -!- SIMILARITY: Belongs to the cobB/cobQ family. CobQ subfamily.
CC
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CC
CC EMBL; AB013230; AAM29789.1; ALT_INIT.
DR HAMAP; MF 00028; -; 1.
DR InterPro; IPR002586; CbiA_P.
DR InterPro; IPR004459; CobQ_synth.
DR Pfam; PF01656; CbiA; 1.
DR TIGRFAMs; TIGR00313; cobQ; 1.
KW Cobalamin biosynthesis; Complete proteome.
SQ SEQUENCE 485 AA; 5324 MW; 329A8E85515528D0 CRC64;
Query Match 6.3%; Score 78; DB 1; Length 485;
Best Local Similarity 23.7%; Pred. No. 38;
Matches 62; Conservative 40; Mismatches 102; Indels 58; Gaps 18;
QY 1 SEKSEETNEK-DLRKKSELOGTA-----LGNLKOIYYNEKAITENKESDD 45
Db 233 SEDSVSLGDKEDSKAEIEIVAVIRLPRISNFTDFEPLEGIVKRVYD---INEELGNDP 289
QY 46 QFL-----ENTILFKGFTGHPWNLDLVLGSKDATNK---YRKGVLDLYGAYGYQCAG 98
Db 290 AIMPGTKNTV-----NDLL-DLRASGMDKKIQAQXG-KVPFPGICGGYQMLG 335
QY 99 -----GTPNKTACMYGGVTLHD--NNRLTEKK--VPINLWIDGKQTTV-PIDKVTSSK 148
Db 336 RTIFDPSGVNGVEAEFEGGLGLDITGTFGRYKRTVQVTKKXNGYGPILPDIGEEIKGY 395
QY 149 ETVQELDLQARHYLHGKFGFLYNSDSFG-GKVQRGGLIVFHSSEGSTVSYDLFDAQG-QY- 205
Db 396 EIHGVTVD--SNRTVFGDDGAIDEGGVIGTYLHGLFDNRNIRNALVRY-LYEKKGLYE 452
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QY 206 PDLTLR---IYRDNKTINSNL 224
Db 453 PDEAISENDAYEEELANVVEQNI 474
RESULT 58
CSDI_ECOLI STANDARD; PRT; 819 AA.
AC P53512;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane usher protein cssD precursor (CS6 fimbria usher
DE protein).
GN CSSD.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=O167:H5 / E10703;
RA Wolf M.K., de Haan L., Casseis F.C., Willshaw G.A., van Gestel E.,
RA Gastra W., Warren R., Boedeker E.C.;
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN THE EXPORT AND ASSEMBLY OF C6 FIMBRIAL
CC SUBUNITS ACROSS THE OUTER MEMBRANE.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
(CC) (By similarity).
CC -!- SIMILARITY: Belongs to the fimbrial export usher family.
CC
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CC
CC EMBL; U04844; AAC45096.1; -.
DR FIR; I83350; I83350.
DR InterPro; IPR000015; Fimb_usher.
DR Pfam; PF00577; Usher; 1.
DR PROSITE; PS01151; FIMBRIAL_USHER; FALSE NEG.
KW Outer membrane; Transmembrane; Fimbria; Transport; Signal.
FT SIGNAL 1 ? POTENTIAL.
FT CHAIN ? 819 OUTER MEMBRANE USHER PROTEIN CSSD.
SQ SEQUENCE 819 AA; 92378 MW; 6E8718FE28C6AA89 CRC64;
Query Match 6.3%; Score 78; DB 1; Length 819;
Best Local Similarity 20.6%; Pred. No. 72;
Matches 53; Conservative 37; Mismatches 97; Indels 70; Gaps 11;
QY 6 EINEKDLKKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLEKGFTHGPWYN 65
Db 206 EFNQNDKKKTWE-----RNYLLEKSFYDKK-----INLVGSYTSNYYNN 248
QY 66 DLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGVTLHDNRLTEKKV 125
Db 249 YSFTGISVSTDTDMYTPSEIDYTPTEIHG-----VADSDSQIIVRQNTIINESV 298
QY 126 P-----INLWIDGKQTTVPIDKVTSSKEVTV-----QELDLQARHYLHGK--- 166
Db 299 PAGPFPFITNLMTYGGQNLVVEITDIYGNRKQYTVSNSSLPVWRKAGLMVYFISGKLT 358
QY 167 -----FGL-YNSDSFGGKVGQRLIVFHSSEGSTVSYDLFDAQGQYPTLL 210
Db 359 KNSEDCGDFFAQGDINYGTHYNSTLFGG-YQPSKYNFNLSTG--IGTDL----GFGAWLL 411
QY 211 RIYRDN-KTINSNLHI 226
Db 412 NVRSRNFKDKNGYNINL 428
```

RESULT 59
 PIP_LACLC STANDARD; PRT; 1902 AA.
 ID PIP_LACLC
 AC P16271;
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE PI-type proteinase precursor (EC 3.4.21.-) (Wall-associated serine proteinase).
 DE proteinase).
 GN FRIP.
 OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
 OC NCBI_TaxID=1359;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=WG2;
 RX MEDLINE=88149035; PubMed=3278687;
 RA Kok J., Leenhouts K.J., Haandrikman A.J., Ledebor A.M., Venema G.;
 RT "Nucleotide sequence of the cell wall proteinase gene of
 Streptococcus cremoris WG2.";
 RL Appl. Environ. Microbiol. 54:231-238 (1988).
 CC -!- FUNCTION: PROTEASE WHICH BREAKS DOWN MILK PROTEINS DURING THE
 GROWTH OF THE BACTERIA ON MILK.
 CC -!- CATALYTIC ACTIVITY: Endopeptidase activity with very broad
 specificity, although some substrate preference have been noted,
 e.g. large hydrophobic residues in the P1 and P4 positions, and
 pro in the P2 position. Best known for its action on caseins,
 although it has been shown to hydrolyze hemoglobin and oxidized
 insulin B-chain.
 CC -!- SUBCELLULAR LOCATION: Attached to the cell wall peptidoglycan by
 an amide bond (Potential).
 CC -!- SIMILARITY: Belongs to peptidase family S8.
 CC
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 CC
 CC EMBL; M24767; AAA17677.1; -.
 CC HSP; P00782; I501.
 CC MEROPS; S08.019; -.
 DR InterPro; IPR001899; Gram_pos_anchor.
 DR InterPro; IPR003137; PA.
 DR InterPro; IPR002029; Peptidase_S8.
 DR Pfam; PF00746; Gram_pos_anchor; 1.
 DR Pfam; PF02225; PA; 1.
 DR Pfam; PF00082; Peptidase_S8; 1.
 DR PRINTS; PRO0723; SUBTILISIN.
 DR TIGRFAMs; TIGR01167; LPXTG_anchor; 1.
 DR PROSITE; PS00847; GRAM_POS_ANCHORING; 1.
 DR PROSITE; PS00136; SUBTILASE_ASP; 1.
 DR PROSITE; PS00137; SUBTILASE_HIS; 1.
 DR PROSITE; PS00138; SUBTILASE_SER; 1.
 KW Hydrolase; Serine protease; Cell wall; Peptidoglycan-anchor; Zymogen;
 KW Signal; Plasmid.
 FT SIGNAL 1 33
 FT PROPEP 34 187
 FT CHAIN 188 1870
 FT PROPEP 1871 1902
 FT ACT_SITE 217 217
 FT ACT_SITE 281 281
 FT ACT_SITE 620 620
 FT SITE 1867 1871
 FT MOD_RES 1870 1870
 FT SEQUENCE 1902 AA; 199910 MW; 2901C7F19B2E5DOB CRC64;
 Query Match 6.3%; Score 78; DB 1; Length 1902;
 Best Local Similarity 24.8%; Pred. No. 2e+02;

Matches 51; Conservative 9; Mismatches 64; Indels 82; Gaps 9;
 QY 46 QFLENTLLFK-----GFFTHPWYNDLLVLDLGLSKDATNKYKGGKVDLYGAYYG 93
 DB 805 QFVEGLFNEKSGDGRNLNLPYMGFRG---WND-----GKIVDSLNG-IT 845
 QY 94 YQCAGS-----TPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKY 145
 DB 846 YSPAGGNFQVFLTNKNTGTQYGGWTD-----ADGNQT----- 881
 QY 146 SKKEVTQELDLQARHYLHGKFLYNSDSFGGKVGRLVHFHSSGSGTYSYVLDFAQGOY 205
 DB 882 -----VDDQATAFSDKKNALYNDISKMYLLRNI-----SNVQVDILDGQGNK 924
 QY 206 PPTLRIYRDNKTIENSENLHIALYLY 231
 DB 925 VTTLSS--STNLTKTYYNAHSQQYIY 948
 RESULT 60
 Y650_METJA STANDARD; PRT; 692 AA.
 ID Y650_METJA
 AC Q57852;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein M0650 precursor.
 GN M0650.
 OS Methanococcus jannaschii.
 OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
 OC Methanocaldococcaceae; Methanocaldococcus.
 OC NCBI_TaxID=2190;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
 RX MEDLINE=96337999; PubMed=8688087;
 RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
 RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,
 RA Kervatage A.R., Dougherty B.A., Tomb J.-P., Adams M.D., Reich C.I.,
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
 RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
 RA Usterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
 RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
 jannaschii.";
 RL Science 273:1058-1073 (1996).
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 CC
 CC EMBL; U67512; AAB98647.1; -.
 DR PIR; B64381; B64381.
 DR TIGR; M0650; -.
 KW Hypothetical protein; Signal; Complete proteome.
 FT SIGNAL 1 24
 FT CHAIN 25 692
 FT SEQUENCE 692 AA; 80607 MW; 25D0A91A08177188 CRC64;
 Query Match 6.3%; Score 77.5; DB 1; Length 692;
 Best Local Similarity 19.5%; Pred. No. 65;
 Matches 52; Conservative 44; Mismatches 95; Indels 75; Gaps 11;
 QY 8 NEKDLRKSLEQGTALGNLKIYIYNEKAITENKESDDQFLENTLLFKGFTGHPWY--- 64
 DB 404 NITDLTKRAMISNDL--ISSIAYGKDCWMLIGLDEVNHLHYPSKSLI---KFDGKKFYDLT 458
 QY 65 -----NDLLVDLGLSKDATNKYKGGKVDL-----YGAYYGVQCAGGTENK 103

Db 459 NISNITCKILKSNKEVILGTRKVLKNGSFITINVTYBKYGLCYFEMDYNPK 518
 QY 104 TACMYGGVTLHDNNRLTEEEKVPIINLWIDGKQTTVPIDKVKTSKKEVTQVELDLQARHYL 163
 Db 519 RYMLVGGVCLY--NHPYSSDAILYKVYDNGSYESLPIN-----DNLHKEI 560
 QY 164 HGKFG-----LYNSDSFGGKVGORGL-----IVFHSSEGSTV--SYDL 198
 Db 561 YGDFGPAVLSLIKYIPKNSFLIKVWGLNDHMLYKNNLTFTFVTKPKPGSIEIDNYTL 620
 QY 199 FDAQGQYPTLLRIYRDKNKTINSEN 224
 Db 621 YIP--NYINT-IBYDNNKLLSTVEL 643

RESULT 61

RNRL_LACLA
 ID RNRL_LACLA STANDARD; PRT; 817 AA.
 AC Q9CH00;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ribonuclease R 1 (EC 3.1.-.-) (RNase R 1) (VacB protein homolog 1).
 GN RNRL OR VACB1 OR LL0942.
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
 OX NCBI_TaxID=1360;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IL1403;
 RX MEDLINE=21235186; PubMed=11337471;
 RA Bolotin A., Wincker P., Manger S., Jallou O., Malarne K.,
 RA Weissenbach J., Ehrlich S.D., Sorokin A.;
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus
 RT lactis ssp. lactis IL1403.";
 RL Genome Res. 11:731-753(2001).
 CC -1- FUNCTION: 3'-5'-exoribonuclease that participates in an essential
 CC cell function. Acts nonspecifically on poly(A), poly(U) and
 CC ribosomal RNAs (By similarity).
 CC -1- SIMILARITY: Belongs to the ribonuclease II (RNB) family.
 CC -1- SIMILARITY: Contains 1 S1 motif domain.

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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: AB006326; AAK05040.1; -
 CC F86742; F86742.
 CC HSP; P05055; ISRO.
 CC InterPro: IPR004476; 3 prime RNase.
 CC InterPro: IPR008994; Nucleic acid OB.
 CC InterPro: IPR001900; Ribonuclease II.
 CC InterPro: IPR003029; S1.
 CC Pfam: PF00773; RNB; 1.
 CC Pfam: PF00575; S1; 1.
 CC SMART: SM00316; S1; 1.
 CC TIGRFAMs: TIGR00358; 3 prime RNase; 1.
 CC PROSITE: PS01175; RIBONUCLEASE_II; 1.
 CC PROSITE: PS0126; S1; 1.
 CC Hydrolase; Exonuclease; Nuclease; RNA-binding; Complete proteome.
 FT DOMAIN 633 717
 SQ SEQUENCE 817 AA; 92250 MW; 44079115EF624D73 CRC64;

Query Match

Best Local Similarity 27.8%; Pred. No. 79;

Matches 27; Conservative 12; Mismatches 37; Indels 21; Gaps 3;

QY 131 IDGKQTTVPIDK----VKTSKKEVTQVELDLQARHYLHGKFLGNSDFGKVGORGLIVF 186

Db 106 LDGDEVFIIDKNAALKGTSAGHVVEIRHVDVHQVGVFVALNDDE---KEQTGLIGF 162
 QY 187 HSSGGSVSYDLFPAQGGYPTLLRIYRDKNKTINSEN 223
 Db 163 VKSRNKKIPY-----RVYLENEGLIPEN 185

RESULT 62

UB32_HUMAN
 ID UB32_HUMAN STANDARD; PRT; 1604 AA.
 AC Q8NFA0; Q9BX85; Q9Y591;
 DT 10-OCT-2003 (Rel. 42, Created)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ubiquitin carboxyl-terminal hydrolase 32 (EC 3.1.2.15) (Ubiquitin
 DE thiolesterase 32) (Ubiquitin-specific processing protease 32)
 DE (Deubiquitinating enzyme 32) (NY-REN-60 antigen).
 GN USP32 OR USP10.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=22506395; PubMed=12604796;
 RA Paulding C.A., Ruvelo M., Haber D.A.;
 RT "The Tre2 (USP6) oncogene is a hominoid-specific gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:2507-2511(2003).
 RN [2]
 RP SEQUENCE OF 331-1604 FROM N.A.
 RC TISSUE=Testis;
 RA Sha J.H.;
 RT "Identification of a novel ubiquitin specific protease gene related to
 RT testes development from human testes cDNA library.";
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 536-1363 FROM N.A.
 RX MEDLINE=99438124; PubMed=10508479;
 RA Scanlan M.J., Gordan J.D., Williamson B., Stockert E., Bander N.H.,
 RA Jorgeneel C.V., Gure A.O., Jager D., Jager E., Knuth A., Chen Y.-T.,
 RA Old L.J.;
 RT "Antigens recognized by autologous antibody in patients with renal-
 RT cell carcinoma.";
 RL Int. J. Cancer 83:456-464(1999).
 CC -1- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O =
 CC ubiquitin + a thiol.
 CC -1- SIMILARITY: Belongs to peptidase family C19.
 CC -1- SIMILARITY: Contains 2 EF-hand calcium-binding domains.

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 CC -----
 CC EMBL: AF533230; AA097922.1; -
 CC EMBL: AF350251; AAK30207.1; -
 CC EMBL: AF155116; AAD42882.1; -
 CC MEROPS: C19.044; -
 CC Genew: HGNC:19143; USP32.
 CC InterPro: IPR006615; DUSP.
 CC InterPro: IPR002048; EF-hand.
 CC InterPro: IPR001394; Peptidase_C19.
 CC InterPro: IPR001125; Recoverin.
 CC Pfam: PF00036; ehand; 2.
 CC Pfam: PF00443; UCH; 1.
 CC PRINTS: PR00450; RECOVERIN.
 CC SMART: SM00695; DUSP; 1.
 CC SMART: SM00054; EPH; 2.

DR PROSITE; PS00018; EF HAND; 2.
 DR PROSITE; PS00972; UCH_2_1; 1.
 DR PROSITE; PS00973; UCH_2_2; 1.
 DR PROSITE; PS0235; UCH_2_3; 1.
 KW Ubl conjugation pathway; Hydrolase; Thiol protease; Multigene family;
 KW Calcium-binding; Repeat.
 FT CA_BIND 241 252 EF-HAND 1 (POTENTIAL).
 FT CA_BIND 277 288 EF-HAND 2 (POTENTIAL).
 FT ACT_SITE 743 743 BY SIMILARITY.
 FT ACT_SITE 1518 1518 BY SIMILARITY.
 FT ACT_SITE 1526 1526 BY SIMILARITY.
 FT CONFLICT 884 884 H -> R (IN REF. 2).
 FT CONFLICT 1167 1167 C -> S (IN REF. 2).
 FT CONFLICT 1604 AA; 181654 MW; A621F764B7632E3 CRC64;
 SQ SEQUENCE 1604 AA; 181654 MW; A621F764B7632E3 CRC64;
 Query Match 6.3%; Score 77.5; DB 1; Length 1604;
 Best Local Similarity 24.3%; Pred. No. 1.8e+02;
 Matches 41; Conservative 18; Mismatches 53; Indels 57; Gaps 9;
 QY 74 KDATNKYGGKVDLYGAYGYQC-----AGTGNKTA-----CMYGGVT--LHDNNRLTE 121
 DB 29 KDAPKRTCG-----LSYYMGQHCFTREVLDGVPKVAEVIYCSFGGTSGKLHFNLI-- 81
 QY 122 EKKVPIINWIDKQTTVIDKVKTSKEVTQVELDQARHYLHGKFGLYNSDSFGKQVQR 181
 DB 82 ---VGLVLLTRGK-----DEERAKVI---FSLFSSSES-GNYVIR 113
 QY 182 GLIVPHSSEGSVSYDLFDAGQYPTTLRIYRDNKTINSENHIALYL 230
 DB 114 -----BEMERMLHVVGKVPDTLRKCFSEGEKYNKFRNWLF 152
 RESULT 63
 ID POLG PSBMV STANDARD; PRT; 3206 AA.
 AC P29152;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Genome polypeptide [Contains: N-terminal protein (P1); Helper
 DE component polypeptide (EC 3.4.22.45) (HC-Pro); Protein P3; 6 kDa
 DE protein 1 (6K1); Cytoplasmic inclusion protein (CI); 6 kDa protein 2
 DE (6K2); Genome-linked protein (VPG); Nuclear inclusion protein A (NI-A)
 DE (NTA) (EC 3.4.22.44) (49 kDa proteinase) (49 kDa-Pro); Nuclear
 DE inclusion protein B (NI-B) (NIB) (RNA-directed RNA polymerase)
 DE (EC 2.7.7.48); Coat protein (CP)].
 OS Pea seed-borne mosaic virus (strain DpD1).
 OS Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
 OC Potyvirus.
 OC NCBI_TaxID=31736;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92044431; PubMed=1940858;
 RA Johansen E., Rasmussen O.F., Heide M., Borkhardt B.;
 RT "The complete nucleotide sequence of pea seed-borne mosaic virus
 RT RNA.";
 RL J. Gen. Virol. 72:2625-2632(1991).
 CC -!- FUNCTION: Helper component-proteinase is required for aphid
 CC transmission and also has proteolytic activity.
 CC -!- FUNCTION: Cytoplasmic inclusion protein has helicase activity. It
 CC may be involved in replication.
 CC -!- FUNCTION: Nuclear inclusion protein A has proteolytic activity,
 CC further restricted by preferences for the amino acids in P6 - P1,
 CC that vary with the species of potyvirus, e.g. Glu-Xaa-Tyr-Xaa-
 CC Gln+(Ser or Gly) for the enzyme from tobacco etch virus. The
 CC natural substrate is the viral polypeptide, but other proteins and
 CC oligopeptides containing the appropriate consensus sequence are
 CC also cleaved.
 CC -!- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC (RNA) (N).
 CC -!- CATALYTIC ACTIVITY: Hydrolyzes a Gly-|-Gly bond at its own C-
 CC terminus, commonly in the sequence -Tyr-Xaa-Val-Gly-|-Gly, in the

CC processing of the potyviral polypeptide.
 CC -!- PTM: VPG is covalently linked to the genomic RNA.
 CC -!- PTM: The viral RNA of potyviruses is expressed as a single
 CC polypeptide which undergoes posttranslational proteolytic
 CC processing resulting in the production of at least eight
 CC individual proteins.
 CC -!- SIMILARITY: HC PROTEINASE BELONGS TO PEPTIDASE FAMILY C6.
 CC -!- SIMILARITY: NI-A PROTEINASE BELONGS TO PEPTIDASE FAMILY C4.
 CC -!- SIMILARITY: Belongs to the potyviruses polypeptide family.
 CC -----
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 CC -----
 CC EMBL; D10930; BAA01726.1; --
 DR PIR; J01331; GNVSPV.
 DR MEROPS; C04.010; --
 DR MEROPS; C06.001; --
 DR InterPro; IPR001410; DEAD.
 DR InterPro; IPR001650; Helicase_C.
 DR InterPro; IPR001730; Peptidase_C4.
 DR InterPro; IPR001456; Peptidase_C6.
 DR InterPro; IPR001592; Poty_coat.
 DR InterPro; IPR002540; Poty_P1.
 DR InterPro; IPR007095; RNA_pol_DS_PS.
 DR InterPro; IPR001205; RNA_pol_P3D.
 DR InterPro; IPR007094; RNA_pol_PSVir.
 DR Pfam; PF00271; helicase_C_1.
 DR Pfam; PF00863; Peptidase_C4; 1.
 DR Pfam; PF00851; Peptidase_C6; 1.
 DR Pfam; PF00757; Poty_coat; 1.
 DR Pfam; PF01577; Poty_P1; 1.
 DR Pfam; PF00680; RNA_dep_RNA_pol; 1.
 DR PRINTS; PR00966; NIAPOTYPTASE.
 DR SMART; SMO0490; HELIC; 1.
 DR SMART; SMO0487; DEXDC; 1.
 DR Hydrolase; Transferase; Thiol protease; RNA-directed RNA polymerase;
 KW Coat protein; Polypeptide; Covalent protein-RNA linkage; Helicase;
 KW ATP-binding.
 FT CHAIN 1 ? N-TERMINAL PROTEIN.
 FT CHAIN 857 ? HELPER COMPONENT PROTEINASE.
 FT CHAIN ? 1266 6 kDa PROTEIN 1.
 FT CHAIN 1267 1902 CYTOPLASMIC INCLUSION PROTEIN.
 FT CHAIN 1903 1955 6 kDa PROTEIN 2.
 FT CHAIN 1956 ? GENOME-LINKED PROTEIN.
 FT CHAIN ? 2395 NUCLEAR INCLUSION PROTEIN A.
 FT CHAIN 2396 2915 NUCLEAR INCLUSION PROTEIN B.
 FT CHAIN 2916 3206 COAT PROTEIN.
 FT SITE 1266 1267 CLEAVAGE (BY 49 kDa PROTEASE).
 FT SITE 1902 1903 CLEAVAGE (BY 49 kDa PROTEASE).
 FT SITE 1955 1956 CLEAVAGE (BY 49 kDa PROTEASE).
 FT SITE 2395 2396 CLEAVAGE (BY 49 kDa PROTEASE).
 FT SITE 2915 2916 CLEAVAGE (BY 49 kDa PROTEASE).
 FT BINDING 2016 2016 COVALENT LINKAGE OF VIRAL RNA (BY
 FT SIMILARITY).
 FT NP_BIND 1351 1358 ATP (POTENTIAL).
 FT SEQUENCE 3206 AA; 364271 MW; 42A3D921BE9A0CBF CRC64;
 Query Match 6.3%; Score 77.5; DB 1; Length 3206;
 Best Local Similarity 25.4%; Pred. No. 4.1e+02;
 Matches 47; Conservative 22; Mismatches 55; Indels 61; Gaps 9;
 QY 38 TENKESDDDFLE-----NTLLFKGFTGHPWYNLLVLDGSKDATNKYKG 82
 DB 1489 TEDLSFDQFVQAQSGGANGCDILKKGHNILVYSSVNEVDRLSKLLVDGFX--VTKVDG 1546
 QY 83 KKVLDYGAHYGYQCAGGTENKTACMYGGVTLHDNNRLTEKK---VPINLWIDGKQTTVP 139

Db 1547 RTMKL-----GGVEI--NTSGTAEKPHFIVATNIENG--VTLD 1581

Qy 140 IDKVKTSKEVTVQELDLQARHVLHGKFLYNSDGFQGVQR-----GLIVFHS 188

Db 1582 IDVVDFGVKV-VAEILDADARTMYNKQAI-----SYGERIQRLGRVGRKQGHALRIGHT 1636

Qy 189 SEGST 193

Db 1637 EKGIT 1641

RESULT 64

V212_FOWPV STANDARD; PRT; 303 AA.

AC Q9J523;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Probable serine/threonine protein kinase PPV212 (EC 2.7.1.-).

GN PPV212.

OS Fowlpox virus (FPV).

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

OC Avipoxvirus.

OX NCBI_TaxID=10261;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20193820; PubMed=10729156;

RA Afonso C.L., Tulman E.R., Lu Z., Zeak L., Kutish G.F., Rock D.L.;

RT "The genome of fowlpox virus."

RL J. Virol. 74:3815-3831(2000).

CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.

CC POXVIRUSES SUBFAMILY.

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CC EMBL; AF198100; AAF44556.1; -

DR HSP; Q06486; ICK1.

DR InterPro; IPR000719; Prot kinase.

DR InterPro; IPR008271; Ser Thr_pkin_AS.

DR Pfam; PF00069; pkinase; 2.

DR ProDom; PD000001; Prot_kinase; 1.

DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.

DR PROSITE; PS00108; PROTEIN KINASE ST; 1.

DR PROSITE; PS00011; PROTEIN KINASE DOM; 1.

DR Transferrase; Serine/threonine-protein kinase; ATP-binding.

FT DOMAIN 25 303 PROTEIN KINASE.

FT ND BIND 31 39 ATP (BY SIMILARITY).

FT BINDING 54 54 ATP (BY SIMILARITY).

FT ACT_SITE 160 160 BY SIMILARITY.

Qy SEQUENCE 303 AA; 34775 MW; 4B1BFD17C5220716 CRC64;

Query Match 6.2%; Score 77; DB 1; Length 303;

Best Local Similarity 19.9%; Pred. No. 27;

Matches 51; Conservative 42; Mismatches 69; Indels 94; Gaps 13;

Qy 10 KDLRKSELOQTALGN--LKOIYYNEK-----AITENKESDDOFLNTLLFKGFFTG 60

Db 18 EDITKNWILGKQLGSGFGFLVQVSCSKSEIDCVAKIELKESG-----GLFCE 66

Qy 61 HPVNDLLVDLGSKDANKYKGGKVDLYG--AYGYQCAGGTENKTACMYGGVTLHDN-- 116

Db 67 INFYNRWKNKTSLDTW--MKQKIDVIGPSFHGF-----GITYKNVE 109

Qy 117 -----NRTEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHY 162

Db 110 YRFALIQRLGRDLENILSEKFN-----TVIKKLAIKILDI--LKF 150

Qy 163 LHQKFLYNSDGFQGVQRGLIVFHSSEGST--VSYDL---PDAQGYPTLLRIYRDNK 217

Db 151 IHSK-----EFSGHDIKAGNILFGKDDKDKVLYLDYGLATKYSSNGKHKE-----Y 195

Qy 218 TINSNLHIALYLYTT 233

Db 196 TINKPHNGTMAFTS 211

RESULT 65

TYPH_MYCPI STANDARD; PRT; 419 AA.

AC P47717;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Thymidine phosphorylase (EC 2.4.2.4) (TdrPase).

GN DEOA.

OS Mycoplasma plium.

OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.

OX NCBI_TaxID=2122;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN=BER;

RX MEDLINE=93352438; PubMed=8349569;

RA Tham T.N., Ferris S., Kovacic R., Montagnier L., Blanchard A.;

RT "Identification of Mycoplasma plium genes involved in the salvage pathways for nucleosides."

RL J. Bacteriol. 175:5281-5285(1993).

CC -!- FUNCTION: THE ENZYMES WHICH CATALYZE THE REVERSIBLE PHOSPHORYLOSIS OF PYRIMIDINE NUCLEOSIDES ARE INVOLVED IN THE DEGRADATION OF THESE COMPOUNDS AND IN THEIR UTILIZATION AS CARBON AND ENERGY SOURCES, OR IN THE RESCUE OF PYRIMIDINE BASES FOR NUCLEOTIDE SYNTHESIS.

CC -!- CATALYTIC ACTIVITY: Thymidine + phosphate = thymine + 2-deoxy-D-ribose 1-phosphate.

CC -!- SUBUNIT: Homodimer (By similarity).

CC -!- SIMILARITY: Belongs to the thymidine/pyrimidine-nucleoside phosphorylase family.

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CC EMBL; L13289; AAA25432.1; -

DR FIR; C53312; C53312.

DR HSP; P77836; 1BRW.

DR InterPro; IPR000312; Glyco_trans_3.

DR InterPro; IPR000053; Thymid_phosphils.

DR Pfam; PF02885; Glycos_trans_3N; 1.

DR Pfam; PF00591; Glycos_transf_3; 1.

DR PIRSF; PIRSF00478; Thymid_phosphils; 1.

DR ProDom; PD001864; Glyco_trans_3; 1.

DR ProDom; PD005916; Thymid_phosphils; 1.

DR PROSITE; PS00647; THYMID_PHOSPHORYLASE; 1.

KW Transferrase; Glycosyltransferase.

Qy SEQUENCE 419 AA; 47278 MW; C1620F2BF33929E3 CRC64;

Query Match 6.2%; Score 77; DB 1; Length 419;

Best Local Similarity 27.8%; Pred. No. 39;

Matches 44; Conservative 22; Mismatches 58; Indels 34; Gaps 10;

Qy 36 AITENKESDDO--FLENTLFGK--FTTCHPWYNDLLVDLGSKDANKYKGGKVD----- 86

Db 44 AIFWFLDNDNELYFLTKAMIDSGIKYKFPYKYLID--KHSTGGI-GDKVSIALLRPI 99

Qy 87 -----LYGAYGYQCAGGTENKTACMYGGVTLHDNRLTEKKV--PINLWDGK 134

Db 100 LVSFGLGVAKLSRGLGF--TGGTIDKLE-----SINVNTDIDLKNSKILNIAMFVQG 153

[illegible]

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Db 213 KUKGKPKFNTKSKYISFGTCNNNDYYINTEKSKAILFHNKIVDTSNILL-----N 267
QY 60 GHPWYNDLLVGLSGDATNKYKGGKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRL 119
Db 268 GHNYENILTSLAISQMKFDQKVSINVLLKFL-----GLPHRFQ-----TVHNNNI 315
QY 120 TEKKVPEINLWI-DGKQTTVPIDKVKTSKEVTVQ 153
Db 316 S-----WINDSKSTNV--DSTKAALKNLKIK 339

RESULT 68
Y314 MYCGE
ID Y314 MYCGE STANDARD; PRT; 443 AA.
AC Q49415; Q49279;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG314.
GN MG314.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
ON NCBI_TaxID=2097;
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33530 / G-37;
RX MEDLINE=96026346; PubMed=7569993;
RA Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A.,
RA Fleischmann R.D., Bult C.J., Kiehl J.F., Sutton G., Kelley J.M.,
RA Pritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhmann J.L.,
RA Nguyen D.T., Uterback T.R., Saudek D.M., Phillips C.A., Merrick J.M.,
RA Tomb J.F., Dougherty B.A., Bort K.F., Hu P.C., Lucier T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RA "The minimal gene complement of Mycoplasma genitalium."
RL Science 270:397-403(1995).
RN [2]
RP SEQUENCE OF 70-171 FROM N.A.
RC STRAIN=ATCC 33530 / G-37.
RX MEDLINE=94075230; PubMed=8253680;
RA Peterson S.N., Hu P.C., Bort K.F., Hutchison C.A. III;
RA "A survey of the Mycoplasma genitalium genome by using random
RA sequencing."
RL J. Bacteriol. 175:7918-7930(1993).
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CC -----
DR EMBL; U39712; AAC71536.1; -.
DR EMBL; U02151; AAD12432.1; -.
DR PIR; G64234; G64234.
DR TIGR; MG314; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 443 AA; 51132 MW; 3EP503F9168015D7 CRC64;

Query Match 6.2%; Score 77; DB 1; Length 443;
Best Local Similarity 21.5%; Pred. No. 42;
Matches 41; Conservative 26; Mismatches 82; Indels 42; Gaps 7;

QY 8 NEXDLRKK-----SELQGTALGNLKQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW 63
Db 19 NNETLTRIKTSDPAKTLAQKLILYFLEEKQKVKTKKPHFLFGS----- 66
QY 64 YNDLLVLDLGSKDATNK-YGKKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNR 118
Db 67 FHDKFIQLGQNLSEKELAAKFDLTDALNLYNVAVKNLFNK-----ELNSFTK 118
QY 119 LTEKKVPIINLWIDGKQTTVPIDKVKTSKEVTVQ-----SKKEVTVQELDLQARHYLHGKFG 168

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Db 119 LAETQVKPSELOENNKTKVDNPSFOTINNQQSLNLENNILQOTLQVRAR---DRAFG 175
QY 169 LYNSDSPFGKV 179
Db 176 RFTSEKLVGKI 186

RESULT 69
ID IBMP FMVD STANDARD; PRT; 512 AA.
AC P09524;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Inclusion body matrix protein (Viroplasma).
GN VI.
OS Figwort mosaic virus (strain Dxs) (FMV).
OC Viruses; Retroid viruses; Caulimoviridae; Caulimovirus.
ON NCBI_TaxID=10650;
RP SEQUENCE FROM N.A.
RX MEDLINE=88040466; PubMed=3671088;
RA Richins R.D., Scholthof H.B., Shepherd R.J.;
RA "Sequence of figwort mosaic virus DNA (caulimovirus group).";
RL Nucleic Acids Res. 15:8451-8466(1987).
CC -1- FUNCTION: ENHANCES THE TRANSLATION OF DOWNSTREAM ORF'S ON
CC POLYICISTRONIC MRNA'S DERIVED FROM FIGWORT MOSAIC VIRUS.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic inclusion bodies.
CC -1- MISCELLANEOUS: THE INCLUSION BODIES ARE THE SITE OF VIRAL DNA
CC SYNTHESIS, VIRION ASSEMBLY AND ACCUMULATION IN THE INFECTED CELL.
CC -1- SIMILARITY: Belongs to the caulimoviruses viroplasma family.
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CC -----
DR EMBL; X06166; CAA29528.1; -.
DR PIR; S01284; WMCVFM.
DR InterPro; IPR002609; Caulimo.VI.
DR Pfam; PF01693; Caulimo.VI.1.
KW Trans-acting factor; Translation regulation.
SQ SEQUENCE 512 AA; 58207 MW; AE34455BF2FB0391 CRC64;

Query Match 6.2%; Score 77; DB 1; Length 512;
Best Local Similarity 23.6%; Pred. No. 50;
Matches 56; Conservative 34; Mismatches 91; Indels 56; Gaps 11;

QY 5 BEINEKDLRKKSELQGTALGNLK-QIYYNE---KAITENKESDDQFLENTLL---FKGF 57
Db 2 EEL--KALRLKEKILELNSVKNQIHAYEESLKATTVNSVQSGEILQTESIECEPAQK 59
QY 58 FTGHPWYND-LLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTENKTACMYGGVTLHDN 116
Db 60 ETPNPVKADSLTLKILGNERNQNPLEGKSKL-----VNLTPK 96
QY 117 NRLTEKKVPIINLWIDGKQTTVPIDKVKTSKEVTV---OELD-----LQARHYLHG 165
Db 97 SDKDKVKSVPANG-SGKDSINPLNPLVALGSKNTILGKQADEEKKPDYLRASNGQS 155
QY 166 KFGLY---NSDSFGG-----KVQRGLVIFHSSSGSTVSVDLFDQAQQYPTLLR 211
Db 156 WFAVYKGPENKEFTTEWEIVADICKRQKSRFRSKQAEVSIISLYNKDIQDPVNFRL 212

RESULT 70
YNN6 YEAST
ID YNN6 YEAST STANDARD; PRT; 425 AA.
AC P53911;

```


FT	CHAIN	32	455	HYPOTHETICAL PEPTIDASE YWAD.
SO	SEQUENCE	455 AA:	49450 MW:	89EE6A6EEB0CCE18 CRC64;

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Db 229 LNIKQDVCLIEBVTGLSEFPVILLKIPQKFLPELPEEVIVSMRTHQKYKFCLEKNGSFA 288
Qy 195 SYDLFDAGQVYDPTLLRIYRDNKNTINSENLHIALYLY 231
Db 289 PYFLFVINGRFVNTL-ITQGNKVLRLADALYFY 324

RESULT 74
SYA_RALSO STANDARD; PRT; 884 AA.
ID SYA_RALSO STANDARD; PRT; 1002 AA.
AC Q8V193.
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ALanyl-tRNA synthetase (EC 6.1.1.7) (Alanine-tRNA ligase) (AlaRS).
GN ALAL OR RSC0737 OR RS05040.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave P., Gouzy J., Mangenot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choisme N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Sigquier P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
CC -!- CATALYTIC ACTIVITY: ATP + L-alanine + tRNA(Ala) = AMP +
CC di-phosphate + L-alanyl-tRNA(Ala).
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
CC
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AL646061; CAD14499.1; -.
DR HAMAP; MF_00036; -.
DR InterPro; IPR003156; DHAL.
DR InterPro; IPR002318; tRNA-synt_2c.
DR InterPro; IPR006193; tRNA_synt_Ala.
DR Pfam; PF02272; DHAL; 1. 2c; 1.
DR Pfam; PF01411; tRNA-synt_2c; 1.
DR PRINTS; PR00980; TRNASYNTHALA.
DR TIGRFAMs; TIGR00344; alaS; 1.
DR PROSITE; PS00860; AA tRNA_LIGASE II Ala; 1.
KW Aminoacyl-tRNA synthetase, Protein Biosynthesis; Ligase; ATP-binding;
KW Complete proteome.
SQ SEQUENCE 884 AA; 96738 MW; 6DF71962D21305880 CRC64;

Query Match 6.2%; Score 76.5; DB 1; Length 884;
Best Local Similarity 25.4%; Pred. No. 1.1e+02;
Matches 51; Conservative 30; Mismatches 73; Indels 47; Gaps 12;

Qy 16 SELOGTALGNLKQIYYNEKATENKESDDQFLENTLLFKGFTT-GHPV-----YND 66
Db 377 SLIDG-ALGELK-----AAGDKQKRLDGLAFKLDHTYGFPLDLTDQVCREND 425
Qy 67 LLDVLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMGVTLHDNNRUTEKKVP 126
Db 426 VIVDEAFAFDMNRQREAAAGK---FKWAAGTLDTY3---DKTFHGVDDQLLSSTSRV 479
Qy 127 INLWIDGKQTIVDKVTKTSKEVTVOELDQARHYLHGKFLGYNLSDSPGKVGQRLIVF 186
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Db 480 TALFVVG--ASVP--EMRFGQTGVVY--LD-----HTFF---YAESGQVGDQGTLL-- 521
Qy 187 HSSEGSTVSYDLFDAGQGYPD 207
Db 522 ---KAATVWFVDVADTQKVLPE 539

RESULT 75
TAGA_VIBCH STANDARD; PRT; 1002 AA.
ID TAGA_VIBCH STANDARD; PRT; 1002 AA.
AC P24019; O68335; Q56595; Q9KTR9;
DT 01-MAR-1992 (Rel. 21, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE ToxR-activated gene A lipoprotein precursor.
GN TAGA OR VC0820.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=98169509; PubMed=9501228;
RA Karolis D.K.R., Johnson J.A., Bailey C.C., Boedeker E.C., Kaper J.B.,
RA Reeves P.R.;
RT "A Vibrio cholerae pathogenicity island associated with epidemic and
RT pandemic strains.";
RL Proc. Natl. Acad. Sci. U.S.A. 95:3134-3139(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
RN [3]
RP SEQUENCE OF 1-576 FROM N.A.
RC STRAIN=Classical Ogawa 395 / ATCC 39541 / Serotype O1;
RX MEDLINE=95189108; PubMed=7883190;
RA Harkey C.W., Everiss K.D., Peterson K.M.;
RT "Isolation and characterization of a Vibrio cholerae gene (tagA) that
RT encodes a ToxR-regulated lipoprotein.";
RL Gene 153:81-84(1995).
RN [4]
RP SEQUENCE OF 1-68 FROM N.A.
RC STRAIN=KF8 56;
RX MEDLINE=91210174; PubMed=1902210;
RA Farset C.R., Mekalanos J.J.;
RT "Expression of the Vibrio cholerae gene encoding aldehyde
RT dehydrogenase is under control of ToxR, the cholera toxin
RT transcriptional activator.";
RL J. Bacteriol. 173:2842-2851(1991).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Potential).
CC -!- SIMILARITY: Contains 1 fibronectin type III domain.
CC -!- CAUTION: Ref.3 sequence differs from that shown in the C-terminus
CC due to a frameshift.
CC -----
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Search completed: August 12, 2004, 13:30:35
Job time : 9.11863 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 12, 2004, 13:23:20 ; Search time 20.2698 Seconds
(without alignments)
3626.866 Million cell updates/sec

Title: US-09-900-766-3

Perfect score: 1238

Sequence: 1 SEKSEENEDLRKSELOG.....RDNKTINSENLHLYVTT 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

SPTREMBL 25.*

1: sp_archea.*

2: sp_bacteria.*

3: sp_fungi.*

4: sp_human.*

5: sp_invertebrate.*

6: sp_mammal.*

7: sp_mhc.*

8: sp_organelle.*

9: sp_phase.*

10: sp_plant.*

11: sp_rodent.*

12: sp_virus.*

13: sp_vertebrate.*

14: sp_unclassified.*

15: sp_rvirus.*

16: sp_bacteriap.*

17: sp_archeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1037	83.8	260	16 Q931M4	Q931M4 staphylococ
2	992	80.1	260	16 Q99SU3	Q99SU3 staphylococ
3	821	66.3	268	2 Q85217	Q85217 staphylococ
4	481.5	38.9	229	16 Q8NW97	Q8NW97 staphylococ
5	453.5	36.6	258	16 Q9EZM4	Q9EZM4 staphylococ
6	389	31.4	179	2 Q52075	Q52075 staphylococ
7	380.5	30.7	260	16 Q99T46	Q99T46 staphylococ
8	380.5	30.7	261	2 Q9EZM8	Q9EZM8 staphylococ
9	360	29.1	217	2 Q8RR76	Q8RR76 staphylococ
10	360	29.1	241	16 Q53585	Q53585 staphylococ
11	339.5	27.4	242	16 Q85383	Q85383 staphylococ
12	333	26.9	240	16 Q9F0L7	Q9F0L7 staphylococ
13	332	26.8	240	16 Q8NXJ5	Q8NXJ5 staphylococ
14	331.5	26.8	218	2 Q8RR75	Q8RR75 staphylococ
15	330.5	26.7	225	2 Q8VW1	Q8VW1 staphylococ
16	324.5	26.2	225	2 Q9L921	Q9L921 streptococ

17	323.5	26.1	225	16 Q99Z21	Q99Z21 streptococ
18	310	25.0	239	16 Q99T47	Q99T47 staphylococ
19	309.5	25.0	242	16 Q8NVW3	Q8NVW3 staphylococ
20	308.5	24.9	256	2 Q8VLW7	Q8VLW7 staphylococ
21	306.5	24.8	242	2 Q93CC6	Q93CC6 staphylococ
22	306	24.7	239	2 Q9EZM7	Q9EZM7 staphylococ
23	302.5	24.4	239	2 Q85331	Q85331 staphylococ
24	301.5	24.4	239	2 Q85335	Q85335 staphylococ
25	300.5	24.3	239	2 Q05157	Q05157 staphylococ
26	300.5	24.3	266	16 Q8NXJ6	Q8NXJ6 staphylococ
27	299.5	24.2	239	2 Q85333	Q85333 staphylococ
28	299	24.2	242	16 Q8NVW2	Q8NVW2 staphylococ
29	298.5	24.1	207	2 Q7X0E8	Q7X0E8 staphylococ
30	298	24.1	242	2 Q93CC5	Q93CC5 staphylococ
31	298	24.1	242	2 Q54476	Q54476 staphylococ
32	295.5	23.9	239	2 Q85332	Q85332 staphylococ
33	294.5	23.8	218	2 Q7X0E7	Q7X0E7 staphylococ
34	294.5	23.8	234	2 Q85X4	Q85X4 staphylococ
35	293.5	23.7	218	2 Q7X0E9	Q7X0E9 staphylococ
36	287.5	23.2	207	2 Q7X0E6	Q7X0E6 staphylococ
37	283.5	22.9	271	2 Q9F0L6	Q9F0L6 staphylococ
38	282.5	22.8	239	2 Q53678	Q53678 staphylococ
39	282.5	22.8	251	16 Q8K6K5	Q8K6K5 streptococ
40	276.5	22.3	239	2 Q85334	Q85334 staphylococ
41	275	22.2	260	2 Q54971	Q54971 streptococ
42	273	22.1	260	2 Q54738	Q54738 streptococ
43	273	22.1	260	16 Q54739	Q54739 streptococ
44	270.5	21.8	236	2 Q54696	Q54696 streptococ
45	269.5	21.8	236	2 P97163	P97163 streptococ
46	268.5	21.7	222	2 Q9S524	Q9S524 streptococ
47	268.5	21.7	222	2 Q938P4	Q938P4 streptococ
48	268.5	21.7	236	2 Q54779	Q54779 streptococ
49	267.5	21.6	222	2 Q9R931	Q9R931 streptococ
50	264	21.3	258	2 Q9ZNF2	Q9ZNF2 streptococ
51	263.5	21.3	236	2 Q57453	Q57453 streptococ
52	256	20.7	233	2 Q8RR77	Q8RR77 staphylococ
53	256	20.7	258	2 Q9EZM3	Q9EZM3 staphylococ
54	244.5	19.7	209	2 Q93Q05	Q93Q05 streptococ
55	241.5	19.5	209	2 Q9LAE0	Q9LAE0 streptococ
56	241.5	19.5	209	2 Q9LAD8	Q9LAD8 streptococ
57	239.5	19.3	209	2 Q9LAC6	Q9LAC6 streptococ
58	239	19.3	209	2 Q9LAD1	Q9LAD1 streptococ
59	237.5	19.2	209	2 Q9LAE1	Q9LAE1 streptococ
60	237.5	19.2	209	2 Q9LAC4	Q9LAC4 streptococ
61	235.5	19.0	209	2 Q9LAC5	Q9LAC5 streptococ
62	232.5	18.8	209	2 Q9LAD6	Q9LAD6 streptococ
63	232	18.7	209	2 Q9LAD2	Q9LAD2 streptococ
64	231.5	18.7	207	2 Q7WY99	Q7WY99 streptococ
65	231.5	18.7	209	2 Q9LAC7	Q9LAC7 streptococ
66	230.5	18.6	209	2 Q9LAD9	Q9LAD9 streptococ
67	230	18.6	233	16 Q8NZ89	Q8NZ89 streptococ
68	229.5	18.5	209	2 Q9LAC9	Q9LAC9 streptococ
69	228.5	18.5	209	2 Q9LAD4	Q9LAD4 streptococ
70	228.5	18.5	259	2 Q936G4	Q936G4 staphylococ
71	227.5	18.4	209	2 Q9LAC8	Q9LAC8 streptococ
72	227.5	18.4	209	2 Q9LAC3	Q9LAC3 streptococ
73	226.5	18.3	256	2 Q9S1H8	Q9S1H8 streptococ
74	225.5	18.2	209	2 Q9LAD5	Q9LAD5 streptococ
75	222.5	18.0	209	2 Q9LAD7	Q9LAD7 streptococ
76	221.5	17.9	209	2 Q9LAD3	Q9LAD3 streptococ
77	220.5	17.8	233	16 Q99XW1	Q99XW1 streptococ
78	216.5	17.5	209	2 Q9LAD0	Q9LAD0 streptococ
79	212	17.1	234	16 Q8K8Q7	Q8K8Q7 streptococ
80	209	16.9	240	16 Q8P2R5	Q8P2R5 streptococ
81	208	16.8	210	2 Q9K2G9	Q9K2G9 streptococ
82	200	16.2	157	16 Q99TP7	Q99TP7 staphylococ
83	194	15.7	136	16 Q99T49	Q99T49 staphylococ
84	193	15.6	236	2 Q9L920	Q9L920 streptococ
85	189	15.3	234	2 Q93RR9	Q93RR9 streptococ
86	189	15.3	234	2 Q8G9K7	Q8G9K7 streptococ
87	179	14.5	232	16 Q99QW1	Q99QW1 streptococ
88	176.5	14.3	235	16 Q8KX2	Q8KX2 streptococ
89	175.5	14.2	256	2 Q9X9R8	Q9X9R8 streptococ

90 175.5 14.2 256 2 Q9S1H9 streptococc
91 163 13.2 206 2 Q54512 streptococc
92 157.5 12.7 108 2 Q9EZM5 streptococc
93 149.5 12.1 167 2 Q7X0E4 streptococc
94 141.5 11.4 167 2 Q7X0E5 streptococc
95 136.5 11.0 167 2 Q7WS59 streptococc
96 136 11.0 62 16 Q99TP8 streptococc
97 125 10.1 132 2 Q9EZM6 streptococc
98 125 10.1 133 16 Q99T48 streptococc
99 123.5 10.0 227 2 Q849U3 streptococc
100 123.5 10.0 262 16 Q8P0S0 streptococc

ALIGNMENTS

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RESULT 1
Q931M4 PRELIMINARY; PRT; 260 AA.
ID Q931M4
AC Q931M4
DT 01-DEC-2001 (T-EMBLrel. 19, Created)
DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Enterotoxin P.
GN SEP OR SAV1948.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizukami-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kihara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003364; BAB58110.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:coxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 260 AA; 30016 MW; 15C2D36270FA8241 CRC64;

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Query Match 83.8%; Score 1037; DB 16; Length 260;
Best Local Similarity 83.3%; Pred. No. 4.1e-73;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLKSKSELOQTALGNLKQIYYNEKAITENKESDDQFLETLFKGFFTG 60
DB 28 SEKSEINEKDLKSKSELOQTALGNLKQIYYNEKAITENKESDDQFLETLFKGFFTD 87

QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATACMYGVTLHDNNRLT 120
DB 88 HSWYNDLLVDFDSKIDVYKGGKVDLYGAYGYQCAGGTPNKATACMYGVTLHDNNRLT 147

QY 121 EEKVPINLWDGKQTTVPIDKVTSKKEVTQVELDQARHYLKGFLGKGLNSDSFGKVQ 180
DB 148 EEKVPINLWDGKQTTVPIDKVTSKKEVTQVELDQARHYLKGFLGKGLNSDSFGKVQ 207

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QY 181 RGLIVFHSBEGSTVSYDLFDAQOQYPTLLRIYRDNKTINSENHLIALYLYTT 233
DB 208 RGLIVFHSBEGSTVSYDLFDAQOQYPTLLRIYRDNKTINSENHLIALYLYTS 260

RESULT 2
Q99SU3 PRELIMINARY; PRT; 260 AA.
ID Q99SU3
AC Q99SU3
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Enterotoxin P.
GN SEP OR SA1761.
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T., Kanamori M.,
RA Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Ui Y.,
RA Takahashi N.K., Sawano T., Inoue R.-I., Kaito C., Sekimizu K.,
RA Hirakawa H., Kihara S., Goto S., Yabuzaki J., Kanehisa M.,
RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
RA Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003365; BAB43036.1; -.
DR PIR; C89984; C89984.
DR HSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:coxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 260 AA; 29708 MW; 087C5B4EC028CFDB CRC64;

Query Match 80.1%; Score 992; DB 16; Length 260;
Best Local Similarity 78.5%; Pred. No. 1.3e-69;
Matches 183; Conservative 18; Mismatches 32; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLKSKSELOQTALGNLKQIYYNEKAITENKESDDQFLETLFKGFFTG 60
DB 28 SEKSEINEKDLKSKSELOQTALGNLKQIYYNEKAITENKESDDQFLETLFKGFFTG 87

QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATACMYGVTLHDNNRLT 120
DB 88 HQWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATACMYGVTLHDNNRLT 147

QY 121 EEKVPINLWDGKQTTVPIDKVTSKKEVTQVELDQARHYLKGFLGKGLNSDSFGKVQ 180
DB 148 EEKVPINLWDGKQTTVPIDKVTSKKEVTQVELDQARHYLKGFLGKGLNSDSFGKVQ 207

QY 181 RGLIVFHSBEGSTVSYDLFDAQOQYPTLLRIYRDNKTINSENHLIALYLYTT 233
DB 208 RGLIEFHPSSGDSYGYDLFDAQOQYPTQLRIYRDNKTIIKSKNHHIDYLYTT 260

RESULT 3
Q85217

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RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus";
RL Lancet 357:1225-1240(2001).
DR EMBL: AF285760; ARG3856.1; -;
DR EMBL: AF003363; BAB57987.1; -;
DR EMBL: AF003135; BAB42911.1; -;
DR PIR: H89968; H89968.
DR HSSP: P13163; 1ESF.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0015070; F:toxin activity; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bctr1 tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph tox_OB.
DR Pfam: PF01123; Staph_strip_toxin; 1.
DR Pfam: PF02876; Staph_strip_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 258 AA; 29676 MW; 8A6C074F31EF82D2 CRC64;

Query Match 36.8%; Score 453.5; DB 16; Length 258;
Best Local Similarity 40.8%; Pred. No. 1.4e-27;
Matches 95; Conservative 45; Mismatches 78; Indels 15; Gaps 6;

QY 6 EINEKDLRKSELOQTALGNLQIYYNEKAITENKSDDOFLNTLLFKGFFTG 60
DB 32 EVDKDLKKKSDLSKLFNLTS--YITD--ITWQDSENKISTQLLNFIILKNIDIS 87

QY 61 HPWYNLLVLDGSKDATNKYKGKVDLYGAYGYQCAGTGNKTCMYGGVTLHNNRLT 120
DB 88 VLKTSLSKVEFNSSDLANQFKGNIDIVGLYFGNKGVLTEKTSCLYGGVTHDGNOLD 147

QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKVTYQELDLQARHYLHGFGLYNSDSFGKVVQ 180
DB 148 EEKVGIVNFKDGVQGGFV--IKTKAKVTYQELDTKVRFKLENLYKIYNKDT--GNIQ 203

QY 181 RGLIVFHS--SEGTSVSYDLFDAGQGYPTLLRIYRDNKTINSENLHIALYLY 231
DB 204 KGCIFPHSHNHQDSFYDLYNKGVSVAEGAEFFQFYSNRTVSSNVHIDVFLY 256

RESULT 6
Q52075 Q52075 PRELIMINARY; PRT; 179 AA.
AC Q52075;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin D.
GN VIRC2.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OG Plasmid pIB485.
OX NCBI_TaxID=1280;
[1]
SEQUENCE FROM N.A.
RX MEDLINE=89359112; PubMed=2549000;
RA Bayles K.W., Iandolo J.J.;
RT "Genetic and molecular analyses of the gene encoding staphylococcal
RT enterotoxin D";
RL J. Bacteriol. 171:4799-4806(1989).
DR EMBL: M94872; AAA98133.1; -;
DR HSSP: P13163; 1SXT.

DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0046821; C:extrachromosomal DNA; IEA.
DR GO: GO:0015070; F:toxin activity; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph tox_OB.
DR Pfam: PF01123; Staph_strip_toxin; 1.
DR Pfam: PF02876; Staph_strip_tox_C; 1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
KW Plasmid.
SQ SEQUENCE 179 AA; 20563 MW; 579FEE11BC08747 CRC64;

Query Match 31.4%; Score 389; DB 2; Length 179;
Best Local Similarity 50.0%; Pred. No. 9.8e-23;
Matches 75; Conservative 22; Mismatches 53; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAITENKSDDOFLNTLLFKGFFTG 60
DB 26 NENIDSVKEKELHKSELSSTALNNKHSYADKNPIIGENKSTGDOFLNTLLKFFTD 85

QY 61 HPWYNLLVLDGSKDATNKYKGKVDLYGAYGYQCAGTGNKTCMYGGVTLHNNRLT 120
DB 86 LINFEDLLINFSKEMQAQHFKNVDVPIRYINCYGGEIDRTACTYGGVTPHEGNK 145

QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKKEV 150
DB 146 ERKKIPINLWINGVQKEVSLDKVQTDKNL 175

RESULT 7
Q99T46 Q99T46 PRELIMINARY; PRT; 260 AA.
AC Q99T46;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin SeO.
GN SEO OR SAVI830 OR SA1548.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878, 158879;
[1]
SEQUENCE FROM N.A.
RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
EX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus";
RL Lancet 357:1225-1240(2001).
DR EMBL: AP003363; BAB57992.1; -;
DR EMBL: AP003135; BAB42916.1; -;
DR PIR: H89969; H89969.
DR HSSP: P13163; 1SXT.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0015070; F:toxin activity; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bctr1 tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR InterPro: IPR006173; Staph tox_OB.
DR Pfam: PF01123; Staph_strip_toxin; 1.
DR Pfam: PF02876; Staph_strip_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.

```
DR PROSITE, PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE, PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 260 AA; 29836 MW; AC927DDCC3E3B8EF CRC64;

Query Match
Best Local Similarity 30.7%; Score 380.5; DB 16; Length 260;
Matches 96; Conservative 31; Mismatches 87; Indels 29; Gaps 8;

QY 8 NEKD-----LRKKSELOQTALGNLQIYYNE----KAITENKESDDQFLENTLLFKGFF 58
Db 29 NEEDPKIESLCKKSSVDPIALHNINDDYNNRFTTVKSIIVTTE---KFLDFDLFLFKSI- 84
QY 59 TGHWP-----YNDLLVLDGSKDANKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGV 111
Db 85 ---NWLDDGISAEFKDLKVEFSSAISKEFLGKTVDIYGVIYKAHCHGEHQVDFACTYGGV 141
QY 112 TLHNNRLTEKKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYN 171
Db 142 TPENNNKLSPEKNIGVAVYKDNVNVNFTI--VTTDKKVTQAQELDIKVRTKLNNAKLY- 198
QY 172 SDSFGGKVORGLIVPHSSEGSTVS--YDLFDAQGYPTDLLRIYRDNKTINSENHLIALY 229
Db 199 -DRMTSDVQKGIKPHSHSEHKESFYDLYFKGNLPDQYLIYNDNKTIDSSDYHIDVY 257
QY 230 LYT 232
Db 258 LFT 260

RESULT 8
Q9EZM8 PRELIMINARY; PRT; 261 AA.
AC Q9EZM8;
DT 01-MAR-2001 (TRENBLrel. 16, Created)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DE 01-OCT-2003 (TRENBLrel. 25, Last annotation update)
SE SEQ.
GN SEC.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A900322;
RA Jaraud S., Peyrat M.A., Lim A., Tristan A., Bes M., Mougel C.,
Etienne J., Vandenesch F., Bonneville M., Lina G.;
RT "egc, A highly prevalent operon of enterotoxin gene, forms a putative
nursery of superantigens in Staphylococcus aureus.";
RL J. Immunol. 166:669-677(2001).
DR EMBL; AF285760; AAG36951.1; -.
DR HSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR Pfam; PF01123; Staph_tox_C; 1.
DR Pfam; PF02876; Staph_tox_OB.
DR PRINTS; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 261 AA; 29949 MW; 24DA4DD766288EC CRC64;

Query Match
Best Local Similarity 30.7%; Score 380.5; DB 2; Length 261;
Matches 96; Conservative 31; Mismatches 87; Indels 29; Gaps 8;

QY 8 NEKD-----LRKKSELOQTALGNLQIYYNE----KAITENKESDDQFLENTLLFKGFF 58
Db 29 NEEDPKIESLCKKSSVDPIALHNINDDYNNRFTTVKSIIVTTE---KFLDFDLFLFKSI- 84
QY 59 TGHWP-----YNDLLVLDGSKDANKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGV 111
Db 85 ---NWLDDGISAEFKDLKVEFSSAISKEFLGKTVDIYGVIYKAHCHGEHQVDFACTYGGV 141
QY 112 TLHNNRLTEKKVPINLWIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYN 171
Db 142 TPENNNKLSPEKNIGVAVYKDNVNVNFTI--VTTDKKVTQAQELDIKVRTKLNNAKLY- 198
QY 172 SDSFGGKVORGLIVPHSSEGSTVS--YDLFDAQGYPTDLLRIYRDNKTINSENHLIALY 229
Db 199 -DRMTSDVQKGIKPHSHSEHKESFYDLYFKGNLPDQYLIYNDNKTIDSSDYHIDVY 257
QY 230 LYT 232
Db 258 LFT 260

RESULT 9
Q8RR76 PRELIMINARY; PRT; 217 AA.
AC Q8RR76;
DT 01-JUN-2002 (T-EMBLrel. 21, Created)
DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Enterotoxin H (fragment).
SEH.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21871379; PubMed=11880405;
RA Omoie K., Ishikawa M., Shimoda Y., Hu D.L., Ueda S., Shinagawa K.;
RT "Detection of seg, seh, and sei genes in Staphylococcus aureus
isolates and determination of the Enterotoxin Productivities of S.
aureus Isolates Harboring seg, seh, or sei Genes.";
RL J. Clin. Microbiol. 40:857-862(2002).
DR EMBL; AB060536; BAB85990.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_tox_C; 1.
DR Pfam; PF02876; Staph_tox_OB.
DR PRINTS; PS00279; BACTRLTOXIN_1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 217 AA; 25143 MW; A8A44E23F31DBE80D CRC64;

Query Match
Best Local Similarity 29.1%; Score 360; DB 2; Length 217;
Matches 84; Conservative 45; Mismatches 83; Indels 12; Gaps 7;

QY 10 KDLRKSELOQTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPWNLDLV 69
Db 1 EDLHDKSELTDALAN--AYQYNHPFIKENIKSDEISGEKDLIFRN--QDMSG-NDLRV 55
QY 70 DLGSKDANKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLTEKKVPINL 129
Db 56 KEATADLAQKFNKVDIYGASFYKCKEISENISECLYGGTTL-NSKLQAGERVIGANV 114
QY 130 WIDGKQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDFGKVGORGLIVPHSS 189
Db 115 WVDGQKTEL--IRTNKNVTLOELDIKRIKILSKDKYIKYKDS---EISGLIEFDWK 169
QY 190 EGSTVSYDLFDAQGYPTDLLRIYRDNKTINSENHLIALYLT 232
```

Query Match

Best Local Similarity 35.6%; Pred. No. 1e-18;
Matches 84; Conservative 37; Mismatches 78; Indels 37; Gaps 9;

QY 8 NEXDLRKKSELQG-TALGNLKQIV-...-YNEKAITENKESDDOFLNTLLFKGFFTHGP 62
Db 17 NIKDL-...-TAAQDIGNVLRNFTKHDYIDLKGVTDNPIANQLB-...-FSTG-- 64
QY 63 WYNLLVDLGSKDATNRYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEE 122
Db 65 -TNDLISENNWDEISKFKGKLDIFGIDYNGPC-...-KSKMYGGATL-SQYLNSA 116
QY 123 KKVPIWLDGKQTVTDIDKVTSSKVTVOELDLQARHLYHGKFGYNSDSG-GK-... 178
Db 117 RKIPINLVWNGKHTISTDKIATNKLVTAGIEDVKLRRLYQEBEYNYGHNTTKGKEYG 176
QY 179 -...-VQRGGLIVFSSSEGTSVSYDLFDAQGGYPTDLLRIYRDNKTIINSENLIH 226
Db 177 YKSXYGSPNGKVLFLHNNKESYSYDLFYTGDLGVPVFLKIYEDNKIESEKPHL 232

RESULT 12
ID Q9FOL7 PRELIMINARY; PRT; 240 AA.
AC Q9FOL7;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Sel (Extracellular enterotoxin L).
GN SEL OR SAV2008 OR SA1816.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699),
OS Staphylococcus aureus (strain N315), and
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878, 158679, 1280;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S.aureus;
RX MEDLINE=20566668; PubMed=11114901;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Hiramatsu K.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus aureus";
RL Lancet 357:1225-1240(2001).
DR EMBL; AF217235; RAG29598.1;
DR EMBL; AF2003364; BAB58170.1;
DR EMBL; AF2003135; BAB43096.1;
DR PIR; G89991; G89991.
DR HSSP; P13163; 1ESP.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0003405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strip_toxin; 1.
DR Pfam; PF02876; Staph_strip_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; Staph Strep toxin 1; 1.
DR PROSITE; PS00278; Staph Strep toxin 2; 1.
DR KW Complete proteome.
SQ SEQUENCE 240 AA; 27478 MW; 85CD62DA731C3D95 CRC64;

DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 240 AA; 27496 MW; F40D62DA73197881 CRC64;

Query Match 26.9%; Score 333; DB 16; Length 240;
Best Local Similarity 35.0%; Pred. No. 3.3e-18;
Matches 77; Conservative 37; Mismatches 72; Indels 34; Gaps 6;

QY 24 GNLKQIY-...-YNEKAITENKESDDOFLNTLLFKGFFTHGPWYND-LLVDLGSKDATN 78
Db 31 GNLRNFTYKVEYVNLKNVKNKSPESHRL-...-YSYKNDTLVAFDFNEIITS 79
QY 79 KYGKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDGKQTV 138
Db 80 DLKGNVDVFGYSKY-...-GNSRT-...-IYGWTKAENNKLDSPRIIPINLWIDGKQTV 133
QY 139 PIDKVTSKKEVTVOELDLQARHLYHGKFGY-...-NSDSFGGKVGQGLIYF 186
Db 134 TTKSVSTDKWVTAQIEDVKLRKYLQDEENIYGHNDTGKKEYGTSKSYSGFDKGSVVF 193
QY 187 HSSEGTSVSYDLFDAQGGYPTDLLRIYRDNKTIINSENLIH 226
Db 194 HMNDGNSFNYSYDLFYTGGLPESFLKIYKDNKTVDSTQFHL 233

RESULT 13
ID Q8XJ5 PRELIMINARY; PRT; 240 AA.
AC Q8XJ5;
DT 01-OCT-2002 (Tremblrel. 22, Created)
DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Extracellular enterotoxin L.
GN SEL2 OR MW0760.
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22040717; PubMed=12044378;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-acquired MRSA";
RL Lancet 359:1819-1827(2002).
DR EMBL; AF004824; BAB594625.1;
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strip_toxin; 1.
DR Pfam; PF02876; Staph_strip_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; Staph Strep toxin 1; 1.
DR PROSITE; PS00278; Staph Strep toxin 2; 1.
DR KW Complete proteome.
SQ SEQUENCE 240 AA; 27478 MW; 85CD62DA731C3D95 CRC64;

Query Match 26.8%; Score 332; DB 16; Length 240;
Best Local Similarity 35.0%; Pred. No. 4e-18;
Matches 77; Conservative 37; Mismatches 72; Indels 34; Gaps 6;

QY 24 GNLKQIY-...-YNEKAITENKESDDOFLNTLLFKGFFTHGPWYND-LLVDLGSKDATN 78
Db 31 GNLRNFTYKVEYVNLKNVKNKSPESHRL-...-YSYKNDTLVAFDFNEIITS 79
QY 79 KYGKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEKKVPINLWIDGKQTV 138

Db 80 DLKGNVDFGYSYK---GNSRT--YGVTVKAENKLDSPRIIPINLIINGKHQTV 133
 QY 139 PIDKVTSKKEVTVQELDLQARHYLHGKFGLY-----NDSFGGKVQORGLIVF 186
 Db 134 TTKSVSTDKKMTVAQEIADVLRKYLODEFNIYGHNDTGKGYCTSKFYSGFDKGSVVF 193
 QY 187 HSEGSTSVSYDLFDAQOQYPTLLRIYRDNKTINSENLIH 226
 Db 194 HINDGSNFSYDLFTYTGGLPESFLKIYKDKNTVDSFPHL 233

RESULT 14

Q8RR75 PRELIMINARY; PRT; 218 AA.
 AC Q8RR75;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Enterotoxin I (Fragment).
 GN SEI.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OC NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21871379; PubMed=11880405;
 RA Omoe K., Ishikawa M., Shimoda Y., Hu D.L., Ueda S., Shinagawa K.;
 RT "Detection of seg, seh, and sei genes in Staphylococcus aureus
 RT Isolates and Determination of the Enterotoxin Productivities of S.
 RT aureus Isolates Harboring seg, seh, or sei Genes.";
 RL J. Clin. Microbiol. 40:857-862(2002).
 DR EMBL: AB060537; BAB8591.1;
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0015070; F:toxin activity; IEA.
 DR GO: GO:0009405; P:pathogenesis; IEA.
 DR InterPro: IPR008992; Bact_endotox.
 DR InterPro: IPR006123; Staph7Strep_toxin.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR Pfam: PF01123; Staph_Strep_toxin; 1.
 DR Pfam: PF02876; Staph_Strep_toxin; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 218 AA; 24909 MW; 1017728FB71BF662 CRC64;

Query Match 26.8%; Score 331.5; DB 2; Length 218;
 Best Local Similarity 35.0%; Pred. No. 3.9e-18;
 Matches 77; Conservative 37; Mismatches 73; Indels 33; Gaps 7;

QY 23 LGNLKQIY----YNNKATENKESDDQFLENTLLFKGFTGHPWNTDLLVLGSKDATN 78
 Db 6 VGNLRFYTKHDIYDLKGYTDKNLPANQLE-----FSTG---TNDLISESNWDNIS 55
 QY 79 KYGKKVLYGAYYGQAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGQKTV 138
 Db 56 KFKGKKLDIFGIDYNGPC-----KSKYMGFGATL-SCGYLNSARKIPINLWNGKHXTI 108
 QY 139 PIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDFG-GK-----VQORGLIVF 186
 Db 109 STDXTANKKLVTQAEIDVLRKYLODEFNIYGHNTTGKGYCTSKFYSGFNNKRVLF 168
 QY 187 HSEGSTSVSYDLFDAQOQYPTLLRIYRDNKTINSENLIH 226
 Db 169 HLNNEKSFYDLFTYTGGLPESFLKIYEDNKIESEKPHL 208

RESULT 15

Q8VWV1 PRELIMINARY; PRT; 225 AA.
 AC Q8VWV1;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Exotoxin I.
 GN SPEI.
 OS Streptococcus pyogenes.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OC NCBI_TaxID=1314;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=M1;
 RX MEDLINE=21259899; PubMed=11359827;
 RA Proft T., Arcus V.L., Handley V., Baker E.N., Fraser J.D.;
 RT "Immunological and biochemical characterization of streptococcal
 RT pyrogenic exotoxins I and J (SPE-I and SPE-J) from Streptococcus
 RT pyogenes.";
 RL J. Immunol. 166:6711-6719(2001).
 DR EMBL: AF438524; AAL31571.1;
 DR GO: GO:0005576; C:extracellular; IEA.
 DR GO: GO:0015070; F:toxin activity; IEA.
 DR GO: GO:0009405; P:pathogenesis; IEA.
 DR InterPro: IPR008992; Bact_endotox.
 DR InterPro: IPR006177; BctrI_tox.
 DR InterPro: IPR006123; Staph7Strep_toxin.
 DR InterPro: IPR006126; Staph/Strep_tox.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR Pfam: PF01123; Staph_Strep_toxin; 1.
 DR Pfam: PF02876; Staph_Strep_toxin; 1.
 DR PRINTS: PR00279; BACTRLTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 SQ SEQUENCE 225 AA; 25654 MW; DB193667890ACDAF CRC64;

Query Match 26.7%; Score 330.5; DB 2; Length 225;
 Best Local Similarity 33.9%; Pred. No. 4.8e-18;
 Matches 75; Conservative 43; Mismatches 80; Indels 23; Gaps 6;

QY 25 NLKQIYYNKAITENKESDDQFLENTLLFKGFTGHPWNTDLLVLGSKDATNKYK 81
 Db 8 NLRNLYSTYDPTTEVKKINEGPPFSGSLFYKNI-----PYGNSIELKVELNSVEKANFFS 63
 QY 82 GKVDLYGAYYGQAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDG---KQTTV 138
 Db 64 GKRVDIPTLEYSPPCSNIKNS---YGGITLSDGNRI-DKKNIPVNFIDGVQQXSYT 119
 QY 139 PIDKVTSKKEVTVQELDLQARHYLHGKFGLY-----NDSFGGKVQORGLIVPHSS 189
 Db 120 DISTVSTDKKEVTIQELDLVLRKYLODEFNIYGHNDTGKGYCTSKFYSGFNNIIFHLN 179
 QY 190 EGSTVSYDLFDAQOQYPTLLRIYRDNKTINSENLIHLYL 230
 Db 180 SGERISYNLFDTGHDRESNLKYSNDKNTAYSQDLHDIYL 220

RESULT 16

Q9L921 PRELIMINARY; PRT; 225 AA.
 ID Q9L921
 AC Q9L921;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE 25.7 kDa protein.
 OS Streptococcus equi.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OC NCBI_TaxID=1336;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CF32;
 RA Artushin S.C., Timoney J.F., Sheoran A.S.;
 RT "Identification and molecular characterization of mitogens from
 RT Streptococcus equi.";
 RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF186180; AAF72808.1;
 DR HSP; P13163; ISXT.

DR GO:GO:0005576; C:extracellular; IEA.
DR GO:GO:0015070; F:toxin activity; IEA.
DR GO:GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox; C; 1.
DR PRINTS; PR00279; BACTRUTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 225 AA; 25684 MW; EB43D47B26FB9F89 CRC64;

Query Match 26.2%; Score 324.5; DB 2; Length 225;
Best Local Similarity 33.5%; Pred. No. 1.4e-17;
Matches 74; Conservative 43; Mismatches 81; Indels 23; Gaps 6;

QY 25 NLKQIYYNEKAITENKESDDQFLENTLLFKGFFTHFWYN---DLLVDLGSKDATNKYK 81
DB 8 NLRNLYSTYDPTVEVKGKINEGPPFSGSLFYKNI---PYGNSSIELKVELNSVEKAFKS 63
QY 82 GKVDLYGAYGYQACAGTGNKTACMYGVTLHNNRLTEKKVPINLWIDG---KQTTV 138
DB 64 GKRVDFITLTPLEYPSPCNISNKKNS---YGGITLSDGNRI-DKXNIPVNIIFIDGVQKYSYT 119
QY 139 PIDKVKTSKKEVTQVELDLQARHYLHGKFLY-----NSDSFGKVGQRLIVPHSS 189
DB 120 DISTVSTDKKEVTIQELDVKSRVYLOKHFNIGYGVDFGRSSRFQSGFEENIIIFHLN 179
QY 190 EGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHLIALYL 230
DB 180 SGERISYNLFTDGHGDRSMLKKYSNDKNTAYSDQLHIDIYL 220

RESULT 17
Q99Z21 ID Q99Z21 PRELIMINARY; PRT; 225 AA.
AC Q99Z21;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Streptococcus exotoxin 1.
GN SPI OR SPI007.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296;
RA Ferretti J.J., McShan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,
Primeaux C., Szate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
Xuan X., Clifton S.W., Roe B.A., McLaughlin R.;
RA "Complete genome sequence of an M1 strain of Streptococcus pyogenes";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
DR EMBL; AE006546; AAK33906.1; -.
DR HSSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox; C; 1.
DR PRINTS; PR00279; BACTRUTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.

DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 225 AA; 25611 MW; CE0D6736CC11CC04 CRC64;

Query Match 26.1%; Score 323.5; DB 16; Length 225;
Best Local Similarity 33.5%; Pred. No. 1.7e-17;
Matches 74; Conservative 43; Mismatches 81; Indels 23; Gaps 6;

QY 25 NLKQIYYNEKAITENKESDDQFLENTLLFKGFFTHFWYN---DLLVDLGSKDATNKYK 81
DB 8 NLRNLYSTYDPTVEVKGKINEGPPFSGSLFYKNI---PYGNSSIELKVELNSVEKAFKS 63
QY 82 GKVDLYGAYGYQACAGTGNKTACMYGVTLHNNRLTEKKVPINLWIDG---KQTTV 138
DB 64 GKRVDFITLTPLEYPSPCNISNKKNS---YGGITLSDGNRI-DKXNIPVNIIFIDGVQKYSYT 119
QY 139 PIDKVKTSKKEVTQVELDLQARHYLHGKFLY-----NSDSFGKVGQRLIVPHSS 189
DB 120 DISTVSTDKKEVTIQELDVKSRVYLOKHFNIGYGVDFGRSSRFQSGFEENIIIFHLN 179
QY 190 EGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHLIALYL 230
DB 180 SGERISYNLFTDGHGDRSMLKKYSNDKNTAYSDQLHIDIYL 220

RESULT 18
Q99T47 ID Q99T47 PRELIMINARY; PRT; 239 AA.
AC Q99T47;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin SEM.
GN SEM OR SAV1829 OR SA1647.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158878, 158879;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=S. aureus (strain Mu50), and S. aureus (strain N315);
RX MEDLINE=21311952; PubMed=11418146;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
Kanamori M., Matsumaru H., Murayama A., Murakami H., Hosoyama A.,
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RA "Whole genome sequencing of methicillin-resistant Staphylococcus
aureus";
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003363; BAB57991.1; -.
DR EMBL; AP003135; BAB42915.1; -.
DR PIR; D89969; D89969.
DR HSSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox; C; 1.
DR PRINTS; PR00279; BACTRUTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 239 AA; 27370 MW; 5F29665125705600 CRC64;

Query Match 25.0%; Score 310; DB 16; Length 239;
Best Local Similarity 32.1%; Pred. No. 2.1e-16;
Matches 70; Conservative 40; Mismatches 82; Indels 26; Gaps 5;

QY 23 LGNLKQIYYNEKAITENK--ESDDQFLENTLLFKGFTTGHWPYNDLLVDLGSKDATNKY 80
 Db 24 VGVNLNRYGSGYPIEDHQSPENNHLSHQLVFS-----MDNSTVTAEFKNVDVKKF 77
 QY 81 KKKKVDLYGAYGYOCAGGTGPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGKOTTVPI 140
 Db 78 KKHADVYGLSYSGVCL-----KNKIYGGVTL-AGDYLEKSRRIPIINLWNGEHTTIST 131
 QY 141 DKVKTSSKEVTVOELDLQARHYLHGKFGLY-----NSDSFGGKQVQGLIVPHS 188
 Db 132 DKVSINKKLVTAQIEDTKRLRYLQBEYNYGNDINKGRNYGNKSKFSGGFGNAGKILFHL 191
 QY 189 SEGSTVSYDLFDAQGYPDTLLRIYRDNKTINSENLIH 226
 Db 192 NDGSSFSYDLFTGTGQAESFLKIYDNKTIVTERFHL 229

RESULT 19

Q8NVM3 PRELIMINARY; PRT; 242 AA.
 ID Q8NVM3
 AC Q8NVM3
 DT 01-OCT-2002 (T-EMBLrel. 22, Created)
 DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Staphylococcal enterotoxin SEG.
 OS SEG2 OR MW1937.
 GN Staphylococcus aureus (strain MW2).
 OC Bacteria; Firmicutes; Bacilliales; Staphylococcus.
 OX NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22040717; PubMed=12044378;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA";
 RL Lancet 359:1819-1827(2002).
 DR EMBL; AB004828; BAB95802.1;
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; BctI_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_exotoxin.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PRINTS; PR01800; STAPHXOTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 242 AA; 28138 MW; PFCC89BB0E7A3BF5 CRC64;

Query Match 25.0%; Score 309.5; DB 16; Length 242;
 Best Local Similarity 33.2%; Pred. No. 2.3e-16;
 Matches 74; Conservative 35; Mismatches 71; Indels 43; Gaps 8;
 QY 25 NLKQIY--YNEK--AITENKESDDQFLENTLLFKGFTTGHWPYNDLLVDLGSKDATNKY 80
 Db 32 NLNRFVANYQPEKLQGVSSGNFSTSHQLE---YIDGKTYLSQFH-----NEY 76
 QY 81 KKK-----KVDLYGAYGYOCAGGTGPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGK 135
 Db 77 EAKRLKDKHVDIFGYSGLC-----NKKYMGGITLANQN-LDKPRNIPINLWNGKQ 129
 QY 136 TTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYN-----SDSFGGKQVQGL 183
 Db 130 NTISTDKVTSQKKEVTAQIEDIKRLKYLQNEYNYGNFKTKKGQYGYKSKFNSGK 189

QY 184 IVFHSSEGSTVSYDLFDAQGYPDTLLRIYRDNKTINSENLIH 226
 Db 190 ITFHLNNEFSFTYDLFTGTGQAESFLKIYDNKTIDAENFHL 232
 RESULT 20
 Q8VLW7 PRELIMINARY; PRT; 256 AA.
 ID Q8VLW7
 AC Q8VLW7
 DT 01-MAR-2002 (T-EMBLrel. 20, Created)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
 DE Staphylococcal enterotoxin Q.
 GN ENIQ.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacilliales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RM4282;
 RX MEDLINE=98385824; PubMed=9720870;
 RA Lindsay J.A., Ruzin A., Ross H.F., Kurepina N., Novick R.P.;
 RT "The gene for toxic shock toxin is carried by a family of mobile
 RT pathogenicity islands in Staphylococcus aureus";
 RL Mol. Microbiol. 29:527-543(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RM4282;
 RA Lindsay J.A., Kreiswirth B.N., Novick R.P.;
 RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-RM4282;
 RA Barry P.C., Novick R.P.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U93688; AAL67620.1;
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; BctI_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR008375; Staph_exotoxin.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PRINTS; PR01800; STAPHXOTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 SQ SEQUENCE 256 AA; 29794 MW; 9E2FI3790823A7DF CRC64;

Query Match 24.9%; Score 308.5; DB 2; Length 256;
 Best Local Similarity 32.4%; Pred. No. 2.9e-16;
 Matches 73; Conservative 32; Mismatches 69; Indels 51; Gaps 7;
 QY 17 ELQGTALGNLK--QIYYNEKAITENKESDDQFLENTLLFKGFTTGHWPYNDLLVDLGS 73
 Db 58 KLQGVSSGNFSTSHQLEVIDGK-----YTLYSQF---HNEYE----- 91
 QY 74 KDATNKYKKVDLYGAYGYOCAGGTGPNKTACMYGGVTLHDNNRLTEKKVPINLWIDG 133
 Db 92 ---AKRLKDKHVDIFGYSGLC-----NKKYMGGITLANQN-LDKPRNIPINLWNG 141
 QY 134 KOTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYN-----SDSFGGKQVQ 181
 Db 142 KONTISTDKVTSQKKEVTAQIEDIKRLKYLQNEYNYGNFKTKKGQYGYKSKFNSG 201
 QY 182 GLIVFHSSEGSTVSYDLFDAQGYPDTLLRIYRDNKTINSENLIH 226
 Db 202 GKITFHLNNEFSFTYDLFTGTGQAESFLKIYDNKTIDAENFHL 246

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RESULT 21
Q93CC6 PRELIMINARY; PRT; 242 AA.
AC Q93CC6;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Seq.
GN SEQ.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COL;
RA Yarwood J.M., McCormick J.K., Paustian M.L., Orwin P.M., Kapur V.,
RT Schlievert P.M.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF410775; AAL04146.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox OB.
DR Pfam; PF01123; Staph_Strep_toxin_1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PRINTS; PR01800; STAPHSTREPTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 242 AA; 28184 MW; F8EEFD4AF8C30D85 CRC64;

Query Match 24.8%; Score 306.5; DB 2; Length 242;
Best Local Similarity 32.4%; Pred. No. 3.9e-16;
Matches 73; Conservative 32; Mismatches 69; Indels 51; Gaps 7;

QY 17 ELQGTALGNLK--QIYYNEKATITENKSDQDQLENTLLPKGFTGHPWYNDLLVDLGS 73
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
44 KLGVSNGNSTSQLEVIDGK-----YTLYSQF---HNEYE----- 77

QY 74 KDATNKYKGVLDYGYGYCCAGTGNKTAACMYGVTLDHNNRLTEKKVPINLWIDG 133
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
78 ---AKRLKHKVDIFGISYSLC-----NFKYMGGITLANQN-LDKPENIPINLWVG 127

QY 134 KQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYN-----SDSFGGKQVR 181
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
128 KQNTISTDKYSTQKEVTAQIDIKRLKYLQNEYNIYGFNKNKTKGQBYGYQSKFNSGFNK 187

QY 182 GLIVFHSSEGSTVSVDLFDAGQGPDTLLRIYRDNKNTINSENLIH 226
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
188 GKITFHLNNEPSFYDLYFYGTGQAESFLKIYDNDKNTIDTENFHL 232

RESULT 22
Q9EZM7 PRELIMINARY; PRT; 239 AA.
AC Q9EZM7;
DT 01-MAR-2001 (TREMELrel. 16, Created)
DT 01-MAR-2001 (TREMELrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE SEM.
GN SEM.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]

SEQUENCE FROM N.A.
STRAIN=900322;
MEDLINE=20571956; PubMed=11123352;
Jarraud S., Peyrat M.A., Lim A., Tristan A., Bes M., Mougell C.,
Etienne J., Vandenesch F., Bonneville M., Lina G.;
"egc, A highly prevalent operon of enterotoxin gene, forms a putative
nursery of superantigens in Staphylococcus aureus.";
J. Immunol. 166:669-677(2001).
EMBL; AF285760; AAG36952.1; -.
HSSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox OB.
DR Pfam; PF01123; Staph_Strep_toxin_1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00277; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 239 AA; 27371 MW; 69240BE23C44028A CRC64;

Query Match 24.7%; Score 306; DB 2; Length 239;
Best Local Similarity 31.7%; Pred. No. 4.2e-16;
Matches 69; Conservative 41; Mismatches 82; Indels 26; Gaps 5;

QY 23 LGLNKQIYYNEKATITENK--ESDQDQLENTLLKGFTHGHPWYNDLLVDLGSKDATNKY 80
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
24 VGVNLNRYGYSPYEDHOSINPENHLHQVFS-----MDNSTVTAETKXNDVDFREF 77

QY 81 KGKKVDLYGAYGYCCAGTGNKTAACMYGVTLDHNNRLTEKKVPINLWIDGKQTTVP 140
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
78 KXHAVDVYGLSYSGYCL-----KNKYIYGGVTL-AGDYLEKRRRIPINLWVNGEHTIST 131

QY 141 DKVKTSSKEVTVOELDQARHYLHGKFGLY-----NSDSFGGKQVORGLIVFHS 188
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
132 DKVSTNKKLVTAQIDIKRLKYLQNEYNIYGFNKNKNGYGNKSKFSSGFNAGKILFHL 191

QY 189 SEGSTVSVDLFDAGQGPDTLLRIYRDNKNTINSENLIH 226
Db :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
192 NDSGSSFYDLYFYGTGQAESFLKIYDNDKNTVETKFEHL 229

RESULT 23
Q06531 PRELIMINARY; PRT; 239 AA.
AC Q06531;
DT 01-NOV-1996 (TREMELrel. 01, Created)
DT 01-NOV-1996 (TREMELrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]_TaxID=1280;
RP SEQUENCE FROM N.A.
RC STRAIN=4446;
MEDLINE=94011313; PubMed=8406814;
Marx J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
"Characterization of novel type C staphylococcal enterotoxins;
biological and evolutionary implications.";
Infect Immun. 61:4254-4262(1993).
EMBL; L13374; AAZ26618.1; -.
HSSP; P34071; ISE2.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox OB.
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RN	[1]
RC	SEQUENCE FROM N.A.
RP	STRAIN=MNCopeland;
RX	MEDLINE=94011313; PubMed=8406814;
RA	Mar J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT	"Characterization of novel type C staphylococcal enterotoxins:
RT	biological and evolutionary implications";
RL	Infect Immun. 61:4254-4262(1993).
DR	EWBL; LJ378; AAA26622.1; -.
DR	HSSP; P34071; ISTE.
DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0015070; F:toxin activity; IEA.
DR	GO; GO:0009405; P:pathogenesis; IEA.
DR	InterPro; IPR008992; Bact_endotox.
DR	InterPro; IPR006177; Ect_x_tox.
DR	InterPro; IPR006123; Staph_Strep_toxin.
DR	InterPro; IPR006126; Staph/Strept_tox.
DR	InterPro; IPR006173; Staph_tox_OB.
DR	Pfam; PF011123; Staph_strip_toxin; 1.
DR	Pfam; PF02876; Staph_strip_tox_C; 1.
DR	PRINTS; PR00279; BACTELTOXIN
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT	NON_TER 1
SQ	SEQUENCE 239 AA; 27651 MW; A21A954386AE8625 CRC64;
	Query Match 24.2%; Score 299.5; DB 2; Length 239;
	Best Local Similarity 32.9%; Pred. No. 1.4e-15;
	Matches 80; Conservative 47; Mismatches 97; Indels 19; Gaps 9;
QY	2 EKSEINEKDLRKKSLOGTALGNLKQIYYNEKAITEKN-ESDDQFLENTLLFKGFFTG 60
DB	1 ESQPDPTPELHKSSSEFTGT-MGNMK--LYLDHYVSATKVKSVDKFLAHDLIYNISDKK 57
QY	61 HPWYNDLLVIGSKDATNKYGKKVDLYGAYGYQC-----AGTTPNKTACMYGGVTIL 113
DB	58 LKNYDKVKVELLNEDLAKYIKDEVVDVIGNYVCYFSKDNVKGVTGGTKCMYGSITK 117
QY	114 HDNNRLTEE--KKVPINLMIDGQTTPVDKVKTSKEVTVQBELDQAARHLYHGKFGLYN 171
DB	118 HEGNHFDNGNLQNVLIRVY-ENKRNTISFE-VQTDKSVTAQELDIAKRNFLINKXKLYE 175
QY	172 SDSFGKVGQGLIVFHSSSGSTVSYLDFPAQGYPD--TLIRYRDNKTIINSENHLIALY 229
DB	176 FNS--SPYETGYIKFIENNNGNTFTFWMPAPGPKFDQSKYLMYNDNKTVDSREVKIEVH 233
QY	230 LYT 232
DB	234 LTT 236
RESULT 28	
Q8NVW2	ID Q8NVW2 PRELIMINARY; PRT; 242 AA.
AC	Q8NVW2;
DT	01-OCT-2002 (TEMBLrel. 22, Created)
DT	01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE	Staphylococcal enterotoxin sek.
GN	SEK2 OR MW1938.
OS	Staphylococcus aureus (strain MW2).
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX	NCBI_TaxID=196620;
RN	[1]
RP	SEQUENCE FROM N.A.
RX	MEDLINE=22040717; PubMed=12044378;
RA	Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA	Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA	Yamanoto K., Hiramatsu K.;
RT	"genome and virulence determinants of high virulence community-
RT	acquired MRSA.";
RL	Lancet 359:1819-1827(2002).
DR	EWBL; AP004828; BAB95803.1; -.

```

179 -----VQRCGLIVFHSBEGSTVSYDLF 199
      : : : : :
      : : : : :
177 YKSFYSGFNKGKVLPHLNDKSFSYDLF 205

QY
DB

RESULT 30
Q93CC5
ID Q93CC5 PRELIMINARY; PRT; 242 AA.
AC Q93CC5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)

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SEK.
DE
GN
OS
OC

11]_--ixaid-1200,	
SEQUENCE FROM N.A.	
STRAIN-COL;	
RA Yarwood J.M., McCormick J.K., Paustian M.L., Orwin P.M., Kapur V.,	
RA Schlievert P.M.;	
RA "Staphylococcus aureus pathogenicity island 3 (sapI3).";	
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.	
EMBL; AF410775; AAL04147.1; --	
GO; GO:0005576; C:extracellular; IEA.	
GO; GO:0015070; P:toxin activity; IEA.	
GO; GO:0009405; P:pathogenesis; IEA.	
InterPro; IPR008992; Bact_endotox.	
InterPro; IPR006177; Bctrr_tox.	
InterPro; IPR006123; Staph/Strep_toxin.	
InterPro; IPR006173; Staph_tox_OB.	
Pfam; PF01123; Stap_strep_toxin; 1.	
Pfam; PF02876; Stap_strep_tox_C; 1.	
PRINTS; PR00279; BACTRILTOXIN.	
PROSITE; PS00378; STAPH_STREP_TOXIN 2; 1.	
SEQUENCE 242 AA: 27727 MW: 207938B999DC9A9A CRC64:	
SO	

Query Match	24.1%	Score 298,	DB 2,	Length 242,
Best Local Similarity	32.3%	Pred. No. 1.8e-15;		
Matches	70;	Conservative 40;	Mismatches 81;	Indels 26; Gaps 7
QY	23	LGNIKQIYYVNEKAITENKSSDQFLENTLLFKGFTGHPWYNDLLVLDGSKDANKYKG	82	
DB	29	IDNLENFTKDKFVDLKDVKDNDTPIANQLQF-----SNESY-DLISESKDFKNKSNFKG	82	
QY	83	KKVDLYGAYGYQCAGGTGPNKTACMGVGLTLHDNNRLTEBKVPYINLWIDGKQTTVPIDK	142	
DB	83	KKLDVFGISYNGQC-----NTRYIYGAVTA-TNEYLDKSRNPINIMINGNHKHTISTNK	135	
QY	143	VKTSKKEVTVOELDLQARHYLHGKFGLY-----NSDSFGK-----VQRLGLVFPHSSE	190	
DB	136	VSTNKKFVTAQEIIVDKURKLOEBEINIIYGHNGTKKGEYGHKSKFYSGNIGKVTFLHNL	195	
QY	191	GSTVSYDLF-DAQQYPTDLLRIYRDNKNTINSENLHI	226	
DB	196	NDTFSYDLFTGDDGLPKSFLKYEDNKTVESEKFLH	232	

DB	136	NDIFSJDLFTIGDUGGAFKSLKJIEUNKIVSEKRAL	233
	RESULT	31	
	O54476		
ID	O54476	PRELIMINARY;	PRT; 242 AA.
AC	O54476;		
DT	01-JUN-1998	(TrEMBLrel. 06, Created)	
DT	01-JUN-1998	(TrEMBLrel. 06, Last sequence update)	
DT	01-OCT-2003	(TrEMBLrel. 25, Last annotation update)	
DE	Enterotoxin.		
DE	Enterotoxin.		
GN	ENT.		
OS	Staphylococcus aureus.		
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.		
OX	NCBI_TaxID=1280;		
RN	[1]		

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DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTGXIN
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR NON_TER
SQ SEQUENCE 239 AA; 27642 MW; C77009F46BC8D645 CRC64;

Query Match
Best Local Similarity 23.9%; Score 295.5; DB 2; Length 239;
Matches 78; Conservative 47; Mismatches 90; Indels 19; Gaps 9;

QY 11 DLRKSELOGTALGNLKKQIYYNEKAITENK-ESDDQFLENTLLFKGFFTGHPWYNDLLV 69
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
10 DLKXSEFTGT-MDNMK--LYDDHVSATKVKSVDFLAHDLIYNISDKLKNYDKVK 66
QY 70 DLGSKDATNKYGGKVDLYGAYGYOC-----AGGTENKTCMYGGVTLHDNNLTTEE 122
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
67 ELLNEDLAKYKDEVDVVGNSYVNCYFSSKDNKVGKGTGCTMGITKXEGHFNHG 126
QY 123 --KKVPINLWIDGKOTTPIDVKYTSKKEVTVOELDQARHYLHGKFLYNSDSFGKVQ 180
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
127 NLQNLVLRVY-ENKRNITISFE-VQTDKGSVTAQELDIKARNFLINKNLVFNFS--SPYE 182
QY 181 RGLIVPHSSEGSIVSDLFDAQGYPD--TLRIYPRDKTIINSENLHIALYLT 232
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
183 TGIKFIENGNFTWYDMMPADPKFDQSKYLMYNDNKTVDKSVKIEVHLTT 236

RESULT 33
Q7X0E7
ID Q7X0E7 PRELIMINARY; PRT; 218 AA.
AC Q7X0E7;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin type I (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AS14;
RA Blaiotta G., Pennacchia C., Casaburi A., Ercolini D., Fusco V., Villani F.;
RT "Detection of staphylococcal enterotoxin type G precursors on
RT Staphylococcus spp. strains isolated from meat and dairy products.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY291445; AAP78526.1; -.
FT NON_TER 218
SQ SEQUENCE 218 AA; 24993 MW; 698B8BCE49754350 CRC64;

Query Match
Best Local Similarity 23.8%; Score 294.5; DB 2; Length 218;
Matches 76; Conservative 36; Mismatches 73; Indels 37; Gaps 9;

QY 8 NEKDLRKXSELQG-TALGNLKIY----YVNEKAITENKESDDQFLENTLLFKGFFTGHP 62
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
17 NIKDL--TYAGDGIQVGNLRNRYFKTHDYIDLKGVTDKNLPANQLE-----FTSG-- 64
QY 63 WYNDLLVDLGSKDATNKYGGKVDLYGAYGYOCAGGTPTKTCMYGGVTLHDNNLTTEE 122
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
65 -TNDLISSENNWDEISKFKGKLLDFIGDYNGPC-----KSKMYGGATL-SQGYLNSA 116
QY 123 KKVPLNLWIDGKOTTPIDVKYTSKKEVTVOELDQARHYLHGKFLYNSDSFG-GK--- 178
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
117 RKIPINLWNGKHKTISTDKATKKLVTAGEIDVKLRRYLQEEYNIYGHNNITGKGYG 176
QY 179 -----VQRLIVPHSSEGSIVSDLFDAQGYPDTLRLI 212
Db ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
177 YKSFYSGFNNGKVLPHLNNEKSFYDLFTYTGNGLPVSVFLKI 218

RESULT 34

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DR EMBL; AY291443; AAP78522.1; -.
FT NON TER 218
SQ SEQUENCE 218 AA; 24994 MW; 698329CE49754350 CRC64;

Query Match 23.7%; Score 293.5; DB 2; Length 218;
Best Local Similarity 34.2%; Pred. No. 3.6e-15;
Matches 76; Conservative 36; Mismatches 73; Indels 37; Gaps 9;

QY 8 NEKDLRKSELOG-TALGNLKOIY----YNEKAITENKESDDQFLENTLLFKGFFTGHP 62
DB 17 NIKDL---TYAQGDIGVGNLRFYTKHDYIDLKGVTDKNLPIANOLE-----FSTG-- 64
QY 63 WYNLLVDLGSKDATNKYKGVLDLYGAYVYQVQAGGTPNKTACMYGGVTLHDNNRLTEE 122
DB 65 -TNDLISESNWDEISKFKGKLDIFGIDYNGPC-----KSKMYGGATL-SGQYLNSA 116
QY 123 KKVPIINLWIDGKQTTVPIDKVTSKKEVTQVELDLOARHYLHGKFGLYNSDSFG-GK--- 178
DB 117 RKIPINLWNGKHKTISTDKIATNKKLVTAQIDVLRVLOEYNIYCHNNTGKKEYG 176
QY 179 -----VQRLIVFHSSEGSTVSVDLFDAGQGYPTLLRI 212
DB 177 YKSKFYSGFNNGKVLPHLNNEKSFSDYFTGDLGVLPSPLKI 218

RESULT 36
Q7X0E6 PRELIMINARY; PRT; 207 AA.
ID AC Q7X0E6;
DT 01-OCT-2003 (Tremblrel. 25, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DE Enterotoxin type I (Fragment)
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BS49;
RA Blaiotta G., Pennacchia C., Casaburi A., Ercolini D., Fusco V.,
RA Villani F.;
RT "Detection of staphylococcal enterotoxin type G precursors on
RT Staphylococcus spp. strains isolated from meat and dairy products."
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY291446; AAP78528.1; -.
FT NON TER 207
SQ SEQUENCE 207 AA; 23867 MW; C815DEC021FAA681 CRC64;

Query Match 23.2%; Score 287.5; DB 2; Length 207;
Best Local Similarity 34.9%; Pred. No. 9.8e-15;
Matches 73; Conservative 34; Mismatches 65; Indels 37; Gaps 9;

QY 8 NEKDLRKSELOG-TALGNLKOIY----YNEKAITENKESDDQFLENTLLFKGFFTGHP 62
DB 17 NIKDL---TYAQGDIGVGNLRFYTKHDYIDLKGVTDKNLPIANOLE-----FSTG-- 64
QY 63 WYNLLVDLGSKDATNKYKGVLDLYGAYVYQVQAGGTPNKTACMYGGVTLHDNNRLTEE 122
DB 65 -TNDLISESNWDEISKFKGKLDIFGIDYNGPC-----KSKMYGGATL-SGQYLNSA 116
QY 123 KKVPIINLWIDGKQTTVPIDKVTSKKEVTQVELDLOARHYLHGKFGLYNSDSFG-GK--- 178
DB 117 RKIPINLWNGKHKTISTDKIATNKKLVTAQIDVLRVLOEYNIYCHNNTGKKEYG 176
QY 179 -----VQRLIVFHSSEGSTVSVDLFD 199
DB 177 YKSKFYSGFNNGKVLPHLNNEKSFSDYDLF 205

RESULT 37
Q9F0L6 PRELIMINARY; PRT; 271 AA.
ID Q9F0L6
AC Q9F0L6;

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DT	01-MAR-2001 (TrEMBLrel. 16, Created)
DT	01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Staphylococcal enterotoxin C-bovine.
SEC	SEC-BOV.
OS	Staphylococcus aureus.
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;	
RN	[1]
RP	SEQUENCE FROM N.A.
FX	MEDLINE=20566668; PubMed=11114901;
RA	Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
RT	Meaney W.J., Smyth C.J.;
RT	"Characterization of a putative pathogenicity island from bovine
ST	Staphylococcus aureus encoding multiple superantigens.";
EL	J. Bacteriol. 183:63-70(2001).
DR	EMSL; AF217235; AAG29599.1; -.
DR	HSSP; P34071; LSE2.
DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0015070; F:toxin activity; IEA.
DR	GO; GO:0009405; P:pathogenesis; IEA.
DR	InterPro; IPR008992; Bact_endotox.
DR	InterPro; IPR006177; Bcrt1_tox.
DR	InterPro; IPR006123; Stap/Strep_toxin.
DR	InterPro; IPR006126; Staph/strept tox.
DR	Pfam; PF011123; Stap_strp_toxin; 1.
DR	Pfam; PF02876; Stap_strp_tox_C; 1.
DR	PRINTS; PR00279; BACTELTOXIN_.
DR	PROSITE; PS02277; STAPH_STREP_TOXIN_1; 1.
DR	PROSITE; PS02278; STAPH_STREP_TOXIN_2; 1.
SQ	SEQUENCE 271 AA; 31267 MW; 3493F622B8042F10 CRC64;
Query Match 22.9%; Score 283.5; DB 2; Length 271;	
Best Local Similarity 31.6%; Pred. No. 2.8e-14;	
Matches 77; Conservative 51; Mismatches 97; Indels 19; Gaps 9;	
QY	1 SEKSEEINEKDRLRKSSLOQTALGNLKOIYYYNFKAITENK-ESDDQPLENTLLFGGFTT 59
DB	32 AESQDPTDPDLHKKASFTG-LMENMKVL--YDDRYSATSKVGVDRFLAHDLIYNSDK 88
QY	60 GHPWNDLLVDLGSKDATNKYGKKVDLYGAYGYQC-----AGGTPNKTCMYGGVT 112
DB	89 KLNKYDKVKTELLNEDLAKKYDEVVDYGSNYVNCYFSKDNNGKVTTGGKTCMYGGIT 148
QY	113 LHDNNRLTEEK--KVPINLMWDGKQTTPVDIKVTSKEVTVQBELDQARHYLHGKFGLY 170
DB	149 KHEGNHFDMGKLQNVLIRVY-ENKRNTISPE-VQTDKKSSTAQELDIAKRNFLKNKLY 206
QY	171 NSDSFGKVGQGLIVFHSSSEGTSVSVDLPDAQGYPD--TLRIYRDNKTINSNLHAL 228
DB	207 EFNs--SPYETGYIKFIENNNGTFWYDMWPAPGDQDFQSXYLMYINDKNTVDSKSVKIEV 264
QY	229 YLYT 232
DB	265 HLTT 268
RESULT 38	
ID	Q53678 PRELIMINARY; PRT; 239 AA.
AC	Q53678;
DT	01-NOV-1996 (TrEMBLrel. 01, Created)
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Enterotoxin (Fragment).
OS	Staphylococcus aureus.
OC	Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;	
RN	[1]
RP	SEQUENCE FROM N.A.
FX	MEDLINE=9401133; PubMed=9406814;
RA	Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;

RC STRAIN-SSI-1 / Serotype M3;
RA Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,
RA Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
RA Hayashi H., Hamada S.,
RT "The genome of invasive Streptococcus pyogenes; a comparative analysis
of S. pyogenes SSI-1, SF370 and MGAS8232.";
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AE014161; AAM79908.1; -
DR EMBL; AP005142; BAC63655.1; -
DR PIR; A60108; A60108.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR Pfam; PF02876; Staph_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; Staph/Strep toxin; 1.
DR PROSITE; PS00278; Staph/Strep toxin; 1.
DR Complete proteome.
KW SEQUENCE 251 AA; 29260 MW; 05E782CDA01BFCD5 CRC64;
SQ
Query Match 22.8%; Score 282.5; DB 16; Length 251;
Best Local Similarity 33.3%; Pred. No. 3.1e-14;
Matches 79; Conservative 45; Mismatches 94; Indels 19; Gaps 10;
QY 4 SSEEINKEKLRKSELOQTAL-GNLKQIYV-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
DB 25 SOEVFAQQDDPSQLRHSRLVKNLQNIPLYEGDPVTHENVKSVQDLHSHLIYN---VS 81
QY 61 HPWYNDLLVGLSKDATNKYKGGKVDLYGAYGYQC-AGGTPNKTKACMYGGVTLHNNRL 119
DB 82 GPNYDKLTKELNQEWATLFDKNDIYGVVYHLCYLCENAAERSACIYGGVTHNEGNHL 141
QY 120 TEEKKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKGLYNSDFGKGV 179
DB 142 EIPKIVKIVKSIDGIC-SLSFD-IETNKQWTAQELDYKVRKYLTDNKQLYTNGP--SKY 197
QY 180 ORGLIVFHSSEGSTVSVDLFD----AQGYPTLLRIYRDNKTINSENHLIALYLT 232
DB 198 ETGYIKFIPKNKESFWDFEPPEFTQSKY----LMYKDNETLDSNTSQIEWLTT 250
RESULT 40
Q06534 PRELIMINARY; PRT; 239 AA.
AC Q06534;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262 (1993).
DR EMBL; L13379; AAA24623.1; -
DR HSP; P34071; ISE2.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
SQ

DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR Pfam; PF02876; Staph_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; Staph/Strep toxin; 1.
DR PROSITE; PS00278; Staph/Strep toxin; 1.
DR NON_TER 1
SQ SEQUENCE 239 AA; 27517 MW; F354742619C8D196 CRC64;
Query Match 22.3%; Score 276.5; DB 2; Length 239;
Best Local Similarity 31.3%; Pred. No. 8.5e-14;
Matches 76; Conservative 50; Mismatches 98; Indels 19; Gaps 9;
QY 2 EKSEINEKDLKSKSELOQTALGNLQIYVYNEKAITENK-ESDDQFLENTLLFKGFFTG 60
DB 1 ESQPDPTDELHKASKFTG-LMENMKVL--YDRYVSATKVSVDKFLAHDLIYINISDKK 57
QY 61 HPWYNDLLVGLSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTKACMYGGVTL 113
DB 58 LKNYDKVKTLLNEDLAKKYKDEVDVYGSNYVNCFFSKDNVGVKVTGGKTCMYGGITK 117
QY 114 HDNNRLTEB--KKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKGLYN 171
DB 118 HEGHFDNGNLQNLVIRVY-ENKRNITISFE-VOTDKKSVTAQELDKARSLINKNLVE 175
QY 172 SDSFGGKVGKORGLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKTINSENHLIALY 229
DB 176 FNS--SPYETGYIKFNIENGNIFWYDMFAPGDKFQSKYLMYNDNKTVDKSVKIEVH 233
QY 230 LYT 232
DB 234 LTT 236
RESULT 41
Q54971 PRELIMINARY; PRT; 260 AA.
ID Q54971;
AC Q54971;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Superantigen.
GN SSA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Wellner;
RA Reda K.B., Kapur V., Mollick J.A., Lamphear J.G., Musser J.M.,
RA Rich R.R.;
RT "Molecular characterization and phylogenetic distribution of the
streptococcal superantigen gene (ssa) from Streptococcus pyogenes.";
RL Infect. Immun. 62:1867-1874 (1994).
DR EMBL; L29565; AAA65928.1; -
DR PDB; 1BXT; 22-DEC-99.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strp_toxin; 1.
DR Pfam; PF02876; Staph_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; Staph/Strep toxin; 1.
DR PROSITE; PS00278; Staph/Strep toxin; 1.
DR SEQUENCE 260 AA; 29797 MW; 2DD96017DE9D4F49 CRC64;
SQ

Query Match		22.2%; Score 275; DB 2; Length 260;
Best Local Similarity		33.8%; Pred. No. 1.2e-13;
Matches		78; Conservative 37; Mismatches 98; Indels 18; Gaps 9;
QY	10 KDLRKKSELOQTALGNLKIYVYNEKAITENKESDDOFLNTLLFKGFFTHPWYNDLLV 69	
Db	35 EQLNKSQFTG-VGNNLRCL-YDNHFVEGTNRVSTGQLQHDLPFIKDLKKNYDSVKT 92	
QY	70 DLGSKDATNKYKGGKVDLYGAYGYOCAGTNP-----KTACMYGGVTLHDNNRLTEBEK 124	
Db	93 EFNKDLATKYNKVDIFGNSYVYCYSEGNCKNAKTCMYGGVTEHRNQI--EGK 150	
QY	125 VPINLWI---DGKQTTVPIDKVTSKKVTVOELDLQARHYLHGKFGCLYNSDSFGGKVQR 181	
Db	151 FP-NITVKYVENENILSFD-ITINKQVTVQELDKTKILVSRKNLYEFNN--SPYET 206	
QY	182 GLIVFHSSEGSTVSYDLFDAQGYPD--TLIRYRDNKTINSENHIALYL 230	
Db	207 GYIKFISSGDSFWYDMMPAPGAIFDQSKYLMYNDNKTVSSSAIAIEVHL 257	
RESULT 43		
Q54739		
ID	Q54739 PRELIMINARY; PRT; 260 AA.	
AC	Q54739; Q54737;	
DT	01-NOV-1996 (T-EMBLrel. 01, Created)	
DT	01-NOV-1996 (T-EMBLrel. 01, Last sequence update)	
DT	01-OCT-2003 (T-EMBLrel. 25, Last annotation update)	
DE	SUPERANTIGEN SSA (streptococcal superantigen SSA-phage associated)	
DE	(SSA precursor).	
GN	SSA OR SPYM3 0920 OR SPS1119.	
OS	Streptococcus pyogenes, and	
OC	Streptococcus pyogenes (serotype M3).	
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;	
OC	Streptococcus.	
OX	NCBI_TaxID=1314, 198466;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	SPECIES=S.pyogenes;	
RX	MEDLINE=94222556; PubMed=8168951;	
RA	Reda K.B., Kapur V., Mollick J.A., Lamphear J.G., Musser J.M.,	
RA	Rich R.R.;	
RT	"Molecular characterization and phylogenetic distribution of the	
RT	streptococcal superantigen gene (ssa) from Streptococcus pyogenes.;"	
RL	Infect. Immun. 62:1867-1874(1994).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	SPECIES=S.pyogenes;	
RX	MEDLINE=96178602; PubMed=8606073;	
RA	Reda K.B., Kapur V., Goela D., Lamphear J.G., Musser J.M., Rich R.R.;	
RT	"Phylogenetic distribution of streptococcal superantigen SSA allelic	
RT	variants provides evidence for horizontal transfer of ssa within	
RT	Streptococcus pyogenes.;"	
RL	Infect. Immun. 64:1161-1165(1996).	
RN	[3]	
RP	SEQUENCE FROM N.A.	
RC	SPECIES=S.pyogenes; STRAIN=MGAS315 / Serotype M3;	
RX	MEDLINE=22133808; PubMed=12122206;	
RA	Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,	
RA	Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Perkins L.D.,	
RA	Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,	
RA	Schlievert P.M., Musser J.M.;	
RT	Genome sequence of a serotype M3 strain of group A Streptococcus:	
RT	phage-encoded toxins, the high-virulence phenotype, and clone	
RT	emergence.;"	
RL	Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).	
RN	[4]	
RP	SEQUENCE FROM N.A.	
RC	SPECIES=S.pyogenes; STRAIN=SSI-1 / Serotype M3;	
RA	Nakagawa I., Kurokawa K., Nakata M., Tomiyasu Y., Yamashita A.,	
RA	Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,	
RA	Hayashi H., Hamada S.;	
RT	"The genome of invasive Streptococcus pyogenes; a comparative analysis	
RT	of S. pyogenes SSI-1, SF370 and MGAS232.;"	
RL	Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.	
RN	EMBL; U48794; AAB02150.1; -	

Query Match		22.2%; Score 275; DB 2; Length 260;
Best Local Similarity		33.8%; Pred. No. 1.2e-13;
Matches		78; Conservative 37; Mismatches 98; Indels 18; Gaps 9;
QY	10 KDLRKKSELOQTALGNLKIYVYNEKAITENKESDDOFLNTLLFKGFFTHPWYNDLLV 69	
Db	35 EQLNKSQFTG-VGNNLRCL-YDNHFVEGTNRVSTGQLQHDLPFIKDLKKNYDSVKT 92	
QY	70 DLGSKDATNKYKGGKVDLYGAYGYOCAGTNP-----KTACMYGGVTLHDNNRLTEBEK 124	
Db	93 EFNKDLATKYNKVDIFGNSYVYCYSEGNCKNAKTCMYGGVTEHRNQI--EGK 150	
QY	125 VPINLWI---DGKQTTVPIDKVTSKKVTVOELDLQARHYLHGKFGCLYNSDSFGGKVQR 181	
Db	151 FP-NITVKYVENENILSFD-ITINKQVTVQELDKTKILVSRKNLYEFNN--SPYET 206	
QY	182 GLIVFHSSEGSTVSYDLFDAQGYPD--TLIRYRDNKTINSENHIALYL 230	
Db	207 GYIKFISSGDSFWYDMMPAPGAIFDQSKYLMYNDNKTVSSSAIAIEVHL 257	
RESULT 42		
Q54738		
ID	Q54738 PRELIMINARY; PRT; 260 AA.	
AC	Q54738;	
DT	01-NOV-1996 (T-EMBLrel. 01, Created)	
DT	01-NOV-1996 (T-EMBLrel. 01, Last sequence update)	
DT	01-OCT-2003 (T-EMBLrel. 25, Last annotation update)	
DE	SUPERANTIGEN SSA.	
GN	SSA.	
OS	Streptococcus pyogenes.	
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;	
OC	Streptococcus.	
OX	NCBI_TaxID=1314;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=MGAS 1842;	
RX	MEDLINE=94222556; PubMed=8168951;	
RA	Reda K.B., Kapur V., Mollick J.A., Lamphear J.G., Musser J.M.,	
RA	Rich R.R.;	
RT	"Molecular characterization and phylogenetic distribution of the	
RT	streptococcal superantigen gene (ssa) from Streptococcus pyogenes.;"	
RL	Infect. Immun. 62:1867-1874(1994).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=MGAS 1842;	
RX	MEDLINE=96178602; PubMed=8606073;	
RA	Reda K.B., Kapur V., Goela D., Lamphear J.G., Musser J.M., Rich R.R.;	
RT	"Phylogenetic distribution of streptococcal superantigen SSA allelic	
RT	variants provides evidence for horizontal transfer of ssa within	
RT	Streptococcus pyogenes.;"	
RL	Infect. Immun. 64:1161-1165(1996).	
DR	EMBL; U48793; AAB02149.1; -	
DR	HSP; P01552; 1SEB	
DR	GO; GO:0005576; C:extracellular; IEA.	
DR	GO; GO:0015070; F:toxin activity; IEA.	
DR	GO; GO:0009405; P:pathogenesis; IEA.	
DR	InterPro; IPR008992; Bact_endotox.	
DR	InterPro; IPR006177; Bctrl_tox.	
DR	InterPro; IPR006123; Staph/Strep_toxin.	
DR	InterPro; IPR006126; Staph/Strep_tox.	
DR	InterPro; IPR006173; Staph_tox.	
DR	PFam; PF01123; Staph_toxin; 1.	
DR	PFam; PF02876; Staph_toxin; 1.	
DR	PRINTS; PR00279; BACTRLTOXIN.	
DR	PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.	
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.	
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.	
DR	SEQUENCE 260 AA; 29836 MW; C12141693842AD6 CRC64;	
Query Match		22.1%; Score 273; DB 2; Length 260;
Best Local Similarity		33.8%; Pred. No. 1.8e-13;
Matches		78; Conservative 37; Mismatches 98; Indels 18; Gaps 9;

[illegible]

01-CC1-2003 (IRMURE1. 25, Last annotation update)
Type A exotoxin precursor (Fragment).
SPEA.
OS Streptococcus pyogenes.
Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_taxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS156, and MGAS500;
RXL MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Selaender R.K., Muser J.M.;
RR "Characterization and cloral distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes."
RL J. Exp. Med. 174:1271-1274 (1991).
DR EMBL; X61556; CAA43754.1; -
DR EMBL; X61557; CAA43755.1; -
DR EMBL; X61560; CAA43756.1; -
DR EMBL; X61555; CAA43753.1; -
DR EMBL; X61558; CAA43756.1; -
DR EMBL; X61559; CAA43757.1; -
DR EMBL; X61554; CAA43752.1; -
DR PIR: A60108; AG0108.
DR HSSP: P08095; IB1Z.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0015070; P:toxin activity; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR Interpro: IPR008992; Eact_endotox.
DR Interpro: IPR006177; Bctrl_tox.
DR Interpro: IPR006123; Staph/Strep_toxin.
DR Interpro: IPR006126; Staph/Strep_tox.
DR Interpro: IPR006173; Staph_tox OB.


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Db      122 EIPKNILVKVSDIGIQ-SLSFD-IETSKWVTAQELDYKVRKHLTDNNQLYTNGP--SKY 177
QY      180 QRGVLIVFHSSEGSTVSYDLFDAGQGYPTDLLRIYRDNTKINS 221
Db      178 ETGYIKRFSKDKETFWDFPEPEFNOVKYLMYKDNLTDS 219

RESULT 48
Q54779 PRELIMINARY; PRT; 236 AA.
AC Q54779; Q54613; Q54736; Q54740; Q54741;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=MGAS624 AND MGAS158 AND MGAS485 AND MGAS491, and MGAS495;
RX MEDLINE=82044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Selander R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes."
RL J. Exp. Med. 174:1271-1274(1991).
DR EMBL; X61569; CAA43767.1; -
DR EMBL; X61572; CAA43770.1; -
DR EMBL; X61568; CAA43768.1; -
DR EMBL; X61570; CAA43768.1; -
DR EMBL; X61571; CAA43769.1; -
DR PIR; A60108; A60108.
DR HSSP; P08095; 1B1Z.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT NON_TER 1 1
FT SIGNAL <1 22 POTENTIAL.
FT CHAIN 23 >236 TYPE A EXOTOXIN.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27468 MW; 29DF2AD575623A84 CRC64;

Query Match 21.7%; Score 268.5; DB 2; Length 236;
Best Local Similarity 32.9%; Pred.No.3.5e-13;
Matches 76; Conservative 44; Mismatches 92; Indels 19; Gaps 10;

QY 4 SEINEKDLRKSELOQTAL-GNLKQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
Db 17 SQEVEAQDDPDSQHRSSLVKXNLQNIYFLYEGDPVTHENVKSDQLSHDLIYN---VS 73
QY 61 HPWYNDLLVLDGSKDATNKYKGVLDYGYAYCYQC-AGGTPNKACMYGGVTLHDNNEL 119
Db 74 GPNYDKLKTENQEMATLFDKNVDIYGYVEYVHLCYLCENAEARSACIYGGVNHGHNEL 133
QY 120 TEKKVPINLWIDGKQTVPIDKVTSKKEVTYQELDLQARHYLHGKFGLYNSDSFGGKV 179
Db 134 EIPKKIVKVSIDIGIQ-SLSFD-IETNKKWVTAQELDYKVRKYLTDNKLQYTNP--SKY 189

RESULT 50
Q52NF2 PRELIMINARY; PRT; 258 AA.
AC Q52NF2
ID Q52NF2
DT 01-MAY-1999 (TrEMBLrel. 10, Created)

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QY 180 QRGVLIVFHSSEGSTVSYDLFD----AQQGYPTDLLRIYRDNTKINSENLHI 226
Db 190 ETGYIKRIPKNSFWDFFPEPEFTQSKY---LMIYKDNLTDSNTSQI 236

RESULT 49
Q9R931 PRELIMINARY; PRT; 222 AA.
AC Q9R931;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Exotoxin A (Fragment).
GN SPEA.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=D709;
RX MEDLINE=99137798; PubMed=9952369;
RA Bessen D.E., Izzo M.W., Fiorentino T.R., Caringal R.M.,
RA Hollingshead S.K., Beall B.;
RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue
RT tropism in group A streptococci";
RL J. Infect. Dis. 179:827-836(1999).
DR EMBL; AF055698; AAD11624.1; -
DR PIR; A60108; A60108.
DR HSSP; P08095; 1B1Z.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006126; Staph/Strep tox.
DR InterPro; IPR006173; Staph tox OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1 1
FT NON_TER 222 222
SQ SEQUENCE 222 AA; 25759 MW; 48BB7ADDCD91FBA3 CRC64;

Query Match 21.6%; Score 267.5; DB 2; Length 222;
Best Local Similarity 33.6%; Pred.No.3.9e-13;
Matches 76; Conservative 43; Mismatches 88; Indels 19; Gaps 10;

QY 4 SEINEKDLRKSELOQTAL-GNLKQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
Db 5 SQEVEAQDDPDSQHRSSLVKXNLQNIYFLYEGDPVTHENVKSDQLSHDLIYN---VS 61
QY 61 HPWYNDLLVLDGSKDATNKYKGVLDYGYAYCYQC-AGGTPNKACMYGGVTLHDNNRL 119
Db 62 GPNYDKLKTENQEMATLFDKNVDIYGYVEYVHLCYLCENAEARSACIYGGVNHGHNEL 121
QY 120 TEKKVPINLWIDGKQTVPIDKVTSKKEVTYQELDLQARHYLHGKFGLYNSDSFGGKV 179
Db 122 EIPKKIVKVSIDIGIQ-SLSFD-IETNKKWVTAQELDYKVRKYLTDNKLQYTNP--SKY 177
QY 180 QRGVLIVFHSSEGSTVSYDLFD----AQQGYPTDLLRIYRDNTKINS 221
Db 178 ETGYIKRIPKNSFWDFFPEPEFTQSKY---LMIYKDNLTDS 219

RESULT 50
Q52NF2 PRELIMINARY; PRT; 258 AA.
AC Q52NF2
ID Q52NF2
DT 01-MAY-1999 (TrEMBLrel. 10, Created)

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DR EMBL; AB060535; BAB85989.1; -.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact endotox.
 DR InterPro; IPR006177; Bctrl tox.
 DR InterPro; IPR006123; Staph/Strep toxin.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 233 AA; 27040 MW; EC85287D63BF60D CRC64;

Query Match 20.7%; Score 256; DB 2; Length 233;
 Best Local Similarity 29.6%; Pred.No.3.3e-12;
 Matches 74; Conservative 50; Mismatches 84; Indels 42; Gaps 12;

Qy 3 KSEINEKDLRKSELOGLALGNLQIYY--YNEKAITENKESDDQFLENTLLFKGFFT 59
 Db 5 KDELKNSVDYKNN--KGT-MGNVNMVLTSPVVEGRGVNSR-----QFLSHDLFF---I 54
 Qy 60 GHPWYNDLLVDSGKDATNKYKGGKVDLYGAYGYQCA-----GTPNKKTACM 107
 Db 55 EYKSYNEVKTTELENTLANNYKDKVDIFGVYFYTCIIPKSEPDINQNFSG-----CCM 109
 Qy 108 YGVVTLH--DNNRLTEKKVPINLMDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHG 165
 Db 110 YGLLTNSSENER--DKLITVQVITDNRQSLG--FTITTNQMVTIQLDYKARHWLTK 164
 Qy 166 KFLGYNDSFGGKVGRLIVFHSSEGSTVSYDLFDAQGYDPT---LLRIYRDNKNTINSE 222
 Db 165 EKLYEFD--GSAFESGYIKFTKNTSFWFLDPFKKELVPPVPYKFLNIYGDNKVVDK 222
 Qy 223 NLHIALYLYT 232
 Db 223 SIRMEVFLNT 232

RESULT 53
 Q9EZM3 PRELIMINARY; PRT; 258 AA.
 ID Q9EZM3
 AC Q9EZM3
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE SEGL29P.
 GN SEGL29P.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OC NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A903222;
 RX MEDLINE=20571956; PubMed=11123352;
 RA Jarraud S., Peyrat M.A., Lim A., Tristan A., Bes M., Mougél C.,
 RA Etienne J., Vandenesch F., Bonneville M., Lina G.,
 RA "egc, A highly prevalent operon of enterotoxin gene, forms a putative
 RT nursery of superantigens in Staphylococcus aureus";
 RL J. Immunol. 166:669-677(2001).
 DR EMBL; AF285760; AAC36957.1; -.
 DR HSP; P01552; ISHB.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact endotox.
 DR InterPro; IPR006177; Bctrl tox.
 DR InterPro; IPR006123; Staph/Strep toxin.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.

Qy 48 LENTLFLKGFTHPW-YNDLLVD-----LGSKDANKYKGGKVDLYGAY--- 91
 Db 3 VDNLSRLNIYSTIVVEYSDIVDFTKSNLVTKQVDJDRFFINSEYANDFKT 62

DR EMBL; AB060535; BAB85989.1; -.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact endotox.
 DR InterPro; IPR006177; Bctrl tox.
 DR InterPro; IPR006123; Staph/Strep toxin.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 233 AA; 27040 MW; ECB85287D63BF60D CRC64;

Query Match 20.7%; Score 256; DB 2; Length 233;
 Best Local Similarity 29.6%; Pred.No.3.3e-12;
 Matches 74; Conservative 50; Mismatches 84; Indels 42; Gaps 12;

Qy 3 KSEINEKDLRKSELOGLALGNLQIYY--YNEKAITENKESDDQFLENTLLFKGFFT 59
 Db 5 KDELKNSVDYKNN--KGT-MGNVNMVLTSPVPEGVGNR---QFLSHDLFP---I 54
 Qy 60 GHPWYNDLLVDSGKDATNKYKGGKVDLYGAYGYQCA-----GTPNKATACM 107
 Db 55 EYKSYNEVKTTELENTLANNYKDKVDIFGVFYFTCIIPKSEPDINQNFSG---CCM 109
 Qy 108 YGVVTLH--DNNRLTEKKVPINLMDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHG 165
 Db 110 YGLLTNSSENER---DKLITVQVITDNRQSLG--FTITTNQNMVTIQLDYKARHWLTK 164
 Qy 166 KFLGYNDSFGGKVGRLIVFHSSEGSTVSYDLFDAQGYPTD---LLRIYRDNKNTINSE 222
 Db 165 EKLYEFD--GSAFESGYIKFTKNTSFWFLDFPKKELVPPVPYKFLNIYGDNKVVDK 222
 Qy 223 NLHIALYLYT 232
 Db 223 SIRMEVFLNT 232

RESULT 53
 Q9EZM3 PRELIMINARY; PRT; 258 AA.
 ID Q9EZM3
 AC Q9EZM3
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE SEGL29P.
 GN SEGL29P.
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OC NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A903222;
 RX MEDLINE=20571956; PubMed=11123352;
 RA Jarraud S., Peyrat M.A., Lim A., Tristan A., Bes M., Mougél C., Etienne J., Vandenesch F., Bonneville M., Lina G., "egc, A highly prevalent operon of enterotoxin gene, forms a putative nursery of superantigens in Staphylococcus aureus."; J. Immunol. 166:669-677(2001).
 DR EMBL; AF285760; AAC36957.1; -.
 DR HSP; P01552; ISHB.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0015070; F:toxin activity; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact endotox.
 DR InterPro; IPR006177; Bctrl tox.
 DR InterPro; IPR006123; Staph/Strep toxin.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.

Qy 48 LENTLFLKGFTHP-VNDLLVD-----LGSKDANKYKGGKVDLYGAY--- 91
 Db 3 VDNNSLRNIYSTIVVEYSDIVDFTKSNLVTKQVDVDFINSEYANDFKT 62

QY 92 -----YGYCCAGGTPNKACMGVGTLLHNNRLTEEEKVPINLWIDGKQTTVP 139
Db 63 GDKIAVFSVPDMNLSKG---KVTAITYGGITPYQKTSI--PKNIPVNLWINGKQISVP 117
QY 140 IDKVKTSKEVTVOELDLQARHYLHGKFLGNSDSFGKVGQGLIVFHSSEGS-TVSYDL 198
Db 118 YNEISTNKTITVTAQEIIDLKVRKFLIAQHOLYSS---GSSYKSGRLVPHNTDNDKYSFDL 174
QY 199 FDAQGYPTDLLRIYRDNKNTINSEN 224
Db 175 FYGVRDKESIFKYKDNKNSFNIDKI 200

RESULT 55
Q9LAE0 PRELIMINARY; PRT; 209 AA.
AC Q9LAE0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-4 (Fragment).
GN SMEZ-4.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9893;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143654; AAF66655.1; -.
DR HSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph_strep_toxin.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 209 AA; 24108 MW; 67EC279B8C4A8247 CRC64;

Query Match 19.5%; Score 241.5; DB 2; Length 209;
Best Local Similarity 28.2%; Pred. No. 3.9e-11;
Matches 58; Conservative 47; Mismatches 64; Indels 37; Gaps 7;
QY 48 LENTLLFKGFTGHPW-YNDLLVD-----LGSKDATNKYKGVLDLYGAY---- 91
Db 3 VDNNSLLRNIYSTIVYEYSDTVIDFKTSHNLVTKKLDVRDARDFINSEMDEYAANDFKD 62
QY 92 -----YGYCCAGGTPNKACMGVGTLLHNNRLTEEEKVPINLWIDGKQTTVP 139
Db 63 GDKIAVFSVPDMNLSKG---KVTAITYGGITPYQKTSI--PKNIPVNLWINGKQISVP 117
QY 140 IDKVKTSKEVTVOELDLQARHYLHGKFLGNSDSFGKVGQGLIVFHSSEGS-TVSYDL 198
Db 118 YNEISTNKTITVTAQEIIDLKVRKFLIAQHOLYSS---GSSYKSGRLVPHNTDNDKYSFDL 174
QY 199 FDAQGYPTDLLRIYRDNKNTINSEN 224
Db 175 FYGVRDKESIFKYKDNKNSFNIDKI 200

RESULT 56
Q9LAD8 PRELIMINARY; PRT; 209 AA.
ID Q9LAD8;
AC Q9LAD8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-7 (Fragment).
GN SMEZ-7.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11574;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143657; AAF66657.1; -.
DR HSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph_strep_toxin.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 209 AA; 24064 MW; 67E977CD5AA934F7 CRC64;

Query Match 19.5%; Score 241.5; DB 2; Length 209;
Best Local Similarity 28.2%; Pred. No. 3.9e-11;
Matches 58; Conservative 47; Mismatches 64; Indels 37; Gaps 7;
QY 48 LENTLLFKGFTGHPW-YNDLLVD-----LGSKDATNKYKGVLDLYGAY---- 91
Db 3 VDNNSLLRNIYSTIVYEYSDTVIDFKTSHNLVTKKLDVRDARDFINSEMDEYAANDFKA 62
QY 92 -----YGYCCAGGTPNKACMGVGTLLHNNRLTEEEKVPINLWIDGKQTTVP 139
Db 63 GDKIAVFSVPDMNLSKG---KVTAITYGGITPYQKTSI--PKNIPVNLWINGKQISVP 117
QY 140 IDKVKTSKEVTVOELDLQARHYLHGKFLGNSDSFGKVGQGLIVFHSSEGS-TVSYDL 198
Db 118 YNEISTNKTITVTAQEIIDLKVRKFLIAQHOLYSS---GSSYKSGRLVPHNTDNDKYSFDL 174
QY 199 FDAQGYPTDLLRIYRDNKNTINSEN 224
Db 175 FYGVRDKESIFKYKDNKNSFNIDKI 200

RESULT 57
Q9LAC6 PRELIMINARY; PRT; 209 AA.
ID Q9LAC6;
AC Q9LAC6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-20 (Fragment).
GN SMEZ-20.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN=10989;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143670; AAF66669.1; -
DR HSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph_strep_toxin.
DR Pfam; PF01123; Staph_strip_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
SQ SEQUENCE 209 AA; 53049A11599BBA68 CRC64;

Query Match 19.3%; Score 239.5; DB 2; Length 209;
Best Local Similarity 28.2%; Pred. No. 5.5e-11;
Matches 58; Conservative 46; Mismatches 65; Indels 37; Gaps 7;

QY 48 LENTLLFKGFFTGHPW-VNDLLVD-----LGSKDANKYKGGKVDLYGAY----- 91
DB 3 VDNNSLRNIYSTIYEDSLTIDFTSHNLVTKLDVDRDFFINSEMDEYAANDFKA 62

QY 92 -----YGYOCAGTPNKTACMYGGVTLHDNNELTEKKVPINLWIDGKQTTVP 139
DB 63 GDIAVFSVPFDWNYLSKG---KVTATYGGITPYQKTSI--PKNIPVNLWNGKQIPVP 117

QY 140 IDVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQGLIVFHSSEGS-TVSYDL 198
DB 118 YNOISNKTVTTAQEIIDLKVRKFLIAHQHLYSS---GSSYKSGRLVFHTNDSKYSFDL 174

QY 199 FDAQGGQYPTDLLRIYRDNKTINSNL 224
DB 175 FYGYRDKESIFKVKYDNKSNFNIDKI 200

RESULT 58
Q9LADI PRELIMINARY; PRT; 209 AA.
AC Q9LADI
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-14 (Fragment).
GN SMEZ-14.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX Streptococcus.
NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=4202;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143664; AAF66664.1; -
DR HSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strip_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
SQ SEQUENCE 209 AA; 24071 MW; FDAFCDLDAAG7271 CRC64;

Query Match 19.2%; Score 237.5; DB 2; Length 209;
Best Local Similarity 28.2%; Pred. No. 7.9e-11;
Matches 58; Conservative 46; Mismatches 65; Indels 37; Gaps 7;

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DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strip_toxin; 1.
DR Pfam; PF02876; Staph_strip_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
SQ SEQUENCE 209 AA; 24122 MW; 0CF5D429E1B96EFE CRC64;

Query Match 19.3%; Score 239; DB 2; Length 209;
Best Local Similarity 29.6%; Pred. No. 6.1e-11;
Matches 60; Conservative 42; Mismatches 65; Indels 36; Gaps 6;

QY 50 NTLFLKGFFTGHPWYNDLLVD-----LGSKDANKYKGGKVDLYGAY----- 91
DB 6 NSLLRNIYSTIYEDSLTIDFTSHNLVTKLDVDRDFFINSEMDEYAANDFKAGDK 65

QY 92 -----YGYOCAGTPNKTACMYGGVTLHDNNELTEKKVPINLWIDGKQTTVPIDK 142
DB 66 IAVFSVPFDWNYLSG---KVIATYGGITPYQKTSI--PKNIPVNLWNGKQISVPYNE 120

QY 143 VKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQGLIVFHSSEGS-TVSYDLFA 201
DB 121 ISTNKTVTTAQEIIDLKVRKFLIAHQHLYSS---GSSYKSGRLVFHTNDSKYSFDLFT 177

QY 202 GQYPTDLLRIYRDNKTINSNL 224
DB 178 GYRDKESIFKVKYDNKSNFNIDKI 200

RESULT 59
Q9LAEL PRELIMINARY; PRT; 209 AA.
AC Q9LAEL
DT 01-OCT-2000 (T-EMBLrel. 15, Created)
DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-3 (Fragment).
GN SMEZ-3.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX Streptococcus.
NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11681;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143653; AAF66654.1; -
DR HSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strip_toxin; 1.
DR Pfam; PF02876; Staph_strip_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
SQ SEQUENCE 209 AA; 24071 MW; FDAFCDLDAAG7271 CRC64;

Query Match 19.2%; Score 237.5; DB 2; Length 209;
Best Local Similarity 28.2%; Pred. No. 7.9e-11;
Matches 58; Conservative 46; Mismatches 65; Indels 37; Gaps 7;

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QY 48 LENTLLFKGFTGHPW-YNDLLVD-----LGSKDATNKYKGGKVDLYGAY---- 91
Db 3 VDNNSLLRNIYSTIYVEYSDTVIDFKTSHNLVTKLDVRDARDFINSEMEYANDFKA 62
QY 92 -----YGYOCAGGTPNKTAACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTP 139
Db 63 GSKIAVFSVPFDWNLKSG---RVATYTYGGITPYQKTSI--PKNIPVNLWINGKQISVP 117
QY 140 IDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKVGQGLIVFHSSEGS-TVSVDL 198
Db 118 YNEISTNKTVTVAQEIIDLKVRKFLIAQHLYSS---GSSYKSGKLIVFHTNDNSDKYSLDL 174
QY 199 FDAQGQYPTLLRIYRDNKNTINSENL 224
Db 175 FVTGYRDKESIFKVKYKDNKSFNIDKI 200

RESULT 60
Q9LAC4
ID Q9LAC4 PRELIMINARY; PRT; 209 AA.
AC Q9LAC4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-22 (Fragment).
GN SMEZ-22.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10463;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143671; AAF66670.1; -.
DR HSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; P:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR Pfam; PF01123; Staph_strep_toxin; OB.
DR Pfam; PF02876; Staph_strep_toxin; 1.
DR PRINTS; PS00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24075 MW; 3611E7C456D6EDB8 CRC64;

Query Match 19.2%; Score 237.5; DB 2; Length 209;
Best Local Similarity 28.2%; Pred. No. 7.9e-11;
Matches 58; Conservative 46; Mismatches 65; Indels 37; Gaps 7;

QY 48 LENTLLFKGFTGHPW-YNDLLVD-----LGSKDATNKYKGGKVDLYGAY---- 91
Db 3 VDNNSLLRNIYSTIYVEYSDTVIDFKTSHNLVTKLDVRDARDFINSEMEYANDFKA 62
QY 92 -----YGYOCAGGTPNKTAACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTP 139
Db 63 GSKIAVFSVPFDWNLKSG---RVATYTYGGITPYQKTSI--PKNIPVNLWINGKQISVP 117
QY 140 IDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKVGQGLIVFHSSEGS-TVSVDL 198
Db 118 YNEISTNKTVTVAQEIIDLKVRKFLIAQHLYSS---GSSYKSGKLIVFHTNDNSDKYSLDL 174
QY 199 FDAQGQYPTLLRIYRDNKNTINSENL 224
Db 175 FVTGYRDKESIFKVKYKDNKSFNIDKI 200

RESULT 60
Q9LAC4
ID Q9LAC4 PRELIMINARY; PRT; 209 AA.
AC Q9LAC4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-22 (Fragment).
GN SMEZ-22.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10463;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143672; AAF66671.1; -.
DR HSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; P:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR Pfam; PF01123; Staph_strep_toxin; OB.
DR Pfam; PF02876; Staph_strep_toxin; 1.
DR PRINTS; PS00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24075 MW; 3611E7C456D6EDB8 CRC64;

Query Match 19.2%; Score 237.5; DB 2; Length 209;
Best Local Similarity 28.2%; Pred. No. 7.9e-11;
Matches 58; Conservative 46; Mismatches 65; Indels 37; Gaps 7;

QY 48 LENTLLFKGFTGHPW-YNDLLVD-----LGSKDATNKYKGGKVDLYGAY---- 91
Db 3 VDNNSLLRNIYSTIYVEYSDTVIDFKTSHNLVTKLDVRDARDFINSEMEYANDFKA 62
QY 92 -----YGYOCAGGTPNKTAACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTP 139
Db 63 GSKIAVFSVPFDWNLKSG---RVATYTYGGITPYQKTSI--PKNIPVNLWINGKQISVP 117
QY 140 IDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKVGQGLIVFHSSEGS-TVSVDL 198
Db 118 YNEISTNKTVTVAQEIIDLKVRKFLIAQHLYSS---GSSYKSGKLIVFHTNDNSDKYSLDL 174
QY 199 FDAQGQYPTLLRIYRDNKNTINSENL 224
Db 175 FVTGYRDKESIFKVKYKDNKSFNIDKI 200
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Db 175 FVTGYRDKESIFKVKYKDNKSFNIDKI 200

RESULT 61
Q9LAC5
ID Q9LAC5 PRELIMINARY; PRT; 209 AA.
AC Q9LAC5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-21 (Fragment).
GN SMEZ-21.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11227;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143671; AAF66670.1; -.
DR HSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; P:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR Pfam; PF01123; Staph_strep_toxin; OB.
DR Pfam; PF02876; Staph_strep_toxin; 1.
DR PRINTS; PS00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24106 MW; 67FD2696FA4BC55A CRC64;

Query Match 19.0%; Score 235.5; DB 2; Length 209;
Best Local Similarity 27.7%; Pred. No. 1.1e-10;
Matches 57; Conservative 47; Mismatches 65; Indels 37; Gaps 7;

QY 48 LENTLLFKGFTGHPW-YNDLLVD-----LGSKDATNKYKGGKVDLYGAY---- 91
Db 3 VDNNSLLRNIYSTIYVEYSDTVIDFKTSHNLVTKLDVRDARDFINSEMEYANDFKT 62
QY 92 -----YGYOCAGGTPNKTAACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTP 139
Db 63 GSKIAVFSVPFDWNLKSG---RVATYTYGGITPYQKTSI--PKNIPVNLWINGKQISVP 117
QY 140 IDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKVGQGLIVFHSSEGS-TVSVDL 198
Db 118 YNEISTNKTVTVAQEIIDLKVRKFLIAQHLYSS---GSSYKSGKLIVFHTNDNSDKYSFDL 174
QY 199 FDAQGQYPTLLRIYRDNKNTINSENL 224
Db 175 FVTGYRDKESIFKVKYKDNKSFNIDKI 200

RESULT 62
Q9LAD6
ID Q9LAD6 PRELIMINARY; PRT; 209 AA.
AC Q9LAD6;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-9 (Fragment).
GN SMEZ-9.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
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OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11299;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL: AF143659; AAF66659.1; -
DR HSSP; P13163; 1SXT.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0015070; F:toxin activity; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006123; Bact_endotox.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006123; Staph/Strep toxin.
DR Pfam; PF01123; Staph/Strep toxin; 1.
DR Pfam; PF02876; Staph/Strep toxin; 1.
DR PRINTS; PR00279; BACTRLTOKIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24213 MW; B21587BA343B5DD5 CRC64;

Query Match 18.8%; Score 232.5; DB 2; Length 209;
Best Local Similarity 28.2%; Pred. No. 1.9e-10;
Matches 59; Conservative 45; Mismatches 66; Indels 37; Gaps 7;

QY 48 LENTLLFKGFFGHPWYNDLLVD-----LGSKDATNKYKGGKVDLYGAY---- 91
DB 3 VDNNSLLNIYSTIVYEYSDTVIDFTKSHNLVTKLDVRDARDFINSEMDYEAANDFKA 62

QY 92 -----YGYQCAGGTPNKATCMYGGVTLHDNNRLTEKKVPINLWIDGKQTTPV 139
DB 63 GDKIAPVSPFDNLYSKG---KVTAYTYGGITPYQKTSI--PKNIPVNLWNRKQIPVP 117

QY 140 IDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVGRLIYVHSEGS-TVSYDL 198
DB 118 YNQISTNKTITVTAQEDIDKVRKFLIAHQHLYSS---GSSYKSGRLVFTNDNSDKYSFOL 174

QY 199 FDAQGYPDTLRIYRDNKTINSEN 224
DB 175 FYGYRDKESIFKLYKDNKSFNIDKI 200

RESULT 63
Q9LAD2 PRELIMINARY; PRT; 209 AA.
AC Q9LAD2
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-13 (Fragment).
GN SMEZ-13.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=95/31;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL: AF143663; AAF66663.1; -
DR HSSP; P13163; 1SXT.
DR GO: GO:0005576; C:extracellular; IEA.

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DR GO: GO:0015070; F:toxin activity; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006123; Bact1_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006123; Staph/Strep toxin.
DR Pfam; PF01123; Staph/Strep toxin; 1.
DR Pfam; PF02876; Staph/Strep toxin; 1.
DR PRINTS; PR00279; BACTRLTOKIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24072 MW; 984C1B4614589A1E CRC64;

Query Match 18.7%; Score 232; DB 2; Length 209;
Best Local Similarity 29.1%; Pred. No. 2.1e-10;
Matches 59; Conservative 42; Mismatches 66; Indels 36; Gaps 6;

QY 50 NTLFLKGFHTGHPWYNDLLVD-----LGSKDATNKYKGGKVDLYGAY---- 91
DB 6 NSLLNIYSTIVYEYSDTVIDFTKSHNLVTKLDVRDARDFINSEMDYEAANDFKAGDK 65

QY 92 -----YGYQCAGGTPNKATCMYGGVTLHDNNRLTEKKVPINLWIDGKQTTPIDK 142
DB 66 IAVFSPFDNLYSKG---KVTAYTYGGITPYQKTSI--PKNIPVNLWNRKQIPVP 120

QY 143 VKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVGRLIYVHSEGS-TVSYDLFDA 201
DB 121 ISTNKTITVTAQEDIDKVRKFLIAHQHLYSS---GSSYKSGKLVFTNDNSDKYSLDLFYV 177

QY 202 QGYPDTLRIYRDNKTINSEN 224
DB 178 GYRDKESIFKLYKDNKSFNIDKI 200

RESULT 64
Q7WY99 PRELIMINARY; PRT; 207 AA.
AC Q7WY99
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z (Fragment).
GN SMEZ.
OS Streptococcus canis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1329;
RN [1]
RP SEQUENCE FROM N.A.
RA Igwe E.I., Gertz B.;
RT "Streptococcal superantigen genes in human pathogenesis group G
RT streptococcus.";
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AJ564198; CAD91900.1; -
FT NON_TER 1
FT NON_TER 207
SQ SEQUENCE 207 AA; 24034 MW; C9D5C7B1603BFDCA CRC64;

Query Match 18.7%; Score 231.5; DB 2; Length 207;
Best Local Similarity 27.7%; Pred. No. 2.3e-10;
Matches 57; Conservative 46; Mismatches 66; Indels 37; Gaps 7;

QY 48 LENTLLFKGFFGHPWYNDLLVD-----LGSKDATNKYKGGKVDLYGAY---- 91
DB 2 VDNNSLLNIYSTIVYEYSDTVIDFTKSHNLVTKLDVRDARDFINSEMDYEAANDFKA 61

QY 92 -----YGYQCAGGTPNKATCMYGGVTLHDNNRLTEKKVPINLWIDGKQTTPV 139
DB 62 GDRIAPVSPFDNLYSKG---KVTAYTYGGITPYQKTSI--PKNIPVNLWNRKQIPVP 116

QY 140 IDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVGRLIYVHSEGS-TVSYDL 198
DB 117 YNQISTNKTITVTAQEDIDKVRKFLIAHQHLYSS---GSSYKSGKLVFTNDNSDKYSLDL 173

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QY 199 FDAQQYPTLLRIYRDNTKNTINSENL 224
Db 174 FYTGVRDKEISFKVYKDNKSFNIDKI 199

RESULT 65
Q9LAC7 PRELIMINARY; PRT; 209 AA.
AC Q9LAC7;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-18 (Fragment).
GN SMEZ-18.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10763;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof T., Mofatt S.L., Weller K.D., Paterson A., Martin D.,
Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143668; AAF6668.1; -.
DR HSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; P:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24214 MW; 5755ED7340D77527 CRC64;

Query Match 18.7%; Score 231.5; DB 2; Length 209;
Best Local Similarity 27.7%; Pred. No. 2.3e-10;
Matches 57; Conservative 46; Mismatches 66; Indels 37; Gaps 7;

QY 48 LENTLLFKGFFGHPW-YNDLLVD-----LGSKDATNKYKGVLDLYGAY----- 91
Db 3 VDNNSLLRNIYSTIVVEYSVTVIDFMTSHNLVTKLVDVRDADFFINSKMDVYAANDFKT 62

QY 92 -----YGYQCAGGTENKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVP 139
Db 63 GDKIATVSPVPPNNVLSK3---KVTATYGGITPQKTSI--PRNIPVNLWINKQIIVP 117

QY 140 IDKVTSKKEVTQBELDQARHYLHGKFLGYNDSFGKVGKQVRLIVFHSSGSG-TVSYDL 198
Db 118 YNQISTNKTVTQAQIDLVKVKFLIAQHOLYSS---GSSYKSGKLVFHTNDNSDKYFSL 174

QY 199 FDAQQYPTLLRIYRDNTKNTINSENL 224
Db 175 FYTGVRDKEISFKVYKDNKSFNIDKI 200

RESULT 66
Q9LAD9 PRELIMINARY; PRT; 209 AA.
AC Q9LAD9;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-5 (Fragment).
GN SMEZ-5.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11244;
RX MEDLINE=20273982; PubMed=10811869;
RA Prof T., Mofatt S.L., Weller K.D., Paterson A., Martin D.,
Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143655; AAF66556.1; -.
DR HSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; P:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24079 MW; 24CA3885469CB9B CRC64;

Query Match 18.6%; Score 230.5; DB 2; Length 209;
Best Local Similarity 27.7%; Pred. No. 2.8e-10;
Matches 57; Conservative 47; Mismatches 65; Indels 37; Gaps 7;

QY 48 LENTLLFKGFFGHPW-YNDLLVD-----LGSKDATNKYKGVLDLYGAY----- 91
Db 3 VDNNSLLRNIYSTIVVEYSVTVIDFMTSHNLVTKLVDVRDADFFINSEMDVYAANDFKD 62

QY 92 -----YGYQCAGGTENKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVP 139
Db 63 GDKIATVSPVPPNNVLSK3---KVTATYGGITPQKTSI--KNIPVNLWINKQIIVP 117

QY 140 IDKVTSKKEVTQBELDQARHYLHGKFLGYNDSFGKVGKQVRLIVFHSSGSG-TVSYDL 198
Db 118 YNEISTNKTVTQAQIDLVKVKFLIAQHOLYSS---GSSYKSGKLVFHTNDNSGKYL 174

QY 199 FDAQQYPTLLRIYRDNTKNTINSENL 224
Db 175 FYTGVRDKEISFKVYKDNKSFNIDKI 200

RESULT 67
Q8NZ89 PRELIMINARY; PRT; 233 AA.
AC Q8NZ89;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z.
GN SMEZ OR SPYM18 2064.
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=186103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS8232 / Serotype M18;
RX MEDLINE=21927593; PubMed=11917108;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
Sylvia G.L., Sturdevant D.B., Ricklefs S.M., Forcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Veasy L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
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RT group A Streptococcus strains associated with acute rheumatic fever
RL Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673 (2002).
DR EMBL; AE010110; AAL98535.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; BactI_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW complete proteome.
SQ SEQUENCE 233 AA; 26859 MW; 23E07C9C06AB866 CRC64;

Query Match 18.6%; Score 230; DB 16; Length 233;
Best Local Similarity 29.1%; Pred. No. 3.5e-10;
Matches 59; Conservative 42; Mismatches 66; Indels 36; Gaps 6;

QY 50 NTLFFKGFTHGHPWYNDLLVD-----LGSKDATNKYKGGKVDLYGAY----- 91
DQ 30 NSLLRNISTYIMYEYSDTVIDFKTSHNLVTKLDVRDARDFINSEMDYEAANDFKDGDK 89

QY 92 -----XGYQACGTPNKTCMYGGVTLHDNNRLTEKKVPINLWIDKQTTVPIDK 142
DQ 90 IAFSVFDFDNYLSEG---KVIAITYGGMPYQKTSI--PKNIPVNLWINGKQISVPYNE 144

QY 143 VKTSKKEVTQVELDQARHYLHGKFLYNSDSFGKVGQRLIVFHSSEGS--TVSYDLFDA 201
DQ 145 ISTNKTTVTAQEIIDLKVRKFLISQHLYS---GSSYKSGKLVEHTDNDNSDKYSLDLFVY 201

QY 202 QGYQYPTLLRIYRDNKTINSEN 224
DQ 202 GYRDKESIFKVKYKDKNSFNIDKI 224

RESULT 68
Q9LAC9 PRELIMINARY; PRT; 209 AA.
AC Q9LAC9
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Mitogenic exotoxin Z-16 (Fragment).
GN SMEZ-16
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10649;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143661; AAF66661.1; -.
DR HSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; BactI_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 209 AA; 24194 MW; E12EF47B3B8D95DE CRC64;

Query Match 18.5%; Score 228.5; DB 2; Length 209;
Best Local Similarity 28.2%; Pred. No. 4e-10;
Matches 58; Conservative 44; Mismatches 67; Indels 37; Gaps 7;

QY 48 LENTLLFKGFTGHPWYNDLLVD-----LGSKDATNKYKGGKVDLYGAY----- 91
DQ 3 VDNNSLLRNISTYIMYEYSDTVIDFKTSHNLVTKLDVRDARDFINSEMDYEAANDFKA 62

QY 92 -----XGYQACGTPNKTCMYGGVTLHDNNRLTEKKVPINLWIDKQTTVP 139
DQ 63 GRIAVSFVDFDNYLSKG---KVTAYTYGGITPYQKTSI--PKNIPVNLWINKQISVP 117

QY 140 IDKVTSKKEVTQVELDQARHYLHGKFLYNSDSFGKVGQRLIVFHSSEGS--TVSYDL 198
DQ 118 YNEISTNKTTVTAQEIIDLKVRKFLISQHLYS---GSSYKSGKLVEHTDNDNSDKYSLDL 174

QY 199 FDAQGYPTLLRIYRDNKTINSEN 224
DQ 175 FYTGDKESIFKVKYKDKNSFNIDKI 200

RESULT 69
Q9LAD4 PRELIMINARY; PRT; 209 AA.
ID Q9LAD4
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-11 (Fragment).
GN SMEZ-11
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9779;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143661; AAF66661.1; -.
DR HSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; BactI_tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 209 AA; 24194 MW; E12EF47B3B8D95DE CRC64;

Query Match 18.5%; Score 228.5; DB 2; Length 209;
Best Local Similarity 28.2%; Pred. No. 4e-10;
Matches 58; Conservative 44; Mismatches 67; Indels 37; Gaps 7;

QY 48 LENTLLFKGFTGHPWYNDLLVD-----LGSKDATNKYKGGKVDLYGAY----- 91
DQ 3 VDNNSLLRNISTYIMYEYSDTVIDFKTSHNLVTKLDVRDARDFINSEMDYEAANDFKA 62

QY 92 -----XGYQACGTPNKTCMYGGVTLHDNNRLTEKKVPINLWIDKQTTVP 139
DQ 63 GRIAVSFVDFDNYLSKG---KVTAYTYGGITPYQKTSI--PKNIPVNLWINKQISVP 117

QY 140 IDKVTSKKEVTQVELDQARHYLHGKFLYNSDSFGKVGQRLIVFHSSEGS--TVSYDL 198
DQ 118 YNEISTNKTTVTAQEIIDLKVRKFLISQHLYS---GSSYKSGKLVEHTDNDNSDKYSLDL 174

QY 199 FDAQGYPTLLRIYRDNKTINSEN 224
DQ 175 FYTGDKESIFKVKYKDKNSFNIDKI 200

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Db 63 GDRIAVSFVPPDMNYSKSG---KVTATYGGVTPYQKTSI--PRNIPVNLWNRKQIPVP 117
Qy 140 IDKVKTSKKEVTQELDLQARHYLHGKFGVNSDFGKVGQVQGLIVFHSSEGS--TVSYDL 198
Db 118 YNQISTNKTVTYTAQEIDLKVRKFLISQHLVSS---GSNYKSGKLVTHTNDNSDKYSLDL 174
Qy 199 FDAQGQYPTDLLRIYRNKNTINSENUL 224
Db 175 FYTGDRKESIFKVKDKNKSFNIDKI 200

RESULT 70
Q936G4 ID Q936G4 PRELIMINARY; PRT; 259 AA.
AC Q936G4;
DT 01-DEC-2001 (TREMELrel. 19, Created)
DT 01-DEC-2001 (TREMELrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Enterotoxin-like protein.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=M;
RX MEDLINE=95050273; PubMed=7961465;
RA Lin W.S., Cunnell T., Lee C.Y.;
RT "Sequence analysis and molecular characterization of genes required for the biosynthesis of type 1 capsular polysaccharide in Staphylococcus aureus."
RL J. Bacteriol. 176:7005-7016(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=M;
RA Luong T.T., Shu O., Bush K., Lee C.Y.;
RT "The Type 1 Capsular Polysaccharide of Staphylococcus aureus is carried in a Staphylococcal Cassette Chromosome Genetic Element."
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: U10927; AAL26674.1; -
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0015070; F:toxin activity; IEA.
DR GO: GO:0005215; F:transporter activity; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR GO: GO:0006810; P:transport; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bctr1 tox.
DR InterPro: IPR005666; Lipocin_cytFABP.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006126; Staph/Strep tox.
DR Pfam: PF01123; Staph Strep toxin; 1.
DR Pfam: PF02876; Staph Strep toxin; 1.
DR PRINTS: PR00279; BACTR1TOXIN.
DR PROSITE: PS00213; LIPOCALIN; 1.
DR PROSITE: PS00277; STAPH STREP TOXIN 1; 1.
DR PROSITE: PS00278; STAPH STREP TOXIN 2; 1.
SQ SEQUENCE 259 AA; 29981 MW; 783E1E4FEF057EDB CRC64;

Query Match 18.5%; Score 228.5; DB 2; Length 259;
Best Local Similarity 28.3%; Pred. No. 5.2e-10;
Matches 69; Conservative 41; Mismatches 109; Indels 25; Gaps 9;

Qy 1 SEKEEINEKDLRKSLOQTALGNLQKIYY-YNEKAITENK-ESDDQFLENTLLFKGFF 58
Db 24 AETQNDENISELNKSSQY---TGSWNIWLYNSDPVNAKKIKLSDKFLSHEFIPIINN 79
Qy 59 TGHWNVDLLDGLSKDATNKKYKGVLDLYGAYGYOC-----AGGTPNTACM 107
Db 80 PSH--YDYVKTDLKSTMASSFDGKEVDIFGVNYFDQCYFLNLIQCDNSQAGAGSKTCM 137
Qy 108 YGGVTLHNNRLTEBEKVPINLWI--DCKQTTPVTDKVKTSKKEVTQELDLQARHYLHGK 166
Db 138 YGGITLNN--TNNRQPIVVKVYENDSVLTFD-INIDKEVTIQELDYKVRNKLISK 194
```

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Qy 167 FGLYNSDSFGKVGQGLIVFHSSEGSTVSYDLDFAQQYPTDLLRIYRNKNTINSENLI 226
Db 195 INLYHLG--GTSYEVGYIKFIENGARYWYDMPPGFTQSKYLMYRGNVEVESAKTEI 252
Qy 227 ALYL 230
Db 253 EVEL 256

RESULT 71
Q9LAC3 ID Q9LAC3 PRELIMINARY; PRT; 209 AA.
AC Q9LAC3;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-17 (Fragment).
GN SMEZ-17.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11686;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weiler K.D., Paterson A., Martin D., Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation, Mosaic Structure, and Significant Antigenic Variation."
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL: AF143667; AAF66667.1; -
DR HSSP: P13163; 1SXT.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0015070; F:toxin activity; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bctr1 tox.
DR InterPro: IPR006123; Staph/Strep toxin.
DR InterPro: IPR006173; Staph tox OB.
DR Pfam: PF01123; Staph Strep toxin; 1.
DR Pfam: PF02876; Staph Strep toxin; 1.
DR PRINTS: PR00279; BACTR1TOXIN.
DR PROSITE: PS00278; STAPH STREP TOXIN 2; 1.
FT NON_TER 1
SQ SEQUENCE 209 AA; 24181 MW; A333F466398D9DC2 CRC64;

Query Match 18.4%; Score 227.5; DB 2; Length 209;
Best Local Similarity 27.7%; Pred. No. 4.8e-10;
Matches 57; Conservative 45; Mismatches 67; Indels 37; Gaps 7;

Qy 48 LENTLLFKGFTGHPW-YNDLLVD-----LGSKDATNKKYKGVLDLYGAY---- 91
Db 3 VDNNSLLRNISTIVYYSSTVIDFKTSHNLVTKKLDVRDARDFPFINSEMDEYAAANDFKA 62
Qy 92 -----YGYQCAGGTENKTACMYGGVTLHNNRLTEEEKVPIINLWIDGKQTPV 139
Db 63 GDRIAVSFVPPDMNYSKSG---KVTATYGGVTPYQKTSI--PRNIPVNLWNRKQIPVP 117
Qy 140 IDKVKTSKKEVTQELDLQARHYLHGKFGVNSDFGKVGQVQGLIVFHSSEGS--TVSYDL 198
Db 118 YNQISTNKTVTYTAQEIDLKVRKFLISQHLVSS---GSNYKSGKLVTHTNDNSDKYSLDL 174
Qy 199 FDAQGQYPTDLLRIYRNKNTINSENUL 224
Db 175 FYTGDRKESIFKVKDKNKSFNIDKI 200

RESULT 72
Q9LAC3 ID Q9LAC3 PRELIMINARY; PRT; 209 AA.
AC Q9LAC3;
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DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-24 (Fragment).
GN SMEZ-24.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10438;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143674; AAF66672.1; -.
DR HSSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0003405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR NON_TER.
FT SIGNAL.
SQ SEQUENCE 209 AA; 24137 MW; 301587A9A995F715 CRC64;

Query Match 18.4%; Score 227.5; DB 2; Length 209;
Best Local Similarity 27.7%; Pred.No. 4.8e-10;
Matches 57; Conservative 45; Mismatches 67; Indels 37; Gaps 7;

QY 48 LENTLFGKFFTGHPM-YNDLLVD-----LGSKDATNKYKGVLDYGYAY---- 91
DB 3 VDNNSLLRNIYSTIVVEYSDTVDFKTSNHLVTKLDVDRDARDFINSEMDEYAANDPKA 62
QY 92 -----YGYOCAGGTENKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQTTP 139
DB 63 GKIAVFSVPFDWNLVSKG---KVTATYGGITPY--KRNIPVNLWLNKQIIVP 117
QY 140 IDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRLIVFHSSEGS-TVSYDL 198
DB 118 YNQISNTKTTVTAQEIIDLKVRKFLIAHQHLYSS---GSSYKSGKLVFHTNDNSDKYSLDL 174
QY 199 FDAQGYPTLLRIYDNKTINSEN 224
DB 175 FYGYRDKESIFKVKYDNKSNFNIDKI 200

RESULT 73
Q9SLH8 PRELIMINARY; PRT; 256 AA.
ID Q9SLH8
AC Q9SLH8;
DT 01-MAY-2000 (TREMELrel. 13, Created)
DT 01-MAY-2000 (TREMELrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE SpeX protein precursor.
GN SPEX.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=12714 type 12;
RX MEDLINE=20374978; PubMed=10913699;
RA Gerlach D., Fleischer B., Wagner M., Schmidt K.H., Vettermann S.,
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RA Reichardt W.;
RT "Purification and Biochemical Characterization of a Basic Superantigen
RT (SPEX/SMEZ3).";
RL FEMS Microbiol. Lett. 188:153-163(2000).
DR EMBL; AJ245405; CAB51744.1; -.
DR HSSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0003405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR SIGNAL.
FT SIGNAL.
SQ SEQUENCE 256 AA; 29706 MW; 873D0BAFB6B6DC332 CRC64;

Query Match 18.3%; Score 226.5; DB 2; Length 256;
Best Local Similarity 28.2%; Pred.No. 7.3e-10;
Matches 58; Conservative 47; Mismatches 64; Indels 37; Gaps 7;

QY 48 LENTLFGKFFTGHPM-YNDLLVD-----LGSKDATNKYKGVLDYGYAY---- 91
DB 50 VDNNSLLRNIYSTIVVEYSDTVDFKTSNHLVTKLDVDRDARDFINSEMDEYAANDPKT 109
QY 92 -----YGYOCAGGTENKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQTTP 139
DB 110 GKIAVFSVPFDWNLVSKG---KVTATYGGITPY--KQLQYLKLSLVNLWLNKQISVP 164
QY 140 IDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRLIVFHSSEGS-TVSYDL 198
DB 165 YNEISTNKTTVTAQEIIDLKVRKFLIAHQHLYSS---GSSYKSGRLVFTHTNDNSDKYSFDL 221
QY 199 FDAQGYPTLLRIYDNKTINSEN 224
DB 222 FYGYRDKESIFKVKYDNKSNFNIDKI 247

RESULT 74
Q9SLAD PRELIMINARY; PRT; 209 AA.
ID Q9SLAD
AC Q9SLAD;
DT 01-OCT-2000 (TREMELrel. 15, Created)
DT 01-OCT-2000 (TREMELrel. 15, Last sequence update)
DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)
DE Mitogenic exotoxin Z-10 (Fragment).
GN SMEZ-10.
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=11580;
RX MEDLINE=20273982; PubMed=10811869;
RA Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA Fraser J.D.;
RT "The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT Mosaic Structure, and Significant Antigenic Variation.";
RL J. Exp. Med. 191:1765-1776(2000).
DR EMBL; AF143660; AAF66660.1; -.
DR HSSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0015070; F:toxin activity; IEA.
DR GO; GO:0003405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bctr1 tox.
DR InterPro; IPR006123; Staph/Strep toxin.
DR InterPro; IPR006173; Staph/Strep toxin.
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DR Pfam; PF01123; Stap_Strp_toxin; 1.
DR Pfam; PF02876; Stap_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAP_STRP_TOXIN_2; 1.
FT NON TER
SQ SEQUENCE 209 AA; 24102 MW; 8B4C953751A56D05 CRC64;

Query Match 18.2%; Score 225.5; DB 2; Length 209;
Best Local Similarity 27.7%; Pred. No. 6.9e-10;
Matches 57; Conservative 46; Mismatches 66; Indels 37; Gaps 7;

Qy 48 LENTLLFKGFTGHPW-YNDLLVD-----LGSKDATNKYKGKVDLYGAY----- 91
Db 3 VDNNSLLENISTVIVYESDIVDFKTSNLTVTKKLDVDRDARDFINSEMEDEYAAANDPKD 62
Qy 92 -----YGVQAGGTPNTACMYGVTLLHDNNRLTTEKKVPINLWDGKQTVP 139
Db 63 GDKIAMPSPVPDWNLYSGK---KVIATYFGWTPCQEEPIS--KNIPVNLWINGKQISVP 117
Qy 140 IDKYTSKKEVTVOELDLQARHYLHGKFLGYNSSDFGKGQGVGLTVFHSSEGS--TVSYDL 198
Db 118 YNEISTNKTVTVAQSIDLKVAKFLIAQHLISS---GSSYSGKGLVFTHTDNSDKYSIDL 174
Qy 199 FDAGQYDPDTLRLRYVRDNKTINSNL 224
Db 175 FYVGYRDKESIFKYVKNKSNINIKI 200

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RESULT	75
ID	Q9LAD7
PRELIMINARY;	PRT; 209 AA.
AC	Q9LAD7;
DT	01-OCT-2000 (TrEMBLrel. 15, Created)
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE	Mitogenic exotoxin Z-8 (Fragment).
GN	SMEZ-8.
OS	Streptococcus pyogenes.
OC	Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC	Streptococcus.
OX	NCBI_TaxID=1314;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	STRAIN=1/5045;
RX	MEDLINE=20273982; PubMed=10811869;
RA	Proft T., Moffatt S.L., Weller K.D., Paterson A., Martin D.,
RA	Fraser J.D.;
RT	"The Streptococcal Superantigen SMEZ Exhibits Wide Allelic Variation,
RT	Mosaic Structure, and Significant Antigenic Variation.";
RL	J. Exp. Med. 191:1765-1776(2000).
DR	HMSB; AF143658; AAF66658.1; -
DR	ENSLP; P31363; 1SXT.
DR	GO; GO:0005576; C:extracellular; IEA.
DR	GO; GO:0015070; F:toxin activity; IEA.
DR	GO; GO:0009405; P:pathogenesis; IEA.
DR	InterPro; IPR008992; Bact_endotox.
DR	InterPro; IPR006177; Bctrl_tox.
DR	InterPro; IPR006123; Staph/Strep toxin.
DR	InterPro; IPR006173; Staph_tox_OB.
DR	Pfam; PF01123; Staph_Strep_toxin; 1.
DR	Pfam; PF02876; Staph_Strep_tox_C; 1.
DR	PRINTS; PR00279; BACTRL_TOXIN
DR	PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT	NON_TER
SQ	SEQUENCE 209 AA; 24091 MW; 7680E9B35513DF28 CRC64;
Query Match	18.0%; Score 222.5; DB 2; Length 209;
Best Local Similarity	27.2%; Pred. No. 1.2e-09;
Matches	56; Conservative 47; Mismatches 66; Indels 37; Gaps
QY	48 LENTLLPKGFFTHPH-VNDLLVD-----LGSKDAFNKYKKVLYGAY---- 91
Dd	3 VDNNSLRNIYITVEYEGDVTWIDFKTSNLHVLTKCLDVARDFDFTINSMDYYAANDFKA 91

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 12, 2004, 13:21:44 ; Search time 29.2786 Seconds
(without alignments)
2248.525 Million cell updates/sec

Title: US-09-900-766-3
Perfect score: 1238
Sequence: 1 SEKSEINEKDLRKSEKELQ.....RDNKTINSENLHLYLYTT 233

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

- Database 1: A_Geneseq_25Jan04.*
- 1: Geneseqp1980s.*
 - 2: Geneseqp1990s.*
 - 3: Geneseqp2000s.*
 - 4: Geneseqp2001s.*
 - 5: Geneseqp2002s.*
 - 6: Geneseqp2003as.*
 - 7: Geneseqp2003bs.*
 - 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1238	100.0	233	6	ABP58457 Engineere
2	1216	98.2	245	2	AAW35375 Staphyloc
3	1210	97.7	233	6	ABP58456 Staphyloc
4	1210	97.7	257	4	AAU14103
5	1210	97.7	257	4	ABO10268 S. aureus
6	1196	96.6	230	4	AAW67339 Staphyloc
7	1194	96.4	245	2	AAW35374 Staphyloc
8	1168	94.3	248	6	ABU79072 S. aureus
9	1151	93.0	230	2	AAW45012 Staphyloc
10	1147	92.6	230	5	ABW76235 Staphyloc
11	1130	91.3	233	6	ABP58455 Engineere
12	1130	91.3	672	6	ABP58454 Engineere
13	1128	91.1	230	2	AAW13204 Staphyloc
14	1049	84.7	233	2	AAW13203 Staphyloc
15	1037	83.8	233	6	ABP58458 Staphyloc
16	1037	83.8	257	4	AAU14104 Peptide s
17	1037	83.8	257	6	ABO10269 S. aureus
18	1037	83.8	257	7	ADU44368 Staphyloc
19	1033	83.4	233	2	AAW06738 Staphyloc
20	1030	83.2	233	4	AAW35373 Staphyloc
21	1030	83.2	233	4	AAW67338 Staphyloc
22	1027	83.0	233	2	AAW45011 Staphyloc
23	1024	82.7	257	6	ABU79068 S. aureus
24	1018	82.2	233	5	ABW76234 Staphyloc
25	1014	81.9	257	5	ABW79501 Staphyloc

26	1014	81.9	257	6	ABU10081 Staphyloc
27	1014	81.9	257	7	ABU62324 S. aureus
28	1014	81.9	257	7	AAE37676 Protein #
29	1010	81.6	233	3	AAE37676 Protein #
30	1010	81.6	233	5	ABW79502 Staphyloc
31	1010	81.6	233	6	ABU10082 Staphyloc
32	1010	81.6	233	7	ABU62325 S. aureus
33	1010	81.6	233	7	AAE37677 Protein #
34	1006	81.3	233	6	ABU10099 Staphyloc
35	1001	80.9	233	6	ABU10098 Staphyloc
36	997	80.5	237	3	AAW70102 Staphyloc
37	992	80.1	233	3	AAW70103 Mutant St
38	663	53.6	258	6	ABU79071 S. aureus
39	657	53.1	228	2	AAW45013 Staphyloc
40	657	53.1	228	4	AAW67340 Staphyloc
41	657	53.1	228	5	ABW76236 Staphyloc
42	649	52.4	228	2	AAW13205 Staphyloc
43	523	42.2	203	6	ABP58459 Staphyloc
44	483.5	39.1	250	6	ABW70958 Staphyloc
45	457	36.9	82	6	ABU10091 Bacterial
46	457	36.9	82	7	ABU62338 S. aureus
47	399	32.2	82	6	ABU10089 Bacterial
48	399	32.2	82	7	ABU62336 S. aureus
49	370	29.9	91	2	AAW42439 Staphyloc
50	360	29.1	217	6	ABP58460 Staphyloc
51	327.5	26.5	259	5	ABP29357 Streptoco
52	310.5	25.1	239	2	AAW06254 Staphyloc
53	310.5	25.1	240	6	ABG71370 Staphyloc
54	305.5	24.7	239	2	AAW06253 Staphyloc
55	305.5	24.7	240	6	ABG71369 Staphyloc
56	304.5	24.6	239	2	AAW06256 Staphyloc
57	304.5	24.6	240	6	ABG71372 Staphyloc
58	304.5	24.6	266	6	ABU79069 S. aureus
59	303.5	24.5	239	4	AAW64647 Synthetic
60	303.5	24.5	239	4	AAW67341 Staphyloc
61	303.5	24.5	255	2	AAW06737 Staphyloc
62	302.5	24.4	239	2	AAW06255 Staphyloc
63	302.5	24.4	240	6	ABG71371 Staphyloc
64	300.5	24.3	239	2	AAW06252 Staphyloc
65	300.5	24.3	240	6	ABG71368 Staphyloc
66	300.5	24.3	266	7	ABU62455 S. aureus
67	298.5	24.1	238	2	AAW45016 Staphyloc
68	298.5	23.9	238	4	AAW67343 Staphyloc
69	296.5	23.9	238	5	ABW76239 Staphyloc
70	296.5	23.9	239	2	AAW13206 Staphyloc
71	296.5	23.9	239	2	AAW45014 Staphyloc
72	296.5	23.9	266	3	AAW92319 Plant-Opt
73	296.5	23.9	266	5	ABW79503 Staphyloc
74	296.5	23.9	266	6	ABU10083 Staphyloc
75	296.5	23.9	266	7	ABU62326 S. aureus
76	296.5	23.9	266	7	AAE37678 Protein #
77	294.5	23.8	239	5	ABW76237 Staphyloc
78	294.5	23.8	266	2	AAW13208 Staphyloc
79	293.5	23.7	266	3	AAW54464 Amino aci
80	293.5	23.7	266	3	AAW54465 Mutant St
81	292.5	23.6	240	3	AAW54465 Mutant St
82	291.5	23.5	239	5	ABW79505 Staphyloc
83	291.5	23.5	239	6	ABU10085 Staphyloc
84	291.5	23.5	239	7	AAE37680 Protein #
85	291.5	23.5	239	7	AAE37680 Protein #
86	290.5	23.5	239	3	ABU70106 Mutant St
87	290.5	23.5	266	7	ABU62454 S. aureus
88	287.5	23.2	266	7	ABU62452 S. aureus
89	287.5	23.2	266	7	ABU62451 S. aureus
90	286.5	23.1	266	5	ABW79504 Staphyloc
91	286.5	23.1	266	6	ABU10084 Staphyloc
92	286.5	23.1	266	7	ABU62327 Staphyloc
93	286.5	23.1	266	7	AAE37679 Protein #
94	285.5	23.1	251	2	AAW12153 Streptoco
95	284.5	23.0	221	2	AAW13209 Streptoco
96	284.5	23.0	221	2	AAW45017 Staphyloc
97	284.5	23.0	221	5	ABW76240 Staphyloc
98	284.5	23.0	251	2	AAW12151 Streptoco

99 284.5 23.0 251 2 AAW12150
100 283 22.9 265 3 AAY70104

Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFLYNSDSFGKRVQ 180
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFLYNSDSFGKRVQ 180

ALIGNMENTS

Qy 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDKNKTINSENHLALVLYTT 233
Db 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDKNKTINSENHLALVLYTT 233

RESULT 1

ID ABP58457 standard; protein; 233 AA.
XX AC ABP58457;
XX DT 14-APR-2003 (first entry)
XX DE Engineered superantigen SEA/E-18 for human cancer therapy.

XX Superantigen; staphylococcal enterotoxin; antibody; cancer; tumour;
XX cytotatic; vaccine; SEA/E-18; mutant; mutein.
XX OS Staphylococcus sp.
XX OS Synthetic.
XX PN WO2003002143-A1.
XX FH 09-JAN-2003.
XX PD 19-JUN-2002; 2002WO-SR001188.
XX PF 28-JUN-2001; 2001SE-00002327.
XX PR (ACTI-) ACTIVE BIOTECH AB.
XX PA Forsberg G, Erlandsson E, Antonsson P, Walse B;
XX PI WPI; 2003-201467/19.
XX DR Conjugate for therapy, has bacterial superantigen with a region in T-cell
PT receptor and four regions to determine binding to class II major
PT histocompatibility complex, antibody to cancer associated cell surface
PT structure.
XX Example 3; Fig 3; 102pp; English.

XX The present sequence is the protein sequence of engineered staphylococcal
CC superantigen SEA/E-18. The superantigen is based on staphylococcal
CC enterotoxin E (SEE, see ABP58456) except for 4 amino acid residues close
CC to the N-terminal that were from enterotoxin A and one substitution in
CC the C-terminal part, D227A. Models of new superantigen variants were
CC constructed using the SEA/E-18 model as the template. These include the
CC new engineered superantigen SEA/E-120 (see ABP58455), which has been
CC genetically fused to the Fab moiety of the tumour reactive antibody 5T4
CC to form a conjugate (see ABP58454) polypeptide. The conjugate is a
CC claimed example of novel conjugates of the invention comprising an
CC engineered bacterial superantigen and an antibody moiety. The conjugates
CC are designed to target and destroy cancer cells, including cancer of the
CC lung, breast, colon, kidney, pancreas, ovary, stomach, cervix and
CC prostate (claimed)
XX Sequence 233 AA;

Query Match 100.0%; Score 1238; DB 6; Length 233;
Best Local Similarity 100.0%; Pred. No. 1e-115;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKKSELOQTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKKSELOQTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Qy 61 HPWYNDLLVGLGSKDANKYKGGKVDLYGAYGVQACAGTTPNKTACMYGVTLHDNNRLT 120
Db 61 HPWYNDLLVGLGSKDANKYKGGKVDLYGAYGVQACAGTTPNKTACMYGVTLHDNNRLT 120

RESULT 2

AAW35375
ID AAW35375 standard; peptide; 245 AA.
XX AC AAW35375;
XX DT 20-APR-1998 (first entry)
XX DE Staphylococcus enterotoxin SEE modified superantigen.

XX SEE; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment;
XX cancer; infection; autoimmune disease; antibody; modified.
XX OS Staphylococcus sp.
XX FH Location/Qualifiers
FT Misc-difference 20
FT /label= R20G
FT /note= "wild-type Arg is replaced by Gly"
FT Misc-difference 21
FT /label= N21T
FT /note= "wild-type Asn is replaced by Thr"
FT Misc-difference 24
FT /label= S24G
FT /note= "wild-type Ser is replaced by Gly"
FT Misc-difference 27
FT /label= R27K
FT /note= "wild-type Arg is replaced by Lys"
XX WO9736932-A1.
XX PD 09-OCT-1997.
XX PF 26-MAR-1997; 97WO-SR000537.
XX PR 29-MAR-1996; 96SE-00001245.
XX PR 12-AUG-1996; 96US-00695692.
XX PA (PIAA) PHARMACIA & UPJOHN AB.
XX PI Antonsson P, Hansson J, Bjoerk P, Dohlesten M, Kalland T;
XX PI Abrahamson L, Forsberg G;
XX WPI; 1997-503052/46.

XX Conjugate of target seeking moiety and modified superantigen - useful for
PT activating the immune system to treat cancer, viral infections, parasitic
PT infestations and autoimmune diseases.
XX Claim 5; Page; 58pp; English:
XX This is a modified Staphylococcus enterotoxin SEE superantigen. The wild-
CC type SEE superantigen is modified to be used in a novel conjugate. The
CC novel conjugate comprises a target seeking moiety and a modified wild
CC type superantigen. This modified superantigen retains its ability to
CC activate a subset of T cells, even though 1 or more wild-type amino acid
CC residues in at least 1 region which functions in determining binding to T
CC cell receptor (TCR) and activation of a subset of T cells has/have been
CC replaced. Such a modified superantigen can optionally be used as part of
CC a conjugate with a target seeking moiety, for activating the immune
CC system to treat a mammalian disease. A pharmaceutical composition can be
CC prepared comprising a modified antibody (preferably a Fab fragment fused
CC to a peptide moiety providing activation of T cells in Vbeta specific
CC manner) in which cysteines providing for interchain cysteine linkages in

CC the native antibody have been replaced (preferably by serine residues) to
 CC prohibit cysteine formation. The modified wild-type superantigen is used
 CC for treating cancer, viral infections, parasitic infestations and
 CC autoimmune disease. The modified wild type superantigen has a lower
 CC immunogenicity and reactivity with neutralising antibodies and has fewer
 CC side-effects when used as a drug, compared to wild type superantigen.
 CC Note: this sequence is not provided in the specification. It has been
 CC created by modifying the wild-type SEE superantigen sequence in Pages 38-
 CC 39 of the specification
 XX
 SQ Sequence 245 AA;

Query Match 98.2%; Score 1216; DB 2; Length 245;
 Best Local Similarity 94.7%; Pred. No. 1.8e-113;
 Matches 232; Conservative 0; Mismatches 1; Indels 12; Gaps 1;

Qy 1 SEKSEINEKDLRKSELOQTALGNLQIYYNNEKAITENKESDDQFLENTLLFKGFFTG 60
 Db 1 SEKSEINEKDLRKSELOQTALGNLQIYYNNEKAITENKESDDQFLENTLLFKGFFTG 60
 Qy 61 HPWYNDLLVLDLGSKDATNKYKGGVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNRRLT 120
 Db 61 HPWYNDLLVLDLGSKDATNKYKGGVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNRRLT 120
 Qy 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDQARHLYLHGKFGLYNSDSFGGKVQ 180
 Db 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDQARHLYLHGKFGLYNSDSFGGKVQ 180
 Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGVPTLLRIYRDNK-----TINSENHLAL 228
 Db 181 RGLIVFHSSEGSTVSVDLFDAGQGVPTLLRIYRDNK-----TINSENHLAL 228
 Qy 229 YLYTT 233
 Db 241 YLYTT 245

RESULT 3
 ID ABP58456 standard; protein; 233 AA.
 AC ABP58456;
 DT 14-APR-2003 (first entry)
 DE Staphylococcal enterotoxin E.
 KW Superantigen; staphylococcal enterotoxin E; antibody; cancer; tumour;
 KW cytostatic; vaccine.
 OS Staphylococcus sp.
 FN WO2003002143-A1.
 PD 09-JAN-2003.
 PF 19-JUN-2002; 2002WO-SE001188.
 PR 28-JUN-2001; 2001SE-00002327.
 PA (ACTI-) ACTIVE BIOTECH AB.
 PI Forsberg G, Erlandsson E, Antonsson P, Walse B;
 XX WPI; 2003-201467/19.
 XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
 PT receptor and four regions to determine binding to class II major
 PT histocompatibility complex, antibody to cancer associated cell surface
 structure.
 XX
 PS Example 3; Fig 4; 102pp; English.

CC The present sequence is the protein sequence of staphylococcal
 CC enterotoxin SEE. The invention provides novel conjugates (see ABP58454)
 CC for human cancer therapy. These comprise an engineered bacterial
 CC superantigen, such as novel SEA/E-120 (see ABP58455), which is based on
 CC SEE, and an antibody moiety, such as tumour reactive antibody 574. The
 CC superantigen is engineered to reduce seroreactivity whilst maintaining
 CC biological activity and production levels. The conjugates are designed to
 CC target and destroy cancer cells, including cancer of the lung, breast,
 CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
 XX
 SQ Sequence 233 AA;

Query Match 97.7%; Score 1210; DB 6; Length 233;
 Best Local Similarity 97.9%; Pred. No. 6.6e-113;
 Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKSELOQTALGNLQIYYNNEKAITENKESDDQFLENTLLFKGFFTG 60
 Db 1 SEKSEINEKDLRKSELOQTALGNLQIYYNNEKAITENKESDDQFLENTLLFKGFFTG 60
 Qy 61 HPWYNDLLVLDLGSKDATNKYKGGVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNRRLT 120
 Db 61 HPWYNDLLVLDLGSKDATNKYKGGVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNRRLT 120
 Qy 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDQARHLYLHGKFGLYNSDSFGGKVQ 180
 Db 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVQLDQARHLYLHGKFGLYNSDSFGGKVQ 180
 Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGVPTLLRIYRDNK-----TINSENHLAL 233
 Db 181 RGLIVFHSSEGSTVSVDLFDAGQGVPTLLRIYRDNK-----TINSENHLAL 233

RESULT 4
 ID AAU14103 standard; peptide; 257 AA.
 AC AAU14103;
 DT 21-NOV-2001 (first entry)
 DE Peptide sequence from Staphylococcus aureus enterotoxin type E.
 KW Anti-retroviral; DP178-like; DP107-like; enterotoxin type E;
 KW antitumorigenic; antiviral; HIV transmission.
 OS Staphylococcus aureus.
 FN WO200151673-A2.
 PD 19-JUL-2001.
 PF 05-JUL-2000; 2000WO-US035727.
 PR 09-JUL-1999; 99US-00350841.
 PA (TRIM-) TRIMERIS INC.
 PI Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
 XX WPI; 2001-442157/47.

XX Identifying a compound that inhibits the formation of or disrupts a
 PT DP107/DP178 complex, especially compounds with antitumorigenic, antiviral
 PT or intracellular modulatory activity, by detecting the formation of a
 PT DP107/DP178 complex.
 XX
 PS Disclosure; Fig 4; 259pp; English.
 XX The present invention relates to peptides which exhibit anti-retroviral
 CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
 CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
 CC amino acids 639-673 of the transmembrane protein gp41 from human

CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DP107 peptide
 CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
 CC also relates to a method of identifying compounds that inhibit the
 CC formation of or disrupts a DP107/DP178 complex. The method comprises
 CC detecting the formation of a DP107/DP178 complex, both in the presence or
 CC absence of a test compound, in a reaction mixture containing DP107 and
 CC DP178 peptides. The method is useful for identifying compounds, including
 CC small molecule compounds, which may themselves exhibit antifeusogenic,
 CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
 CC peptides are useful to inhibit human and non-human retroviral,
 CC particularly HIV, transmission to uninfected cells. The present sequence
 CC represents a peptide sequence from *Staphylococcus aureus* enterotoxin type
 XX E
 XX
 SQ Sequence 257 AA;

Query Match 97.7%; Score 1210; DB 4; Length 257;
 Best Local Similarity 97.9%; Pred. No. 7.6e-113;
 Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 Db 25 SEKSEINEKDLRKKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
 QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
 Db 85 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
 QY 121 EEKVPINLWIDGQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 Db 145 EEKVPINLWIDGQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIALYLYTT 233
 Db 205 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIALYLYTT 257

RESULT 5
 ABO10268
 ID ABO10268 standard; protein; 257 AA.
 XX ABO10268;
 XX
 DT 19-AUG-2003 (first entry)
 XX
 DE S. aureus enterotoxin E.
 KW HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;
 KW Epstein-Barr virus infection; heptad repeat motif.

XX *Staphylococcus aureus*.
 XX US6518013-B1.
 XX 11-FEB-2003.
 XX 07-JUN-1995; 95US-00485546.
 XX 07-JUN-1993; 93US-00073028.
 XX 07-JUN-1994; 94US-00255208.
 XX 20-DEC-1994; 94US-00360107.
 XX (TRIM-) TRIMERIS INC.
 XX Barney SO, Lambert DM, Petteway SR;
 XX WPI; 2003-465599/44.
 XX Inhibiting transmission of Epstein-Barr virus to a cell, by contacting
 XX the cell with a peptide consisting of a region of Epstein-Barr virus
 XX protein.
 XX Example; Fig 41; 716pp; English.

XX The invention relates to inhibiting (M) transmission of an Epstein-Barr
 CC virus to a cell, comprising contacting the cell with an effective
 CC concentration of a peptide consisting of a region of 16-39 consecutive
 CC amino acids of an Epstein-Barr virus protein for an effective period of
 CC time, where the region is recognised by one or more of ALLMOT15,
 CC 107x178x4 or PL2IP sequence search motifs, the peptide further comprises
 CC an amino terminal X, and a carboxy terminal Z in which X comprises an
 CC amino group, acetyl group, 9-fluorenylmethoxycarbonyl group, hydrophobic
 CC group or macromolecular carrier group, and Z comprises a carboxyl group,
 CC amido group, hydrophobic group, or macromolecular carrier group, and
 CC fusion of the virus to the cell is inhibited. The peptides were
 CC identified by analysing the structure/motifs present in the HIV-1
 CC glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat
 CC motif containing peptides were used to design the motifs cited above,
 CC which in turn were used to analyse proteins from other pathogenic
 CC organisms and HIV isolates, looking for DP107/178 structural analogues.
 CC The method is useful for inhibiting transmission of Epstein-Barr virus to
 CC a cell and Epstein-Barr virus infection. The present sequence is a
 CC protein from a pathogenic organism analysed for regions analogous to
 CC DP107 or DP178
 XX
 SQ Sequence 257 AA;

Query Match 97.7%; Score 1210; DB 6; Length 257;
 Best Local Similarity 97.9%; Pred. No. 7.6e-113;
 Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 Db 25 SEKSEINEKDLRKKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
 QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
 Db 85 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
 QY 121 EEKVPINLWIDGQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 Db 145 EEKVPINLWIDGQTTPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIALYLYTT 233
 Db 205 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIALYLYTT 257

RESULT 6
 AAB67339
 ID AAB67339 standard; peptide; 230 AA.
 XX AAB67339;
 XX
 DT 23-APR-2001 (first entry)
 XX
 DE *Staphylococcus aureus* enterotoxin E protein.
 KW Tumour; cancer; immune; enterotoxin.
 XX *Staphylococcus aureus*.
 XX US6180097-B1.
 XX 30-JAN-2001.
 XX 30-OCT-1998; 98US-00183437.
 XX 03-OCT-1989; 89US-00416530.
 XX 17-JAN-1990; 90US-00465577.
 XX 17-JAN-1991; 91WO-US000342.
 XX 01-JUN-1992; 92US-00891718.
 XX 02-MAR-1993; 93US-00025144.
 XX 31-JAN-1994; 94US-00189424.
 XX 19-JUN-1995; 95US-00491746.

PA (TERM/) TERVAN D S.
 XX Terman DS;
 PI
 DR WPI; 2001-158657/16.
 XX
 XX
 XX
 PT Tumor cell capable of stimulating antitumor immune reactivity in vitro or
 PT in vivo comprises exogenous nucleic acids encoding a superantigen and a
 PT costimulatory molecule.
 XX
 XX
 PS Disclosure; Fig 2; 16pp; English.
 XX
 XX The present invention relates to a tumour cell capable of stimulating
 CC antitumor immune reactivity in vitro or in vivo contains and expresses an
 CC exogenous nucleic acid molecule encoding a superantigen or its active
 CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
 CC molecule that activates T cells in conjunction with an antigenic
 CC stimulus. The invention may be used for cancer therapy by stimulating an
 CC anticancer immune response in vivo or ex vivo
 XX
 XX Sequence 230 AA;
 SQ
 Query Match 96.6%; Score 1196; DB 4; Length 230;
 Best Local Similarity 97.8%; Pred. No. 1.7e-111;
 Matches 225; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 4 SEEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGHPW 63
 Db 1 SEEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGHPW 60
 QY 64 YNDLLVDLGSKDATNKYKGVLDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNRLTEEK 123
 Db 61 YNDLLVDLGSKDATNKYKGVLDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNRLTEEK 120
 QY 124 KVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRL 183
 Db 121 KVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRL 180
 QY 184 IVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENLHIALYLYTT 233
 Db 181 IVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENLHIALYLYTT 230
 RESULT 7
 AAW35374
 ID AAW35374 standard; peptide; 245 AA.
 XX
 AC AAW35374;
 XX
 XX 20-APR-1998 (first entry)
 XX
 XX Staphylococcus enterotoxin SEE wild-type superantigen.
 DE
 XX SEE; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment;
 XX cancer; infection; autoimmune disease; antibody.
 XX
 XX Staphylococcus sp.
 OS
 XX
 XX Key Location/Qualifiers
 FH
 FT Misc-difference 20 /note= "can be mutated at this position"
 FT
 FT Misc-difference 21 /note= "can be mutated at this position"
 FT
 FT Misc-difference 24 /note= "can be mutated at this position"
 FT
 FT Misc-difference 27 /note= "can be mutated at this position"
 FT
 FT
 XX W09736932-A1.
 PN
 XX
 XX 09-OCT-1997.
 PD
 XX
 XX 26-MAR-1997; 97WO-SE000537.
 PF

XX 29-MAR-1996; 96SE-00001245.
 PR 12-AUG-1996; 96US-00695692.
 XX
 XX (PHAA) PHARMACIA & UPJOHN AB.
 XX
 XX Antonsson P, Hansson J, Bjoerk P, Dohlsten M, Kalland T;
 PI Abrahmsen L, Forsberg G;
 XX
 XX WPI; 1997-503052/46.
 XX
 XX Conjugate of target seeking moiety and modified superantigen - useful for
 PT activating the immune system to treat cancer, viral infections, parasitic
 PT infestations and autoimmune diseases.
 XX
 PS Claim 4; Page 38-39; 58pp; English.
 XX
 CC This is the wild-type Staphylococcus enterotoxin SEE superantigen. This
 CC SEE superantigen can be modified to be used in a novel conjugate. The
 CC novel conjugate comprises a target seeking moiety and a modified wild
 CC type superantigen. The modified superantigen retains its ability to
 CC activate a subset of T cells, even though 1 or more wild-type amino acid
 CC residues in at least 1 region which functions in determining binding to T
 CC cell receptor (TCR) and activation of a subset of T cells has/have been
 CC replaced. Such a modified superantigen can optionally be used as part of
 CC a conjugate with a target seeking moiety, for activating the immune
 CC system to treat a mammalian disease. A pharmaceutical composition can be
 CC prepared comprising a modified antibody, (preferably a Fab fragment fused
 CC to a peptide moiety providing activation of T cells in vbeta specific
 CC manner) in which cysteines providing for interchain cysteine linkages in
 CC the native antibody have been replaced (preferably by serine residues) to
 CC prohibit cysteine formation. The modified wild-type superantigen is used
 CC for treating cancer, viral infections, parasitic infestations and
 CC autoimmune disease. The modified wild type superantigen has a lower
 CC immunogenicity and reactivity with neutralising antibodies and has fewer
 CC side-effects when used as a drug, compared to wild type superantigen
 XX
 SQ Sequence 245 AA;
 Query Match 96.4%; Score 1194; DB 2; Length 245;
 Best Local Similarity 93.1%; Pred. No. 2.9e-111;
 Matches 228; Conservative 1; Mismatches 4; Indels 12; Gaps 1;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTG 60
 Db 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTG 60
 QY 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNRLT 120
 Db 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYCCAGGTPNKTACMYGGVTLHDNNRLT 120
 QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
 Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNK-----TINSENHIAL 228
 Db 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNK-----TINSENHIAL 240
 QY 229 YLYTT 233
 Db 241 YLYTT 245
 RESULT 8
 ABU79072
 ID ABU79072 standard; protein; 248 AA.
 XX
 AC ABU79072;
 XX
 XX 18-JUN-2003 (first entry)
 DT
 XX
 XX S. aureus SEE (staphylococcus enterotoxin E) protein.

XX Superantigen; SAg: staphylococcal enterotoxin; tumour; cancer; apoptosis;
XX gene therapy; mammalian cell receptor; tumour associated lipid; anergy;
XX T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;
XX APC; antitumour.
XX
XX Staphylococcus aureus.
XX
XX US2002177551-A1.
XX
XX 28-NOV-2002.
XX
XX 30-MAY-2001; 2001US-00870759.
XX
XX 31-MAY-2000; 2000US-0208128P.
XX
XX (TERM/) Terman D S.
XX
XX Terman DS;
XX
XX WPI; 2003-361759/34.
XX
XX N-PSDB; ACA64698.
XX
XX A mammalian cell receptor, useful in the treatment of cancer by binding
XX to tumor associated lipids where the binding induces anergy or apoptosis
XX in T cells and antigen presenting cells.
XX
XX Disclosure; Page; 167pp; English.
XX
XX The invention relates to a mammalian cell receptor, useful in the
XX treatment of cancer, which binds to tumour associated lipids and induces
XX anergy or apoptosis in the T cells and antigen presenting cells (APCs).
XX Also included are a mammalian cell useful in the treatment of cancer
XX where the receptor which binds tumour associated lipids and induces
XX cellular inactivation or death is deleted or functionally deactivated,
XX producing (M1) a tumouricidal immunocyte population in vivo in a mammal
XX (by allowing tumour associated lipids to contact immunocytes in which
XX receptors for immunosuppressive fatty acids, ceramides, glycolipids,
XX sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
XX sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
XX deleted), a construct useful in the treatment of cancer comprising a
XX superantigen (Sag) nucleotide inserted into a virus, a mammalian T cell
XX useful in the treatment of cancer (where an adaptor protein which
XX inhibits T cell activation by tumour associated antigens is deleted or
XX functionally deactivated), a composition useful in the treatment of
XX cancer (comprising a lipid raft conjugated to a superantigen), producing
XX (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
XX allowing tumour associated lipids to contact immunocytes, in which
XX receptors for the lipids are inactivated or deleted to produce a
XX tumouricidal immunocyte population, and administering the tumouricidally
XX activated immunocytes to the host), producing (M3) a tumouricidal APC
XX population ex vivo in a mammal (by allowing a tumour associated lipid to
XX contact APCs, in which receptors for the tumour associated lipids are
XX inactivated or deleted to produce a tumouricidally activated population,
XX and administering APCs to the host), producing a tumouricidal T cell
XX population ex vivo in a mammal (by allowing a tumour associated lipids to
XX contact T cells, in which adaptor proteins, which inhibit T cell
XX activation by tumour associated antigens, are deleted or functionally
XX deactivated to produce a tumouricidal population of T cells, and
XX administering the tumouricidally activated T cells to the host, or
XX allowing a superantigen-lipid raft to contact T cells ex vivo, and
XX administering the tumouricidally activated T cells to the host), treating
XX (M5) cancer in a mammal (by administering a lipid binding molecule which
XX binds immunosuppressive tumour associated lipids in vivo), producing (M6)
XX a tumouricidal T cell population in vivo in a mammal (by allowing a
XX tumour associated antigen to contact immunocytes in which adaptor
XX proteins which inhibit T cell activation by tumour associated antigens
XX are deleted or functionally deactivated) and producing (M7) a
XX tumouricidal T cell population ex vivo in a mammal comprising allowing a
XX superantigen-lipid raft conjugate to contact immunocytes in vivo. The
XX receptors, methods and compositions are useful for treating cancers and
XX tumours. Bacterial superantigens are co-administered or administered as
XX fusion constructs with anti-tumour proteins or motifs. The present

CC sequence represents a bacterial superantigen protein (e.g. a
CC staphylococcal enterotoxin). Note: The sequence data for this patent did
CC not form part of the printed specification, but was obtained in
CC electronic format from the US patent office website at
CC "seqdata.uspto.gov/sequence.html?DocID=20020177551"
XX
XX SQ Sequence 248 AA;
XX
XX Query Match 94.3%; Score 1168; DB 6; Length 248;
XX Best Local Similarity 98.2%; Pred. No 1.2e-108;
XX Matches 220; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 1 SEKSEINEKDLRKSELOGTALGNLKIYYNEKAITENKESDDQFLENTLLFKGFTG 60
XX DB 25 SEKSEINEKDLRKSELOGTALGNLKIYYNEKAITENKESDDQFLENTLLFKGFTG 84
XX
XX QY 61 HPWYNDLLVDLGSKDATNKYKKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
XX DB 85 HPWYNDLLVDLGSKDATNKYKKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 144
XX
XX QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
XX DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204
XX
XX QY 181 RGLIVFHSSEGSVSYDLFDAQGYPDTLRLRYRDNKTIENSEL 224
XX DB 205 RGLIVFHSSEGSVSYDLFDAQGYPDTLRLRYRDNKTIENSEL 248
XX
XX RESULT 9
XX AAR45012
XX ID AAR45012 standard; protein; 230 AA.
XX
XX AC AAR45012;
XX
XX DT 25-MAR-2003 (revised)
XX DT 08-JUN-1994 (first entry)
XX
XX DE Staphylococcal enterotoxin SEE.
XX
XX KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
XX autoimmune disease; toxicity; Protein A; perfusion system.
XX
XX OS Staphylococcus aureus.
XX
XX FH Key Location/Qualifiers
XX FT Misc-difference 120 /note= "Given in the specification as J, no further
XX details given"
XX FT Misc-difference 121 /note= "Given in the specification as J, no further
XX details given"
XX FT Misc-difference 123 /note= "Given in the specification as O, no further
XX details given"
XX FT Misc-difference 124 /note= "Given in the specification as U, no further
XX details given"
XX
XX W09324136-A1.
XX
XX 09-DEC-1993.
XX
XX 01-JUN-1993; 93WO-US005213.
XX
XX 01-JUN-1992; 92US-00891718.
XX
XX (TERM/) Terman D S.
XX PA (STON/) STONE J L.
XX
XX Terman DS, Stone JL;
XX WPI; 1993-405418/50.
XX

XX Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
 PT in a patient or for the treatment of auto-immune diseases.
 PT
 XX
 XX Disclosure; Fig 1; 90pp; English.
 XX
 CC The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer in
 CC a patient. These SEs, and homologues of them, can be used as tumouricidal
 CC agents for treating cancers and autoimmune disease. They exhibit
 CC tumouricidal activity and toxicity identical to that observed for the
 CC Protein A pertussis system. They may be administered by i.v. injection.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 XX Sequence 230 AA;

Query Match 93.0%; Score 1151; DB 2; Length 230;
 Best Local Similarity 93.9%; Pred. No. 5.5e-107;
 Matches 216; Conservative 4; Mismatches 10; Indels 0; Gaps 0;
 QY 4 SEINEKDLRKSELOGTALGNLKQIYYNNEKAITENKESDDQFLENTLLFKGFTGHPW 63
 Db 1 SEINEKDLRKSELOGTALGNLKQIYYNNEKAITENKESDDQFLENTLLFKGFTGHPW 60
 QY 64 YNDLLVDSKDATNKYKGGKVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTEEK 123
 Db 61 YNDLLVDSKDATNKYKGGKVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTEEX 120
 QY 124 KVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKGLYNSDSFGKQVORGL 183
 Db 121 XVXXKXWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKGLYNSDSFGKQVORGL 180
 QY 184 IVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHIALYLYTT 233
 Db 181 IVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHIDYLYTT 230

RESULT 10
 ABB76235
 ID ABB76235 standard; protein; 230 AA.
 AC ABB76235;
 XX
 XX 09-AUG-2002 (first entry)
 XX
 DE Staphylococcus aureus enterotoxin E.
 XX
 XX Enterotoxin E; SEE; superantigen; antigen; tumour; cancer; antitumour;
 KW therapy.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 120
 FT /note= "given as 'J' in the specification"
 FT Misc-difference 121
 FT /note= "given as 'J' in the specification"
 FT Misc-difference 123
 FT /note= "given as 'O' in the specification"
 FT Misc-difference 124
 FT /note= "given as 'U' in the specification"
 FT Misc-difference 125
 FT /note= "given as 'V' in the specification"
 XX
 PN US2002051765-A1.
 XX
 XX 02-MAY-2002.
 XX
 XX 19-DEC-2000; 2000US-00741503.
 XX
 XX 03-OCT-1989; 89US-00416530.
 PR 17-JAN-1990; 90US-00466577.
 PR 17-JAN-1991; 91WO-US000342.

PR 01-JUN-1992; 92US-00891718.
 PR 02-MAR-1993; 93US-00025144.
 PR 31-JAN-1994; 94US-00189424.
 PR 19-JUN-1995; 95US-00491746.
 XX
 XX (TERM/) TERMAN D S.
 XX
 XX Terman DS;
 XX
 DR WPI; 2002-415198/44.
 XX
 XX Reagent for treating cancer without the need for e.g. radiotherapy;
 PT comprises a specific V beta subset of T cells sensitized to a growing
 PT tumor and stimulated with superantigens.
 PT
 XX
 XX Disclosure; Fig 2; 17pp; English.

XX The present sequence is the protein sequence of enterotoxin E (SEE) of
 CC Staphylococcus aureus. Similarity is shown, in several stretches of
 CC sequence, between staphylococcal enterotoxins, streptococcal pyrogenic
 CC exotoxins and staphylococcal exfoliative toxins (see ABB76234-44). In the
 CC present invention, synthetic polypeptides useful in tumour therapy and in
 CC blocking or destroying autoreactive T and B lymphocyte populations are
 CC characterised by substantial structural homology to staphylococcal
 CC enterotoxin A and enterotoxin B, and to streptococcal pyrogenic
 CC exotoxins, with statistically significant sequence homology and
 CC similarity (Z value of Lipman and Pearson algorithm in Monte Carlo
 CC analysis exceeding 6) to include alignment of cysteine residues and
 CC similar hydrophathy profiles. These superantigens are used to treat solid
 CC tumours, including their metastases, without radiation, surgery or
 CC standard chemotherapeutic agents. A claimed method of human cancer
 CC treatment involves contacting haematopoietic cells from a patient with
 CC one or more superantigens ex vivo to generate stimulated cells, selecting
 CC a specific V beta subset of cells, and reintroducing these cells into the
 CC patient to induce an in vivo therapeutic, tumoricidal reaction

XX Sequence 230 AA;

Query Match 92.6%; Score 1147; DB 5; Length 230;
 Best Local Similarity 93.9%; Pred. No. 1.4e-106;
 Matches 216; Conservative 3; Mismatches 11; Indels 0; Gaps 0;
 QY 4 SEINEKDLRKSELOGTALGNLKQIYYNNEKAITENKESDDQFLENTLLFKGFTGHPW 63
 Db 1 SEINEKDLRKSELOGTALGNLKQIYYNNEKAITENKESDDQFLENTLLFKGFTGHPW 60
 QY 64 YNDLLVDSKDATNKYKGGKVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTEEK 123
 Db 61 YNDLLVDSKDATNKYKGGKVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTEEX 120
 QY 124 KVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKGLYNSDSFGKQVORGL 183
 Db 121 XVXXKXWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKGLYNSDSFGKQVORGL 180
 QY 184 IVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHIALYLYTT 233
 Db 181 IVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHIDYLYTT 230

RESULT 11
 ABP58455
 ID ABP58455 standard; protein; 233 AA.
 XX
 XX ABP58455;
 AC
 XX
 XX 14-APR-2003 (first entry)
 XX
 XX Engineered superantigen SEA/E-120 for human cancer therapy.
 DE
 XX
 XX Superantigen; staphylococcal enterotoxin; antibody; cancer; tumour;
 KW cytostatic; vaccine; SEA/E-120; mutant; mutein.
 XX
 OS Staphylococcus sp.

XX WO2003002143-A1.
 XX 09-JAN-2003.
 XX 19-JUN-2002; 2002WO-SE001188.
 XX 28-JUN-2001; 2001SE-00002327.
 XX (ACTI-) ACTIVE BIOTECH AB.
 XX Forsberg G, Erlandsson B, Antonsson P, Walse B;
 XX WPI; 2003-201467/19.
 XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
 PT receptor and four regions to determine binding to class II major
 PT histocompatibility complex, antibody to cancer associated cell surface
 PT structure.
 XX Claim 12; Fig 10; 102pp; English.

CC The present sequence is a conjugate of a bacterial superantigen and an
 CC antibody moiety, and has been designed to target and destroy cancer
 CC cells. The bacterial superantigen is SEA/E-120 (see also AB58455), which
 CC was derived from staphylococcal enterotoxin E (SEE) by the incorporation
 CC of the following amino acid substitutions to reduce seroreactivity whilst
 CC maintaining production levels and biological activity: R20G, N21T, S24G,
 CC R27K, K79E, K81S, K83S and D227S. SEA/E-120 was genetically fused to the
 CC Fab moiety of the tumour reactive antibody 5T4. Substitutions were made
 CC in the 5T4 sequence to obtain higher yields: in the heavy chain, H4LP,
 CC S44G, L69T and V113G; and in the light chain, F10S, T45K, I63S, F73L,
 CC T77S, L78V and L83A. An expression vector comprising DNA encoding the
 CC conjugate can be used to transform host cells for recombinant production
 CC of the conjugate. The conjugate is useful for treating cancer, including
 CC cancer of the lung, breast, colon, kidney, pancreas, ovary, stomach,
 CC cervix and prostate (claimed)

XX Sequence 672 AA;
 SQ

Query Match 91.3%; Score 1130; DB 6; Length 672;
 Best Local Similarity 91.4%; Pred. No. 3.2e-104;
 Matches 213; Conservative 9; Mismatches 11; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELQGTALGNLQIYYNKAITENKESDDQFLENTLLFKGFTG 60
 DB 226 SEKSEINEKDLRKSELQGTALGNLQIYYNKAITENKESDDQFLENTLLFKGFTG 285
 QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 120
 DB 286 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 345
 QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTQVQLDQARHYLHGKFGLYNSDSFGKVKQ 180
 DB 346 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTQVQLDQARHYLHGKFGLYNSDSFGKVKQ 405
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHIALYLYTT 233
 DB 406 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHIALYLYTT 458

RESULT 13
 AAR13204
 ID AAR13204 standard; protein; 230 AA.
 XX
 AC AAR13204;
 XX
 DT 15-OCT-1991 (first entry)
 XX Staphylococcal enterotoxin E.
 DE
 DE
 XX
 KW SEE; cancer treatment; pyrogen; tumouricide.
 XX

OS Staphylococcus aureus.
 XX WO9110680-A.
 PN 25-JUL-1991.
 XX 17-JAN-1990; 90US-00466577.
 XX 17-JAN-1990; 90US-00466577.
 XX (TERM/) TERMAN D S.
 PA Terman DS;
 XX WPI; 1991-237984/32.
 DR
 XX Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumoricidal activity as
 PT Staphylococcal protein A without potential toxic reactions.
 XX Disclosure; Fig 1; 74pp; English.

CC SEE was isolated and purified from S.aureus. It can be used for treating
 CC cancer, activating cytokine mediators and procoagulant systems,
 CC augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be
 CC administered intravenously, optionally with ibuprofen to attenuate toxic
 CC reaction to SEE. Synthetic polypeptides having structural homology to
 CC Staphylococcal exotoxins are claimed, provided the homology includes
 CC statistically significant sequence homology, alignment of Cysteine
 CC residues and similar hydropathy profiles. See AAR13203-R13211

XX Sequence 230 AA;
 SQ

Query Match 91.1%; Score 1128; DB 2; Length 230;
 Best Local Similarity 91.7%; Pred. No. 1.1e-104;
 Matches 211; Conservative 7; Mismatches 12; Indels 0; Gaps 0;

QY 4 SEBINEKDLRKSELQGTALGNLQIYYNKAITENKESDDQFLENTLLFKGFTGHPW 63
 DB 1 SEBINEKDLRKSELQGTALGNLQIYYNKAITENKESDDQFLENTLLFKGFTGHPW 60
 QY 64 YNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTEEK 123
 DB 61 YNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTEEX 120
 QY 124 KVPINLWIDGKQTTVPIDKVKTSKKEVTQVQLDQARHYLHGKFGLYNSDSFGKVKQVGL 183
 DB 121 XVQXBKWDGKQTTVPIDKVKTSKKEVTQVQLDQARHYLHGKFGLYNSDSFGKVKQVGL 180
 QY 184 IVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHIALYLYTT 233
 DB 181 IVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHIALYLYTT 230

RESULT 14
 AAR13203
 ID AAR13203 standard; protein; 233 AA.
 XX
 AC AAR13203;
 XX
 DT 15-OCT-1991 (first entry)
 XX Staphylococcal enterotoxin A.
 DE
 DE
 XX SEA; cancer treatment; pyrogen; tumouricide.
 XX Staphylococcus aureus.
 OS
 PN WO9110680-A.
 XX 25-JUL-1991.
 XX 17-JAN-1990; 90US-00466577.

XX 17-JAN-1990; 90US-00466577.
XX (TERM/) Terman D S.
XX Terman DS;
XX WPI; 1991-237984/32.
XX
XX Treating cancer with enterotoxin from Staphylococcus aureus -
XX administered by IV injection, having same tumoricidal activity as
XX Staphylococcal protein A without potential toxic reactions.
XX
XX Disclosure; Fig 1; 74pp; English.
XX
XX SEA was isolated and purified from S aureus. It can be used for treating
XX cancer, activating cytokine mediators and procoagulant systems,
XX augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be
XX administered intravenously, optionally with ibuprofen to attenuate toxic
XX reaction to SEA. Synthetic polypeptides having structural homology to
XX Staphylococcal exotoxins are claimed, provided the homology includes
XX statistically significant sequence homology, alignment of Cysteine
XX residues and similar hydropathy profiles. See also AAR13204-R13211
XX
XX Sequence 233 AA;
XX
Query Match 84.7%; Score 1049; DB 2; Length 233;
Best Local Similarity 84.1%; Pred. No. 9.7e-97;
Matches 196; Conservative 16; Mismatches 21; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLKKSELOQTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 1 SEKSEINEKDLKKSELOQTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
QY 61 HPWNLDLVDLGSKDATNKYKGVLDYGYGYQACAGTGNKTACMYGGVTLHDNNRLT 120
DB 61 HSWNDLLVDLGSKDIDVKYKGVLDYGYGYQACAGTGNKTACMYGGVTLHDNNRLT 120
QY 121 EEKVPINLMDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 180
DB 121 EEKVPINLMDGKQNTVPLETKNKNQNTVOELDLQARHYLHGKFLYNSDSFGKQV 180
QY 181 RGLIVHSSSGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHLIALYLYTT 233
DB 181 RGLIVHSTSTPSVNDLFDAGQYQNTLLRIYRDNKTINSENHDIYLYTS 233
RESULT 15
ID ABP58458 standard; protein; 233 AA.
XX
XX AC ABP58458;
XX DT 14-APR-2003 (first entry)
XX DE Staphylococcal enterotoxin A.
XX
XX Superantigen; staphylococcal enterotoxin A; antibody; cancer; tumour;
XX cytostatic; vaccine.
XX OS Staphylococcus sp.
XX PN WO2003002143-A1.
XX PD 09-JAN-2003.
XX PF 19-JUN-2002; 2002WO-SE001188.
XX PR 28-JUN-2001; 2001SE-00002327.
XX PA (ACTI-) ACTIVE BIOTECH AB.
XX
XX Forsberg G, Erlandsson E, Antonsson P, Walse B;
PI

XX WPI; 2003-201467/19.
XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
XX receptor and four regions to determine binding to class II major
XX histocompatibility complex, antibody to cancer associated cell surface
XX structure.
XX
XX Example 3; Fig 3; 102pp; English.
XX
XX The present sequence is the protein sequence of staphylococcal
XX enterotoxin A (SEA). The invention provides novel conjugates (see
XX ABP58454) for human cancer therapy. These comprise an engineered
XX bacterial superantigen, such as novel SEA/E-120 (see ABP58455), and an
XX antibody moiety, such as tumour reactive antibody 574. Bacterial
XX enterotoxins such as SEA, SEE, SED and SEH were used in the molecular
XX modelling of the engineered superantigens. The superantigens were
XX engineered to reduce seroreactivity whilst maintaining biological
XX activity and production levels. The novel conjugates were designed to
XX target and destroy cancer cells, including cancer of the lung, breast,
XX colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
XX
XX Sequence 233 AA;
XX
Query Match 83.8%; Score 1037; DB 6; Length 233;
Best Local Similarity 83.3%; Pred. No. 1.6e-95;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLKKSELOQTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 1 SEKSEINEKDLKKSELOQTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
QY 61 HPWNLDLVDLGSKDATNKYKGVLDYGYGYQACAGTGNKTACMYGGVTLHDNNRLT 120
DB 61 HSWNDLLVDLGSKDIDVKYKGVLDYGYGYQACAGTGNKTACMYGGVTLHDNNRLT 120
QY 121 EEKVPINLMDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKQV 180
DB 121 EEKVPINLMDGKQNTVPLETKNKNQNTVOELDLQARHYLHGKFLYNSDSFGKQV 180
QY 181 RGLIVHSSSGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHLIALYLYTT 233
DB 181 RGLIVHSTSTPSVNDLFDAGQYQNTLLRIYRDNKTINSENHDIYLYTS 233
RESULT 16
ID AAU14104 standard; peptide; 257 AA.
XX
XX AC AAU14104;
XX DT 21-NOV-2001 (first entry)
XX DE Peptide sequence from Staphylococcus aureus enterotoxin A.
XX
XX Anti-retroviral; DP178-like; DP107-like; enterotoxin A; antifusogenic;
XX antiviral; HIV transmission.
XX OS Staphylococcus aureus.
XX PN WO200151673-A2.
XX PD 19-JUL-2001.
XX PF 05-JUL-2000; 2000WO-US035727.
XX PR 09-JUL-1999; 99US-00350841.
XX PA (TRIM-) TRIMERIS INC.
XX
XX Jeff's P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
XX WPI; 2001-442157/47.
XX
DR

XX Identifying a compound that inhibits the formation of or disrupts a
PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral
PT or intracellular modulatory activity, by detecting the formation of a
PT DP107/DP178 complex.

XX Disclosure; Fig 42; 259pp; English.

XX The present invention relates to peptides which exhibit anti-retroviral
CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
CC amino acids 639-673 of the transmembrane protein gp41 from human
CC immunodeficiency virus 1 (HIV-1) isolate IAI. The DP107 peptide
CC corresponds to amino acids 558-595 of gp41 from HIV-1IAI. The invention
CC also relates to a method of identifying compounds that inhibit the
CC formation of or disrupts a DP107/DP178 complex. The method comprises
CC detecting the formation of a DP107/DP178 complex, both in the presence or
CC absence of a test compound, in a reaction mixture containing DP107 and
CC DP178 peptides. The method is useful for identifying compounds, including
CC small molecule compounds, which may themselves exhibit antifusogenic,
CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
CC peptides are useful to inhibit human and non-human retroviral,
CC particularly HIV, transmission to uninfected cells. The present sequence
CC represents a peptide sequence from *Staphylococcus aureus* enterotoxin A

XX Sequence 257 AA;

Query Match 83.8%; Score 1037; DB 4; Length 257;
Best Local Similarity 83.3%; Pred. No. 1.8e-95;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELGQTALGNLKOIYYNEKAITENKESDDQFLENTLLPKGFPTG 60
DB 25 SEKSEINEKDLRKSELGQTALGNLKOIYYNEKAITENKESHDFLOHTLLPKGFPTD 84

QY 61 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGTGNKTACMYGGVTLHNNRLT 120
DB 85 HSWYNDLLVDFPSKDIYDKYKGVLDLYGAYGYQCAGTGNKTACMYGGVTLHNNRLT 144

QY 121 BEKKVPINLWDGKQTVPIIDKVKTSKKEVTVOELDLQARHYLHGKFGVNSDSFGKVKQ 180
DB 145 BEKKVPINLWDGKQTVPIETVTKNKNVTVOELDLQARRYLQEKYINLNSDVFDFGKVQ 204

QY 181 RGLIVFHSSEGSTVSYDVFDAQGGYPTDILLRIYRDNKTINSENHLIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQQGYSNLTLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 17
ID ABO10269
XX ABO10269;
XX AC ABO10269;
XX DT 19-AUG-2003 (first entry)
XX S. aureus enterotoxin A.
DE HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;
KW Epstein-Barr virus infection; heptad repeat motif.
XX Staphylococcus aureus.
OS US6518013-B1.
PN 11-FEB-2003.
XX 07-JUN-1995; 95US-00485546.
XX 07-JUN-1993; 93US-00073028.
XX 07-JUN-1994; 94US-00255208.
PR 20-DEC-1994; 94US-00360107.
XX

PA (TRIM-) TRIMERIS INC.
XX Barney SO, Lambert DM, Petteway SR;
XX WPI; 2003-465599/44.
XX Inhibiting transmission of Epstein-Barr virus to a cell, by contacting
PT the cell with a peptide consisting of a region of Epstein-Barr virus
PT protein.
XX Example; Fig 42; 716pp; English.

XX The invention relates to inhibiting (M) transmission of an Epstein-Barr
CC virus to a cell, comprising contacting the cell with an effective
CC concentration of a peptide consisting of a region of 16-39 consecutive
CC amino acids of an Epstein-Barr virus protein for an effective period of
CC time, where the region is recognised by one or more of ALLMOTI15,
CC 107x178x4 or PIZIP sequence search motifs, the peptide further comprises
CC an amino terminal X, and a carboxy terminal Z in which X comprises an
CC amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic
CC group or macromolecular carrier group, and Z comprises a carboxyl group,
CC amido group, hydrophobic group, or macromolecular carrier group, and
CC fusion of the virus to the cell is inhibited. The peptides were
CC identified by analysing the structure/motifs present in the HIV-1
CC glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat
CC motif containing peptides were used to design the motifs cited above,
CC which in turn were used to analyse proteins from other pathogenic
CC organisms and HIV isolates, looking for DP107/178 structural analogues.
CC The method is useful for inhibiting transmission of Epstein-Barr virus to
CC a cell and Epstein-Barr virus infection. The present sequence is a
CC protein from a pathogenic organism analysed for regions analogous to
CC DP107 or DP178

XX Sequence 257 AA;

Query Match 83.8%; Score 1037; DB 6; Length 257;
Best Local Similarity 83.3%; Pred. No. 1.8e-95;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELGQTALGNLKOIYYNEKAITENKESDDQFLENTLLPKGFPTG 60
DB 25 SEKSEINEKDLRKSELGQTALGNLKOIYYNEKAITENKESHDFLOHTLLPKGFPTD 84

QY 61 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGTGNKTACMYGGVTLHNNRLT 120
DB 85 HSWYNDLLVDFPSKDIYDKYKGVLDLYGAYGYQCAGTGNKTACMYGGVTLHNNRLT 144

QY 121 BEKKVPINLWDGKQTVPIIDKVKTSKKEVTVOELDLQARHYLHGKFGVNSDSFGKVKQ 180
DB 145 BEKKVPINLWDGKQTVPIETVTKNKNVTVOELDLQARRYLQEKYINLNSDVFDFGKVQ 204

QY 181 RGLIVFHSSEGSTVSYDVFDAQGGYPTDILLRIYRDNKTINSENHLIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQQGYSNLTLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 18
ID ADD44368
XX ADD44368 standard; protein; 257 AA.
XX AC ADD44368;
XX DT 15-JAN-2004 (first entry)
XX *Staphylococcus aureus* enterotoxin A protein.
DE enterotoxin A; ent A; food poisoning; bacterium; food; milk; fruit juice;
KW ice cream.
XX *Staphylococcus aureus*.
OS WO2003080865-A1.
XX

PD 02-OCT-2003.

XX 26-MAR-2002; 2002WO-IB001150.

XX 26-MAR-2002; 2002WO-IB001150.

XX (COUL) COUNCIL SCI & IND RES.

XX Padmapriya BP, Ramesh A, Chandrashekar A, Varadaraj MC;

XX WPI; 2003-779273/73.

XX N-PSDB; ADD44369.

XX Novel oligonucleotide primers directed against enterotoxin A gene of

PT Staphylococcus aureus and heat stable enterotoxin gene of *Yersinia*

PT enterocolitica, useful for detecting food poisoning causing bacteria.

XX Example 2; Page 14-15; 34pp; English.

XX The invention relates to novel oligonucleotide primers directed against

CC enterotoxin A gene (ent A) of *Staphylococcus aureus* and heat stable

CC enterotoxin gene (yst) of *Yersinia enterocolitica*. The novel

CC oligonucleotide primers are useful for simultaneously detecting food

CC poisoning bacterial species *Staphylococcus aureus* and/or *Yersinia*

CC enterocolitica in food systems e.g., milk, fruit juices and ice creams,

CC without prior enrichment for preventing food poisoning outbreak. The PCR

CC detection method is useful for detecting the bacteria strains in quantity

CC as low as one cell. The method can be directly used for detecting

CC bacterial strains. The oligonucleotide primers allow quick and highly

CC sensitive detection of the food poisoning bacterial species. This

CC sequence represents the protein derived from the enterotoxin A gene from

CC *Staphylococcus aureus* of the invention.

XX SQ Sequence 257 AA;

Query Match 83.8%; Score 1037; DB 7; Length 257;

Best Local Similarity 83.3%; Pred. No. 1.8e-95;

Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKXELQGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60

DB 25 SEKSEINEKDLRKXELQGTALGNLKOIYYNEKAITENKESHDFLOHTILFKGFFTD 84

QY 61 HPYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGTGNKTAGCMYGGVTLHDNRILT 120

DB 85 HSYNDLLVDFDSKDIDVKYKGVLDLYGAYGYQCAGTGNKTAGCMYGGVTLHDNRILT 144

QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDQARHVLHGKFLYNSDSFGGKVQ 180

DB 145 EEKVPINLWIDGKQNTVPLETVTKNKQNTVPQELDQARRYLQEKYLYNSDVFDEGKVQ 204

QY 181 RGLIVFHSSSGSTVSVDLFDQAQQYPTLLRIYRDNKTINSENHLIALYLT 233

DB 205 RGLIVFHTSTEPSVNYDLFGAQQYNTLLRIYRDNKTINSENHIDILYLYTS 257

RESULT 19

AAW06738

ID AAW06738 standard; protein; 233 AA.

XX AC AAW06738;

XX 08-MAR-1997 (first entry)

XX Staphylococcus enterotoxin A.

XX Enterotoxin A; superantigen; antigen; cytokine; chemokine; T cell;

XX lymphocyte; monocyte; natural killer cell; gene therapy; cancer; vaccine;

XX adjuvant.

XX Staphylococcus sp.

XX W09636366-A1.

XX 21-NOV-1996.

XX 20-MAY-1996; 96WO-US007432.

XX 18-MAY-1995; 95US-00446918.

XX 29-DEC-1995; 95US-00580806.

XX (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.

XX Dow SW, Elmelle RE, Potter TA;

XX WPI; 1997-011857/01.

XX N-PSDB; AAT45699.

XX Recombinant molecule encoding superantigen and opt. cytokine or

PT chemokine - controls activity of effector cells (T cells, monocytes,

PT natural killer cells), used for gene therapy of cancer.

XX Example 1; Page 98-99; 131pp; English.

XX A CDNA clone (AAT45699) codes for staphylococcal enterotoxin A (AAW06738)

CC superantigen. Nucleic acids encoding superantigens (see also AAW06737,

CC AAW06739), esp. truncated forms of the superantigen lacking the leader

CC peptide, can be used in the gene therapy of cancer, infectious diseases

CC and immunological disorders. The nucleic acid, optionally in combination

CC with cytokine or chemokine nucleic acids, is delivered to an animal using

CC e.g. liposomes. It acts by controlling the activity of effector cells,

CC such as T-cells, macrophages, monocytes and/or natural killer cells.

CC Localised prodn. of an effective but non-toxic amount of encoded proteins

CC allows safe treatment of the animal

XX SQ Sequence 233 AA;

Query Match 83.4%; Score 1033; DB 2; Length 233;

Best Local Similarity 83.2%; Pred. No. 3.9e-95;

Matches 193; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKXELQGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 61

DB 2 EKSEINEKDLRKXELQGTALGNLKOIYYNEKAITENKESHDFLOHTILFKGFFTD 61

QY 62 PNYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGTGNKTAGCMYGGVTLHDNRILT 121

DB 62 SWYNDLLVDFDSKDIDVKYKGVLDLYGAYGYQCAGTGNKTAGCMYGGVTLHDNRILT 121

QY 122 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDQARHVLHGKFLYNSDSFGGKVQ 181

DB 122 EKKVPINLWIDGKQNTVPLETVTKNKQNTVPQELDQARRYLQEKYLYNSDVFDEGKVQ 181

QY 182 GLIVFHSSSGSTVSVDLFDQAQQYPTLLRIYRDNKTINSENHLIALYLT 233

DB 182 GLIVFHTSTEPSVNYDLFGAQQYNTLLRIYRDNKTINSENHIDILYLYTS 233

RESULT 20

AAW35373

ID AAW35373 standard; peptide; 233 AA.

XX AC AAW35373;

XX 20-APR-1998 (first entry)

XX Staphylococcus enterotoxin SEA wild-type superantigen.

XX SEA; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment;

XX cancer; infection; autoimmune disease; antibody.

XX Staphylococcus sp.

XX W09736932-A1.

XX 09-OCT-1997.

XX PF 26-MAR-1997; 97WO-SE000537.
XX PR 29-MAR-1996; 96SE-00001245.
XX PR 12-AUG-1996; 96US-00695692.
XX PA (PHAA) PHARMACIA & UPJOHN AB.
XX PI Antonsson P, Hansson J, Bjoerk P, Dohlstén M, Kalland T;
XX PI Abrahmsen L, Forsberg G;
XX DR WPI; 1997-503052/46.
XX PT Conjugate of target seeking moiety and modified superantigen - useful for
XX PT activating the immune system to treat cancer, viral infections, parasitic
XX PT infestations and autoimmune diseases.
XX PS Claim 8; Page 36-37; 58pp; English.
XX CC This is the wild-type Staphylococcus enterotoxin SEA superantigen. This
XX CC SEA superantigen can be modified to be used in a novel conjugate. The
XX CC novel conjugate comprises a target seeking moiety and a modified wild
XX CC type superantigen. The modified superantigen retains its ability to
XX CC activate a subset of T cells, even though 1 or more wild-type amino acid
XX CC residues in at least 1 region which functions in determining binding to T
XX CC cell receptor (TCR) and activation of a subset of T cells has/have been
XX CC replaced. Such a modified superantigen can optionally be used as part of
XX CC a conjugate with a target seeking moiety, for activating the immune
XX CC system to treat a mammalian disease. A pharmaceutical composition can be
XX CC prepared comprising a modified antibody (preferably a Fab fragment fused
XX CC to a peptide moiety providing activation of T cells in *in vivo* specific
XX CC manner) in which cysteines providing for interchain cysteine linkages in
XX CC the native antibody have been replaced (preferably by serine residues) to
XX CC prohibit cysteine formation. The modified wild-type superantigen is used
XX CC for treating cancer, viral infections, parasitic infestations and
XX CC autoimmune disease. The modified wild type superantigen has a lower
XX CC immunogenicity and reactivity with neutralising antibodies and has fewer
XX CC side-effects when used as a drug, compared to wild type superantigen
XX SQ Sequence 233 AA;

Query Match 83.2%; Score 1030; DB 2; Length 233;
Best Local Similarity 82.8%; Pred. No. 7.8e-95;
Matches 193; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTD 60
QY 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 61 HSWYNDLLVDFDSKDIYDKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 121 EEKVPINLWLDGKQNTVPLETVKTNKNTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 181 RGLIVFHSSGTSVSYDLFPAQGGYPTLLRIYRDNKTINSENHLALYLYTT 233
DB 181 RGLIVFHTSTEPSVNYDLFGAQQGYNSNTLLRIYRDNKTINSENHDIYLYTS 233

RESULT 22
AAB67338
ID AAB67338 standard; peptide; 233 AA.
XX AC AAB67338;
XX DT 23-APR-2001 (first entry)
XX DE Staphylococcus aureus enterotoxin A protein.
XX KW Tumour; cancer; immune; enterotoxin.

XX OS Staphylococcus aureus.
XX PN US6180097-B1.
XX PD 30-JAN-2001.
XX PF 30-OCT-1998; 98US-00183437.
XX PR 03-OCT-1989; 89US-00416530.
XX PR 17-JAN-1990; 90US-00466577.
XX PR 17-JAN-1991; 91WO-US000342.
XX PR 01-JUN-1992; 92US-00891718.
XX PR 02-MAR-1993; 93US-00025144.
XX PR 31-JAN-1994; 94US-00189424.
XX PR 19-JUN-1995; 95US-00491746.
XX PA (TERM/) Terman D S.
XX PI Terman DS;
XX DR WPI; 2001-158657/16.
XX PT Tumor cell capable of stimulating antitumor immune reactivity *in vitro* or
XX PT *in vivo* comprises exogenous nucleic acids encoding a superantigen and a
XX PT costimulatory molecule.
XX PS Disclosure; Fig 2; 16pp; English.
XX CC The present invention relates to a tumour cell capable of stimulating
XX CC antitumor immune reactivity *in vitro* or *in vivo* contains and expresses an
XX CC exogenous nucleic acid molecule encoding a superantigen or its active
XX CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
XX CC molecule that activates T cells in conjunction with an antigenic
XX CC stimulus. The invention may be used for cancer therapy by stimulating an
XX CC anticancer immune response *in vivo* or *ex vivo*
XX SQ Sequence 233 AA;

Query Match 83.2%; Score 1030; DB 4; Length 233;
Best Local Similarity 82.8%; Pred. No. 7.8e-95;
Matches 193; Conservative 16; Mismatches 24; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLOHTLLFKGFFTD 60
QY 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 61 HSWYNDLLVDFDSKDIYDKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 121 EEKVPINLWLDGKQNTVPLETVKTNKNTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 181 RGLIVFHSSGTSVSYDLFPAQGGYPTLLRIYRDNKTINSENHLALYLYTT 233
DB 181 RGLIVFHTSTEPSVNYDLFGAQQGYNSNTLLRIYRDNKTINSENHDIYLYTS 233

RESULT 22
AAR45011
ID AAR45011 standard; protein; 233 AA.
XX AC AAR45011;
XX DT 25-MAR-2003 (revised)
XX DT 08-JUN-1994 (first entry)
XX DE Staphylococcal enterotoxin SEA.
XX KW Staphylococcal enterotoxin; SE; cancer; tumoricidal agent;
XX KW autoimmune disease; toxicity; Protein A; perfusion system.

XX OS Staphylococcus aureus.
XX FH Key Location/Qualifiers
XX FT Misc-difference 49
XX FT /note= "Given in the specification as O, no further
XX PN details given"
XX PN WO3324136-A1.
XX PD 09-DEC-1993.
XX PF 01-JUN-1993; 93WO-US005213.
XX PR 01-JUN-1992; 92US-00891718.
XX PA (TERM/) TERMAN D S.
XX PA (STON/) STONE J L.
XX PI Terman DS, Stone JL;
XX XX WPI; 1993-405418/50.
XX XX
XX XX Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
XX XX in a patient or for the treatment of auto-immune diseases.
XX PS Disclosure; Fig 1; 90pp; English.
XX XX
XX XX The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
XX CC which may be used in the methods of the invention for treating cancer in
XX CC a patient. These SEs, and homologues of them, can be used as tumouricidal
XX CC agents for treating cancers and autoimmune disease. They exhibit
XX CC tumouricidal activity and toxicity identical to that observed for the
XX CC protein A perfusion system. They may be administered by i.v. injection.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Sequence 233 AA;

Query Match 83.0%; Score 1027; DB 2; Length 233;
Best Local Similarity 82.8%; Pred. No. 1.6e-94;
Matches 193; Conservative 15; Mismatches 25; Indels 0; Gaps 0;

OY 1 SEKSEENEDLRKSELOQTALGNLQIYYNEKAITENKSDDOFLENTLLKGFETG 50
DB 1 SEKSEENEDLRKSELOQTALGNLQIYYNEKAITENKSDDOFLENTLLKGFETG 60

OY 61 HPWYNLLVLDLGSKDATNKYKGRKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRIT 120
DB 61 HSWYNLLVLDLGSKDIDVYKGRKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRIT 120

OY 121 BEKVPINLMDGKQTTVPIDKVKTSKVTVOELQARHYLHGFGLVNSDSFGKQV 180
DB 121 BEKVPINLMDGKQNTVPLETKNKGVTVOELDPQARRYLQEKINLYNSDVFQKQV 180

OY 181 RGLIVFHSSEGSTVSYDLFDAQGQYPTLLRIYRDNKTINSENHLALVLYTT 233
DB 181 RGLIVFHTSTEPSVYDLFGAQGQYSNTLLRIYRDNKTINSENHDIYLYTS 233

RESULT 23
ABU79068
ID ABU79068 standard; protein; 257 AA.
AC ABU79068;
XX AC
XX DT 18-JUN-2003 (first entry)
XX DE S. aureus SEA (staphylococcus enterotoxin A) protein.
XX XX Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis;
XX KW gene therapy; mammalian cell receptor; tumour associated lipid; anergy;
XX KW T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;
XX KW APC; antitumour.

XX OS Staphylococcus aureus.
XX PN US2002177551-A1.
XX XX 28-NOV-2002.
XX PF 30-MAY-2001; 2001US-00870759.
XX PR 31-MAY-2000; 2000US-0208128P.
XX PA (TERM/) TERMAN D S.
XX PI Terman DS;
XX XX WPI; 2003-361759/34.
XX XX N-PSDB; ACA64694.
XX XX A mammalian cell receptor, useful in the treatment of cancer by binding
XX PT to tumor associated lipids where the binding induces energy or apoptosis
XX FT in T cells and antigen presenting cells.
XX PS Disclosure; Page; 167pp; English.
XX XX
XX XX The invention relates to a mammalian cell receptor, useful in the
XX CC treatment of cancer, which binds to tumour associated lipids and induces
XX CC energy or apoptosis in the T cells and antigen presenting cells (APCs).
XX CC Also included are a mammalian cell useful in the treatment of cancer
XX CC where the receptor which binds tumour associated lipids and induces
XX CC cellular inactivation or death is deleted or functionally deactivated,
XX CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal
XX CC (by allowing tumour associated lipids to contact immunocytes in which
XX CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,
XX CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
XX CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
XX CC deleted), a construct useful in the treatment of cancer comprising a
XX CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
XX CC useful in the treatment of cancer (where an adaptor protein which
XX CC inhibits T cell activation by tumour associated antigens is deleted or
XX CC functionally deactivated), a composition useful in the treatment of
XX CC cancer (comprising a lipid raft conjugated to a superantigen), producing
XX CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
XX CC allowing tumour associated lipids to contact immunocytes, in which
XX CC receptors for the lipids are inactivated or deleted to produce a
XX CC tumouricidal immunocyte population, and administering the tumouricidal
XX CC population ex vivo in a mammal (by allowing a tumour associated lipid to
XX CC contact APCs, in which receptors for the tumour associated lipids are
XX CC inactivated or deleted to produce a tumouricidally activated population,
XX CC and administering APCs to the host), producing a tumouricidal T cell
XX CC population ex vivo in a mammal (by allowing a tumour associated lipids to
XX CC contact T cells, in which adaptor proteins, which inhibit T cell
XX CC activation to produce a tumouricidal population of T cells, and
XX CC administering the tumouricidally activated T cells to the host, or
XX CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
XX CC administering the tumouricidally activated T cells to the host), treating
XX CC (M5) cancer in a mammal (by administering a lipid binding molecule which
XX CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
XX CC a tumouricidal T cell population in vivo in a mammal (by allowing a
XX CC tumour associated antigen to contact immunocytes in which adaptor
XX CC proteins which inhibit T cell activation by tumour associated antigens
XX CC are deleted or functionally deactivated) and producing (M7) a
XX CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
XX CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
XX CC receptors, methods and compositions are useful for treating cancers and
XX CC tumours. Bacterial superantigens are co-administered or administered as
XX CC fusion constructs with anti-tumour proteins or motifs. The present
XX CC sequence represents a bacterial superantigen protein (e.g. a
XX CC staphylococcal enterotoxin). Note: The sequence data for this patent did
XX CC not form part of the printed specification, but was obtained in
XX CC electronic format from the US patent office website at
XX CC "seqdata.uspto.gov/sequence.html?docID=20020177551"


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XX SQ Sequence 257 AA;
Query Match 82.7%; Score 1024; DB 6; Length 257;
Best Local Similarity 82.4%; Pred. No. 3.6e-94;
Matches 192; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITENKESDDOFLNTLLFKGFTG 60
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITENKESDDOFLNTLLFKGFTN 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144
QY 121 BEKKVPINLWDGKQTTVPIDKVTSKKVTVOELDLQARHYLHGKGLYNSDSFGKVKQ 180
DB 145 BEKKVPINLWDGKQTTVPIDKVTSKKVTVOELDLQARHYLHGKGLYNSDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGOVPTLLRIYRDNKTINSENHLIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNDYDLFGAQGQSNLTLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 24.
ABB76234
ID ABB76234 standard; protein; 233 AA.
XX ABB76234;
AC ABB76234;
XX
DT 09-AUG-2002 (first entry)
DE Staphylococcus aureus enterotoxin A.
XX
KW Enterotoxin A; SEA; superantigen; antigen; tumour; cancer; antitumour;
KW therapy.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT Misc-difference 49
FT /note= "amino acid residue given as 'O' in the
FT specification"
XX
PN US2002051765-A1.
XX
PD 02-MAY-2002.
XX
PF 19-DEC-2000; 2000US-00741503.
XX
PR 03-OCT-1989; 89US-00416530.
PR 17-JAN-1990; 90US-00466577.
PR 17-JAN-1991; 91WO-US000342.
PR 01-JUN-1992; 92US-00891718.
PR 02-MAR-1993; 93US-00025144.
PR 31-JAN-1994; 94US-00189424.
PR 19-JUN-1995; 95US-00491746.
XX
PA (TERM/) TERMAN D S.
XX
PI Terman DS;
XX
XX WPI; 2002-415198/44.
DR
PT Reagent for treating cancer without the need for e.g. radiotherapy,
PT comprises a specific V beta subset of T cells sensitized to a growing
PT tumor and stimulated with superantigens.
XX
XX Disclosure; Fig 2; 17pp; English.
PS
XX
CC The present sequence is the protein sequence of enterotoxin A (SEA) of
CC Staphylococcus aureus. Similarity is shown, in several stretches of
CC sequence, between staphylococcal enterotoxins, streptococcal pyrogenic
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CC exotoxins and staphylococcal exfoliative toxins (see ABB76234-44). In the
CC present invention, synthetic polypeptides useful in tumour therapy and in
CC blocking or destroying autoreactive T and B lymphocyte populations are
CC characterised by substantial structural homology to staphylococcal
CC enterotoxin A and enterotoxin B, and to streptococcal pyrogenic
CC exotoxins, with statistically significant sequence homology and
CC similarity (Z value of Lipman and Pearson algorithm in Monte Carlo
CC analysis exceeding 6) to include alignment of cysteine residues and
CC similar hydropathy profiles. These superantigens are used to treat solid
CC tumours, including their metastases, without radiation, surgery or
CC standard chemotherapeutic agents. A claimed method of human cancer
CC treatment involves contacting haematopoietic cells from a patient with
CC one or more superantigens ex vivo to generate stimulated cells, selecting
CC a specific V beta subset of cells, and reintroducing these cells into the
CC patient to induce an in vivo therapeutic, tumouricidal reaction
XX
SQ Sequence 233 AA;
Query Match 82.2%; Score 1018; DB 5; Length 233;
Best Local Similarity 82.4%; Pred. No. 1.3e-93;
Matches 192; Conservative 15; Mismatches 26; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITENKESDDOFLNTLLFKGFTG 60
DB 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNKAITENKESDDOFLNTLLFKGFTD 60
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
DB 61 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
QY 121 BEKKVPINLWDGKQTTVPIDKVTSKKVTVOELDLQARHYLHGKGLYNSDSFGKVKQ 180
DB 121 BEKKVPINLWDGKQTTVPIDKVTSKKVTVOELDLQARHYLHGKGLYNSDSFGKVKQ 180
QY 181 RGLIVFHSSEGSTVSYDLFDAQGOVPTLLRIYRDNKTINSENHLIALYLYTT 233
DB 181 RGLIVFHTSTEPSVNDYDLFGAQGQSNLTLLRIYRDNKTINSENHIDIYLYTS 233

RESULT 25
ABB79501
ID ABB79501 standard; protein; 257 AA.
XX ABB79501;
AC ABB79501;
XX
DT 23-SEP-2002 (first entry)
DE Staphylococcal enterotoxin A vaccine, periplasmic (A489270P).
XX
KW Enterotoxin A; superantigen; antigen; toxin; vaccine; A489270P;
KW attenuation; mutant; mutein.
XX
OS Staphylococcus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..25
FT /label= Signal_peptide
FT Protein 26..257
FT /label= Mature_protein
FT Misc-difference 72
FT /note= "wild-type Leu substituted by Arg"
FT Misc-difference 94
FT /note= "wild-type Asp substituted by Arg"
FT Misc-difference 116
FT /note= "wild-type Tyr substituted by Ala"
XX
PN US6399332-B1.
XX
XX 04-JUN-2002.
XX
XX 01-SEP-1998; 98US-00144776.
XX
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PR 25-JUN-1997; 97US-00882431.
 PA (USSA) US SEC OF ARMY.
 PI Ulrich RG, Olson MA, Bavari S;
 XX WPI; 2002-546281/58.
 DR N-PSDB; ABN84222.
 XX
 PT Novel isolated and purified superantigen toxin DNA fragment which has
 PT been genetically altered, useful for producing vaccine for treatment of
 PT superantigen toxin-associated bacterial diseases.
 XX
 XX Claim 4; Col 33-35; 46pp; English.
 XX
 CC The present sequence is the protein sequence of staphylococcal
 CC enterotoxin A (SEA) vaccine, periplasmic (A489270P). The vaccine
 CC comprises 3 amino acid substitutions introduced into the SEA sequence:
 CC L48R, Y89A and D70R. These mutations reduce the binding of the toxin to
 CC major histocompatibility complex (MHC) Class II and/or T cell receptors.
 CC The full-length expressed product is secreted into the periplasmic space
 CC of *Escherichia coli* host cells, and the leader peptide is recognised and
 CC cleaved by a native mechanism. The vaccine is used to protect against
 CC superantigen toxin infections. Superantigen attributes are absent, but
 CC the superantigen is effectively recognised by the immune system and an
 CC appropriate antibody response is produced. In examples from the
 CC invention, attenuated superantigen toxins were shown to protect animals
 CC against challenge with wild-type toxin. Methods of producing and using
 CC the altered superantigen toxins as vaccines, and in diagnosis and
 CC therapy, are provided. A multivalent vaccine consisting of altered
 CC superantigen toxins from SEA, SEB, SEC-1, T8ST-1 and streptococcal SPEA
 CC is predicted to provide protective immunity against the majority of
 CC bacterial superantigen toxins
 XX
 SQ Sequence 257 AA;
 Query Match 81.9%; Score 1014; DB 5; Length 257;
 Best Local Similarity 82.0%; Pred. No. 3.6e-93;
 Matches 191; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
 DB 25 SEKSEINEKDLRKSELOQTALGNLKQIYYNEKAITENKESDDQFROHTILFKGFTD 84
 QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
 DB 85 HSWYNDLLVRFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
 QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
 DB 145 EEKVPINLWLDGKQNTVPLETVKTNKNVTVQELDLQARRYLQEKYNLNSDVFQKVQ 204
 QY 181 RGLIVFHSSEGSVSYDLFDAQCYQPDTLRIYRDNKTINSENHLALVLYTT 233
 DB 205 RGLIVFHTSTEPSVNDLFGAQCQYSNTLLRIYRDNKTINSENHIDILYTS 257
 RESULT 26
 ABU10081
 ID ABU10081 standard; protein; 257 AA.
 XX
 AC ABU10081;
 XX
 DT 11-AUG-2003 (first entry)
 XX
 DE Staphylococcal enterotoxin A #1.
 XX
 DE Enterotoxin A; superantigen-associated bacterial infection; vaccine;
 KW superantigen toxin.
 XX
 OS Staphylococcus sp.
 XX
 XX US2003009015-A1.

XX 09-JAN-2003.
 PD
 XX 25-JUN-1997; 97US-00882431.
 PF
 XX 25-JUN-1997; 97US-00882431.
 PR
 XX (ULRI//) ULRICH R G.
 PA (OLSO//) OLSON M A.
 PA (BAVA//) BAVARI S.
 XX
 PI Ulrich RG, Olson MA, Bavari S;
 XX
 XX WPI; 2003-401542/38.
 DR N-PSDB; ACA61177.
 XX
 CC New superantigen toxin and/or DNA fragment with an altered binding of the
 CC encoded altered toxin to either MHC class II or T cell antigen receptor,
 CC useful for treating or ameliorating superantigen-associated bacterial
 CC infection.
 XX
 XX Claim 10; Page 18-19; 50pp; English.
 XX
 CC The invention relates to an isolated and purified superantigen toxin
 CC and/or DNA fragment, which has been altered so that the binding of the
 CC encoded toxin to either major histocompatibility complex (MHC) class II
 CC or T cell antigen receptor is altered. The superantigen toxins, DNA
 CC fragments, and vaccines are useful for treating or ameliorating
 CC superantigen-associated bacterial infection. The DNA fragments are
 CC particularly useful for producing vaccine against superantigen toxin
 CC infections. The transformed host cells are useful for analysing the
 CC effectiveness of drugs and agents that affect the binding of
 CC superantigens to MHC class II or T-cell antigen receptors. The present
 CC sequence represents the amino acid sequence of staphylococcal enterotoxin
 CC A #1
 XX
 SQ Sequence 257 AA;
 Query Match 81.9%; Score 1014; DB 6; Length 257;
 Best Local Similarity 82.0%; Pred. No. 3.6e-93;
 Matches 191; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
 DB 25 SEKSEINEKDLRKSELOQTALGNLKQIYYNEKAITENKESDDQFROHTILFKGFTD 84
 QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
 DB 85 HSWYNDLLVRFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
 QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
 DB 145 EEKVPINLWLDGKQNTVPLETVKTNKNVTVQELDLQARRYLQEKYNLNSDVFQKVQ 204
 QY 181 RGLIVFHSSEGSVSYDLFDAQCYQPDTLRIYRDNKTINSENHLALVLYTT 233
 DB 205 RGLIVFHTSTEPSVNDLFGAQCQYSNTLLRIYRDNKTINSENHIDILYTS 257
 RESULT 27
 ABU62324
 ID ABU62324 standard; protein; 257 AA.
 XX
 AC ABU62324;
 XX
 DT 27-AUG-2003 (first entry)
 XX
 DE S. aureus periplasmic enterotoxin A mutant #1.
 XX
 KW SEA; staphylococcal enterotoxin A; mutein; mutant; vaccine;
 KW superantigen toxin; MHC; superantigen-associated bacterial infection;
 KW bacterial infection; antibacterial.
 XX

OS Staphylococcus aureus.
 OS Synthetic.
 XX Key Location/Qualifiers
 FH Peptide 1..24
 FT /label= Signal_peptide
 FT Protein 25..257
 FT /label= Mature_SEA_mutant #1
 FT Misc-difference 66
 FT /note= "Wild-type Leu substituted by Glu"
 FT Misc-difference 72
 FT /note= "Wild-type Leu substituted by Arg"
 FT Misc-difference 94
 FT /note= "Wild-type Asp substituted by Arg"
 FT Misc-difference 113
 FT /note= "Wild-type Tyr substituted by Gly"
 FT Misc-difference 116
 FT /note= "Wild-type Tyr substituted by Ala"
 XX
 FN US2003036644-A1.
 XX
 XX 20-FEB-2003.
 XX
 XX 26-NOV-2001; 2001US-00002784.
 XX
 XX 25-JUN-1997; 97US-00882431.
 XX 01-SEP-1998; 98US-00144776.
 XX
 XX (ULRI/) ULRICH R G.
 XX
 XX Ulrich RG;
 XX
 XX WPI; 2003-492125/46.
 XX N-PSDB; ACD28894.
 XX
 PT New superantigen toxin DNA fragment, useful for preparing a composition
 PT for treating or preventing bacterial infection.
 XX
 PS Disclosure; Page 22-23; 69pp; English.
 XX
 CC The invention relates to an isolated and purified superantigen toxin DNA
 CC fragment is altered so that binding of the encoded altered toxin to
 CC either the MHC class II or T cell antigen receptor is altered. Also
 CC included are a recombinant DNA construct (comprising a vector and an
 CC cell transfected with the recombinant superantigen toxin DNA fragment), a host
 CC superantigen toxin, an altered TSGT-1 (toxic shock syndrome toxin)
 CC superantigen toxin peptide, diagnosing superantigen-associated bacterial
 CC infection, a vaccine (comprising an altered superantigen toxin for
 CC producing antigenic and immunogenic response resulting in the protection
 CC of a mammal against superantigen-associated bacterial infection),
 CC treating/ameliorating a superantigen-associated bacterial infection, an
 CC antiserum isolated from individuals immunised with one or more altered
 CC TSGT-1 superantigen toxin and an antibody which recognises altered TSGT-
 CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
 CC SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and
 CC SEBb). The superantigen toxin DNA fragment is useful for preparing a
 CC composition for treating or preventing bacterial infection. The present
 CC sequence represents the L42E/L48R/D70R/Y89G/Y92A (with reference to the
 CC mature protein sequence) mutant of periplasmic SEA
 XX
 SQ Sequence 257 AA;
 Query Match 81.9%; Score 1014; DB 7; Length 257;
 Best Local Similarity 82.0%; Pred. No. 3.6e-93;
 Matches 191; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDOFLNTLLPKGFTG 60
 Db 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESHDFQHTILFKGFTD 84
 QY 61 HPWYNDLLVGLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
 Db 85 HSWYNDLLVRFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
 QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVKQ 180
 Db 145 EEKKVPINLWIDGKQNTVPLETVKTKNKNVTQVELDLQARRYLOEKYNLYNSDVFQKVKQ 204
 QY 181 RGLIVFHSSEGSTVSYDLFDAGQGYPDTLRIYRDNKTINSENHLIALYLYTT 233
 Db 205 RGLIVFHTSTEPSVNYDLFDAGQGYNTLLRIYRDNKTINSENMHIDIYLYTS 257
 RESULT 28
 AAE37676
 ID AAE37676 standard; protein; 257 AA.
 XX
 AC AAE37676;
 XX
 DT 06-OCT-2003 (first entry)
 XX
 DE Protein #1 related to the invention.
 XX
 XW Superantigen toxin; vaccine; infection; gene therapy.
 XX
 OS Unidentified.
 XX
 XX WO2003056015-A1.
 XX
 PD 10-JUL-2003.
 XX
 XX 26-NOV-2001; 2001WO-US046540.
 XX
 XX 26-NOV-2001; 2001US-00002784.
 XX
 XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
 XX
 XX Ulrich RG;
 XX
 XX WPI; 2003-492125/46.
 XX N-PSDB; AAD56764.
 XX
 PT New superantigen toxin DNA fragment, useful for preparing a composition
 PT for treating or preventing bacterial infection.
 XX
 PS Disclosure; Page 108-109; 141pp; English.
 XX
 CC The invention provides a superantigen toxin DNA fragment which has been
 CC genetically altered such that binding of the encoded altered toxin to
 CC either the MHC class II or T cell antigen receptor is disrupted or
 CC altered. DNA fragments of the invention are useful in the production of
 CC vaccines against bacterial superantigen toxin infections. They are also
 CC useful in gene therapy. The present sequence is a protein related to the
 CC invention
 XX
 SQ Sequence 257 AA;
 Query Match 81.9%; Score 1014; DB 7; Length 257;
 Best Local Similarity 82.0%; Pred. No. 3.6e-93;
 Matches 191; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDOFLNTLLPKGFTG 60
 Db 25 SEKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESHDFQHTILFKGFTD 84
 QY 61 HPWYNDLLVGLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
 Db 85 HSWYNDLLVRFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
 QY 121 EEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVKQ 180
 Db 145 EEKKVPINLWIDGKQNTVPLETVKTKNKNVTQVELDLQARRYLOEKYNLYNSDVFQKVKQ 204
 QY 181 RGLIVFHSSEGSTVSYDLFDAGQGYPDTLRIYRDNKTINSENHLIALYLYTT 233
 Db 205 RGLIVFHTSTEPSVNYDLFDAGQGYNTLLRIYRDNKTINSENMHIDIYLYTS 257

Db 205 RGLIVFHTSTEPSVNYDLFGAQQGYVNTLLRIYRDNKTINSENHDIYLYTS 257

RESULT 29
AAV54463
ID AAV54463 standard; protein; 233 AA.
XX AAV54463;
XX 25-APR-2000 (first entry)
XX Amino acid sequence of a mutant Staphylococcal enterotoxin A.
XX Mutant; SEA gene; enterotoxin A; SEB gene; nucleic acid vaccine;
KW Venezuelan equine encephalitis virus; vaccine vector; vaccine;
KW Staphylococcal intoxication; Staphylococcus exotoxin.
XX Staphylococcus aureus.
XX Key Location/Qualifiers
FH Misc-difference 2 /note= "Glu encoded by AGAA"
FT Misc-difference 4 /note= "Ser encoded by C"
FT
FT
XX WO200002523-A2.
XX 20-JAN-2000.
XX 09-JUL-1999; 99WO-US015569.
XX 10-JUL-1998; 98US-0092416P.
XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX
XX Lee JS, Pushko P, Smith JF, Ulrich RG;
XX WPI; 2000-160826/14.
XX N-PSDB; AA245833.
XX New DNA construct useful as vaccines against enterotoxins of
PT Staphylococcus aureus which causes gastrointestinal distress, or toxic
PT shock syndrome.
XX Disclosure; Page 28; 30pp; English.
XX The present sequence is represents a mutant Staphylococcal enterotoxin A.
CC It is encoded by a mutant SEA gene. The mutant gene product is unable to
CC bind to the MHC on T-cells, and so is non-toxic. Mutant SEA and SEB genes
CC were inserted into a Venezuelan equine encephalitis (VEE) replicon
CC vector, to produce vaccine vectors. The mutant gene product is unable to
CC bind to the MHC on T-cells, and so is non-toxic. Self-replicating RNA
CC derived from the recombinant VEE vectors can be used as a nucleic acid
CC vaccine, or to transfect cells along with RNA from helper plasmids. The
CC recombinant proteins produced are used as vaccines for providing immunity
CC against Staphylococcal intoxication or as a diagnostic tool for detection
CC of Staphylococcus exotoxin. The transformed host cells are used to
CC analyse the effectiveness of drugs and agents which inhibit S. aureus
CC exotoxins or release of exotoxins. Infectious alpha-virus particles
CC comprising the mutant SEA or SEB genes are used for providing immunity
CC against Staphylococcal exotoxins by generating a protective immune
CC reaction in humans or animals. The vaccines are used to reduce disease
CC symptoms or reduce severity of disease caused by enterotoxins of S.
XX aureus
XX Sequence 233 AA;
SQ Query Match 81.6%; Score 1010; DB 3; Length 233;
Best Local Similarity 81.9%; Pred. No. 8e-93;
Matches 190; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
2 EKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHDOFROHTILFKGFFTDH 61

Db 2 EKSEINEKDLRKSELOQTALGNLQIYYNEKAKTENKESHDOFROHTILFKGFFTDH 61

OY 62 PYNDLLVLDGSKDATNKYKGGKVDLYGAYGYCAGGTPNKTACWYGGVTLHDNNRLTE 121
Db 62 SWYNDLLVRFDSKDIYDKYKGGKVDLYGAYGYCAGGTPNKTACWYGGVTLHDNNRLTE 121
OY 122 EKVPINLWIDGKQTTVPIDPKVTKSKVEVTVOELDLQARHYLHGKFLYNSDSFGKQVOR 181
Db 122 EKVPINLWIDGKQTTVPIDPKVTKSKVEVTVOELDLQARHYLHGKFLYNSDSFGKQVOR 181
OY 182 GLIVFHTSTEPSVNYDLFGAQQGYVNTLLRIYRDNKTINSENHDIYLYTT 233
Db 182 GLIVFHTSTEPSVNYDLFGAQQGYVNTLLRIYRDNKTINSENHDIYLYTS 233

RESULT 30
ABB79502
ID ABB79502 standard; protein; 233 AA.
XX ABB79502;
XX 23-SEP-2002 (first entry)
XX Staphylococcal enterotoxin A vaccine, cytoplasmic (A489270C).
DE Enterotoxin A; superantigen; antigen; toxin; vaccine; A489270C;
KW attenuation; mutant; mutein.
XX Staphylococcus sp.
OS Synthetic.
XX Key Location/Qualifiers
FH Misc-difference 1 /note= "encoded by AT, apparent frameshift"
FT Misc-difference 48 /note= "wild-type Leu substituted by Arg"
FT Misc-difference 70 /note= "wild-type Asp substituted by Arg"
FT Misc-difference 92 /note= "wild-type Tyr substituted by Ala"
XX US6399332-B1.
XX 04-JUN-2002.
XX 01-SEP-1998; 98US-00144776.
XX 25-JUN-1997; 97US-00882431.
XX (USSA) US SEC OF ARMY.
XX Ulrich RG, Olson MA, Bavari S;
XX WPI; 2002-546281/58.
XX N-PSDB; ABN84223.
XX Novel isolated and purified superantigen toxin DNA fragment which has
PT been genetically altered, useful for producing vaccine for treatment of
PT superantigen toxin-associated bacterial diseases.
XX Claim 5; Col 37-39; 46pp; English.
XX The present sequence is the protein sequence of staphylococcal
CC enterotoxin A (SEA) vaccine, cytoplasmic (A489270C). The vaccine
CC comprises 3 amino acid substitutions introduced into the SEA sequence:
CC L48R, Y89A and D70R. These mutations reduce the binding of the toxin to
CC major histocompatibility complex (MHC) Class II and/or T cell receptors.
CC The protein is expressed as a nonsecreted product within host Escherichia
CC coli cells. The vaccine is used to protect against superantigen toxin
CC infections. Superantigen attributes are absent, but the superantigen is
CC effectively recognised by the immune system and an appropriate antibody
CC response is produced. In examples from the invention, attenuated
CC superantigen toxins were shown to protect animals against challenge with

CC wild-type toxin. Methods of producing and using the altered superantigen
 CC toxins as vaccines, and in diagnosis and therapy, are provided. A
 CC multivalent vaccine consisting of altered superantigen toxins from SEA,
 CC SEB, SEC-1, TSST-1 and streptococcal SPa is predicted to provide
 CC protective immunity against the majority of bacterial superantigen toxins
 XX
 SQ Sequence 233 AA;

Query Match 81.6%; Score 1010; DB 5; Length 233;
 Best Local Similarity 81.9%; Pred. No. 8e-93;
 Matches 190; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
 QY 2 EKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
 Db 2 EKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
 QY 62 PWYNDLLVLDGSKDNTKYGKGVLDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLTE 121
 Db 62 SWYNDLLVRFDSKDIDVYKYGKGVLDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLTE 121
 QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVR 181
 Db 122 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVR 181
 QY 182 GLIVFHSSEGSTVSYDLFDAQGYDPTLLRIYRDNKTINSENHIALYLYTT 233
 Db 182 GLIVFHSSTEPSVNDLFGAQQGYNTLLRIYRDNKTINSENHIDYLYTS 233

RESULT 31
 ABU10082
 ID ABU10082 standard; protein; 233 AA.
 AC ABU10082;
 XX
 XX 11-AUG-2003 (first entry)
 DE Staphylococcal enterotoxin A #2.
 KW Enterotoxin A; superantigen-associated bacterial infection; vaccine;
 KW superantigen toxin.
 XX Staphylococcus sp.

Key Location/Qualifiers
 FT Misc-difference 1 /note= "Encoded by AT"
 XX US2003009015-A1.
 XX 09-JAN-2003.
 XX 25-JUN-1997; 97US-00882431.
 XX 25-JUN-1997; 97US-00882431.
 XX (ULRI/) ULRICH R G.
 XX (OLSO/) OLSON M A.
 XX (BAVA/) BAVARI S.
 XX Ulrich RG, Olson MA, Bavari S;
 XX WPI; 2003-401542/38.
 XX N-PSDB; ACA61178.

New superantigen toxin and/or DNA fragment with an altered binding of the
 FT encoded altered toxin to either MHC class II or T cell antigen receptor,
 FT useful for treating or ameliorating superantigen-associated bacterial
 FT infection.
 XX
 XX Claim 11; Page 20-21; 50pp; English.
 XX The invention relates to an isolated and purified superantigen toxin

CC and/or DNA fragment, which has been altered so that the binding of the
 CC encoded toxin to either major histocompatibility complex (MHC) class II
 CC or T cell antigen receptor is altered. The superantigen toxins, DNA
 CC fragments, and vaccines are useful for treating or ameliorating
 CC superantigen-associated bacterial infection. The DNA fragments are
 CC particularly useful for producing vaccine against superantigen toxin
 CC infections. The transformed host cells are useful for analysing the
 CC effectiveness of drugs and agents that affect the binding of
 CC superantigens to MHC class II or T-cell antigen receptors. The present
 CC sequence represents the amino acid sequence of staphylococcal enterotoxin
 CC A #2
 XX
 SQ Sequence 233 AA;

Query Match 81.6%; Score 1010; DB 6; Length 233;
 Best Local Similarity 81.9%; Pred. No. 8e-93;
 Matches 190; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
 QY 2 EKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
 Db 2 EKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
 QY 62 PWYNDLLVLDGSKDNTKYGKGVLDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLTE 121
 Db 62 SWYNDLLVRFDSKDIDVYKYGKGVLDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLTE 121
 QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVR 181
 Db 122 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVR 181
 QY 182 GLIVFHSSEGSTVSYDLFDAQGYDPTLLRIYRDNKTINSENHIALYLYTT 233
 Db 182 GLIVFHSSTEPSVNDLFGAQQGYNTLLRIYRDNKTINSENHIDYLYTS 233

RESULT 32
 ABU62325
 ID ABU62325 standard; protein; 233 AA.
 XX
 AC ABU62325;
 XX
 XX 27-AUG-2003 (first entry)
 DE S. aureus cytoplasmic enterotoxin A mutant #1.
 XX SEA; staphylococcal enterotoxin A; mutein; mutant; vaccine;
 KW superantigen toxin; MHC; superantigen-associated bacterial infection;
 KW bacterial infection; antibacterial.
 XX Staphylococcus aureus.
 OS Synthetic.

Key Location/Qualifiers
 FT Misc-difference 1.2 /note= "Encoded by ATGAG"
 FT Misc-difference 42 /note= "Wild-type Leu substituted by Glu"
 FT Misc-difference 48 /note= "Wild-type Leu substituted by Arg"
 FT Misc-difference 70 /note= "Wild-type Asp substituted by Arg"
 FT Misc-difference 89 /note= "Wild-type Tyr substituted by Gly"
 FT Misc-difference 92 /note= "Wild-type Tyr substituted by Ala"
 XX US2003036644-A1.
 XX 20-FEB-2003.
 XX 26-NOV-2001; 2001US-0002784.
 XX 25-JUN-1997; 97US-00882431.

PR 01-SEP-1998; 98US-00144776.
 PA (ULRI/) ULRICH R G.
 XX
 PI Ulrich RG;
 XX
 DR WPI; 2003-492125/46.
 DR N-PSDB; ACD28895.
 XX
 XX New superantigen toxin DNA fragment, useful for preparing a composition
 PT for treating or preventing bacterial infection.
 XX
 PS Disclosure; Page 24-25; 68pp; English.
 XX
 CC The invention relates to an isolated and purified superantigen toxin DNA
 CC fragment is altered so that binding of the encoded altered toxin to
 CC either the MHC class II or T cell antigen receptor is altered. Also
 CC included are a recombinant DNA construct (comprising a vector and an
 CC isolated and purified altered superantigen toxin DNA fragment), a host
 CC cell transformed with the recombinant DNA construct, producing altered
 CC superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
 CC superantigen toxin peptide, diagnosing superantigen-associated bacterial
 CC infection, a vaccine (comprising an altered superantigen toxin for
 CC producing antigenic and immunogenic response resulting in the protection
 CC of a mammal against superantigen-associated bacterial infection),
 CC treating/ameliorating a superantigen-associated bacterial infection, an
 CC antiserum isolated from individuals immunised with one or more altered
 CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-
 CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
 CC SEB, SECL) and streptococcal pyrogenic enterotoxin a and b (SPEa and
 CC SPEb). The superantigen toxin DNA fragment is useful for preparing a
 CC composition for treating or preventing bacterial infection. The present
 CC sequence represents the L42E/L48R/D70R/Y89G/Y92A mutant of cytoplasmic
 CC SEA
 XX
 SQ Sequence 233 AA;
 Query Match 81.6%; Score 1010; DB 7; Length 233;
 Best Local Similarity 81.9%; Pred. No. 8e-93;
 Matches 190; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
 QY 2 EKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTILFKGFTGH 61
 DB 2 EKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFROHTILFKGFTDH 61
 QY 62 PWYNDLLVLDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
 DB 62 SWYNDLLVRFDSKDIVDKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
 QY 122 EKKVPINLMDGKQTTVPIDKVKTSKKEVTVOELDLQABHYLHGKFLYNSDSFGKQVOR 181
 DB 122 EKKVPINLMDGKQNTVPLETVKTNKXQNTVQELDLQARYLOEKYLNLSVDFGKQVOR 181
 QY 182 GLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNKTINSENHIALYLYTT 233
 DB 182 GLIVFHTSTEPSVNYDLFGAQGYSTLLRIYRDNKTINSENHIDILYLYTS 233
 RESULT 33
 AAEE37677
 ID AAE37677 standard; protein; 233 AA.
 XX
 AC AAE37677;
 XX
 DT 06-OCT-2003 (first entry)
 DE Protein #2 related to the invention.
 XX
 KW Superantigen toxin; vaccine; infection; gene therapy.
 XX Unidentified.
 OS
 XX Key Location/Qualifiers
 FT

FT Misc-difference 1 /note= "Encoded by AT"
 XX
 XX WO2003056015-A1.
 PD 10-JUL-2003.
 XX
 XX 26-NOV-2001; 2001WO-US046540.
 PF
 XX 26-NOV-2001; 2001US-00002784.
 PR
 PA (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
 XX
 XX Ulrich RG;
 XX
 DR WPI; 2003-492125/46.
 DR N-PSDB; AAD56765.
 XX
 XX New superantigen toxin DNA fragment, useful for preparing a composition
 PT for treating or preventing bacterial infection.
 XX
 PS Disclosure; Page 110-112; 141pp; English.
 XX
 CC The invention provides a superantigen toxin DNA fragment which has been
 CC genetically altered such that binding of the encoded altered toxin to
 CC either the MHC class II or T cell antigen receptor is disrupted or
 CC altered. DNA fragments of the invention are useful in the production of
 CC vaccines against bacterial superantigen toxin infections. They are also
 CC useful in gene therapy. The present sequence is a protein related to the
 CC invention
 XX
 SQ Sequence 233 AA;
 Query Match 81.6%; Score 1010; DB 7; Length 233;
 Best Local Similarity 81.9%; Pred. No. 8e-93;
 Matches 190; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
 QY 2 EKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTILFKGFTGH 61
 DB 2 EKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFROHTILFKGFTDH 61
 QY 62 PWYNDLLVLDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
 DB 62 SWYNDLLVRFDSKDIVDKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
 QY 122 EKKVPINLMDGKQTTVPIDKVKTSKKEVTVOELDLQABHYLHGKFLYNSDSFGKQVOR 181
 DB 122 EKKVPINLMDGKQNTVPLETVKTNKXQNTVQELDLQARYLOEKYLNLSVDFGKQVOR 181
 QY 182 GLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNKTINSENHIALYLYTT 233
 DB 182 GLIVFHTSTEPSVNYDLFGAQGYSTLLRIYRDNKTINSENHIDILYLYTS 233
 RESULT 34
 ABU10099
 ID ABU10099 standard; protein; 233 AA.
 XX
 AC ABU10099;
 XX
 DT 11-AUG-2003 (first entry)
 DE Staphylococcus enterotoxin A K14E substitution mutant.
 XX
 KW Staphylococcus enterotoxin A; superantigen-associated bacterial infection; mutant;
 KW superantigen toxin; vaccine; mutein.
 XX
 OS Staphylococcus sp.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FT Misc-difference 14 /note= "Wild-type Lys substituted by Glu"
 FT

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XX PN US2003009015-A1.
XX PD 09-JAN-2003.
XX PF 25-JUN-1997; 97US-00882431.
XX PR 25-JUN-1997; 97US-00882431.
XX PA (ULRI/) ULRICH R G.
XX PA (OLSO/) OLSON M A.
XX PA (BAVA/) BAVARI S.
XX PI Ulrich RG, Olson MA, Bavari S;
XX WPI; 2003-401542/38.
XX New superantigen toxin and/or DNA fragment with an altered binding of the
XX encoded altered toxin to either MHC class II or T cell antigen receptor,
XX useful for treating or ameliorating superantigen-associated bacterial
XX infection.
XX Example 7; Page; 50pp; English.
XX The invention relates to an isolated and purified superantigen toxin
XX and/or DNA fragment, which has been altered so that the binding of the
XX encoded toxin to either major histocompatibility complex (MHC) class II
XX or T cell antigen receptor is altered. The superantigen toxins, DNA
XX fragments, and vaccines are useful for treating or ameliorating
XX superantigen-associated bacterial infection. The DNA fragments are
XX particularly useful for producing vaccine against superantigen toxin
XX infections. The transformed host cells are useful for analysing the
XX effectiveness of drugs and agents that affect the binding of
XX superantigens to MHC class II or T-cell antigen receptors. The present
XX sequence represents the amino acid sequence of the staphylococcus
XX enterotoxin A K4E mutant. Note: The present sequence is not present in
XX the specification but was created by the indexer from the wild-type
XX staphylococcus enterotoxin A sequence (see ACA61178)
XX SQ Sequence 233 AA;
XX Query Match 81.3%; Score 1006; DB 6; Length 233;
XX Best Local Similarity 81.5%; Pred. No. 2e-92;
XX Matches 189; Conservative 17; Mismatches 26; Indels 0; Gaps 0;
QY 2 EKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDOFLNLLFKGFTGH 61
Db 2 EKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDOFRQHILFKGFTDH 61
QY 62 PWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTE 121
Db 62 SWYNDLLVRFDSKDIDVKYKGVLDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFLYNSDSFGKQVOR 181
Db 122 EKKVPINLWDGKQTTVPLETVTNKNKNTVQELDLQARHYLQEKYLNLYNSDVFQKQVOR 181
QY 182 GLIVFHSSEGSTVSYDLFDAQGYQVPTLLRIYRDNKNTINSENHLIALVLYTT 233
Db 182 GLIVFHTSTEPSVNYDLFQAQGYQVNTLLRIYRDNKNTINSENHMDIYLYTS 233
RESULT 35
ABU10098
ID ABU10098 standard; protein; 233 AA.
XX ABU10098;
XX AC
XX DT 11-AUG-2003 (first entry)
XX Staphylococcus enterotoxin A Y64A substitution mutant.
XX Enterotoxin A; superantigen-associated bacterial infection; mutant;

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KW superantigen toxin; vaccine; mutain.
XX Staphylococcus sp.
XX Synthetic.
XX Key Location/Qualifiers
FT Misc-difference 64 /note= "Wild-type Tyr substituted by Ala"
XX US2003009015-A1.
XX 09-JAN-2003.
XX 25-JUN-1997; 97US-00882431.
XX 25-JUN-1997; 97US-00882431.
XX (ULRI/) ULRICH R G.
XX PA (OLSO/) OLSON M A.
XX PA (BAVA/) BAVARI S.
XX PI Ulrich RG, Olson MA, Bavari S;
XX WPI; 2003-401542/38.
XX New superantigen toxin and/or DNA fragment with an altered binding of the
XX encoded altered toxin to either MHC class II or T cell antigen receptor,
XX useful for treating or ameliorating superantigen-associated bacterial
XX infection.
XX Example 7; Page; 50pp; English.
XX The invention relates to an isolated and purified superantigen toxin
XX and/or DNA fragment, which has been altered so that the binding of the
XX encoded toxin to either major histocompatibility complex (MHC) class II
XX or T cell antigen receptor is altered. The superantigen toxins, DNA
XX fragments, and vaccines are useful for treating or ameliorating
XX superantigen-associated bacterial infection. The DNA fragments are
XX particularly useful for producing vaccine against superantigen toxin
XX infections. The transformed host cells are useful for analysing the
XX effectiveness of drugs and agents that affect the binding of
XX superantigens to MHC class II or T-cell antigen receptors. The present
XX sequence represents the amino acid sequence of the staphylococcus
XX enterotoxin A Y64A mutant. Note: The present sequence is not present in
XX the specification but was created by the indexer from the wild-type
XX staphylococcus enterotoxin A sequence (see ACA61178)
XX SQ Sequence 233 AA;
XX Query Match 80.9%; Score 1001; DB 6; Length 233;
XX Best Local Similarity 81.5%; Pred. No. 6.4e-92;
XX Matches 189; Conservative 16; Mismatches 27; Indels 0; Gaps 0;
QY 2 EKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDOFLNLLFKGFTGH 61
Db 2 EKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDOFRQHILFKGFTDH 61
QY 62 PWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTE 121
Db 62 SWYNDLLVRFDSKDIDVKYKGVLDLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFLYNSDSFGKQVOR 181
Db 122 EKKVPINLWDGKQTTVPLETVTNKNKNTVQELDLQARHYLQEKYLNLYNSDVFQKQVOR 181
QY 182 GLIVFHSSEGSTVSYDLFDAQGYQVPTLLRIYRDNKNTINSENHLIALVLYTT 233
Db 182 GLIVFHTSTEPSVNYDLFQAQGYQVNTLLRIYRDNKNTINSENHMDIYLYTS 233
RESULT 36
AAV70102
ID AAV70102 standard; protein; 257 AA.

```

XX AC AAY70102;
XX DT 05-JUN-2000 (first entry)
XX DE Staphylococcal enterotoxin A.
XX KW Superantigen toxin; SAG; Staphylococcal enterotoxin A; SEA; cytostatic;
XX KW antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;
XX KW antibody; toxoid; staphylococcal/streptococcal toxin; diagnosis;
XX KW treatment; superantigen-associated bacterial infection.
XX OS Staphylococcus sp.
XX FH Key Location/Qualifiers
XX FT Peptide 2..25
XX FT Protein /label= Leader_peptide
XX FT Protein 26..253
XX FT /label= Mature Staphylococcal enterotoxin A
XX FT /note= "Includes transcription start site residue, Met"
XX FT Misc-difference 42
XX FT /note= "Encoded by TTG"
XX FT Misc-difference 125
XX FT /note= "Encoded by CCA"
XX PN WO200009154-A1.
XX PD 24-FEB-2000.
XX XX 13-AUG-1998; 98WO-US016766.
XX XX 13-AUG-1998; 98WO-US016766.
XX PA (REED-) REED ARMY INST RES WALTER.
XX PI Ulrich RG, Olson MA, Bavari S;
XX DR WPI; 2000-224177/19.
XX DR N-PSDB; AA251105.
XX PT Nucleic acid encoding superantigen toxin useful as a vaccine and for
XX PT diagnosis of superantigen-associated bacterial infections.
XX PS Claim 7; Page 72-73; 118pp; English.
XX CC The present amino acid sequence is the Staphylococcal enterotoxin A
XX CC (SEA), a bacterial superantigen toxin (SAG). The coding region of the SAG
XX CC toxin when altered by site directed mutagenesis, results in disruption of
XX CC binding of the toxin to both the MHC class II or T-cell antigen receptor.
XX CC SEA has antibacterial and cytostatic activity. This sequence is useful
XX CC for the production of SEA vaccines and specific antibodies. This vaccine
XX CC overcomes the disadvantages of the chemically inactivated toxoids and is
XX CC designed to protect individuals against one or several related
XX CC staphylococcal and streptococcal toxins. It is used for the diagnosis and
XX CC treatment or amelioration of superantigen-associated bacterial
XX CC infections
XX SQ Sequence 257 AA;
Query Match 80.5%; Score 997; DB 3; Length 257;
Best Local Similarity 81.1%; Pred. No. 1.9e-91;
Matches 189; Conservative 16; Mismatches 28; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLKKELQGTALGNLKQIYYNEKAITENKSDDOFLENTILFKGFFTG 60
DB 25 SEKSEINEKDLKKELQGTALGNLKQIYYNEKAITENKSDDOFLENTILFKGFFTG 84
QY 61 HPWYNDLLVGLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 120
DB 85 HSNYNDLLVAFDSKDIYDKYKGGKVDLYGAYGYQCAGGTFNKTACMYGGVTLHNNRLT 144
QY 121 EEKKVPINLWLDGKQNTVPLETVKTKNKNVTQELDLQARRYLOEKYNLYNSDVFSGKVQ 180
DB 145 EEKKVPINLWLDGKQNTVPLETVKTKNKNVTQELDLQARRYLOEKYNLYNSDVFSGKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDILLRIYRDKNKTINSENHLIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQGYNTLLRIYRDKNKTINSENHMLIDVLYTS 257
RESULT 37
AAY70103
ID AAY70103 standard; protein; 233 AA.
XX AC AAY70103;
XX DT 05-JUN-2000 (first entry)
XX DE Mutant Staphylococcal enterotoxin A for vaccine A489270P.
XX KW Superantigen toxin; SAG; Staphylococcal enterotoxin A; SEA; cytostatic;
XX KW antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;
XX KW antibody; toxoid; staphylococcal/streptococcal toxin; diagnosis; mutant;
XX KW treatment; superantigen-associated bacterial infection; A489270P.
XX OS Staphylococcus sp.
XX FH Key Location/Qualifiers
XX FT Protein 1..233
XX FT /label= Mature Staphylococcal enterotoxin_A
XX FT /note= "Mutant sequence without the leader peptide"
XX FT Misc-difference 2
XX FT /note= "Encoded by AG"
XX FT Misc-difference 18
XX FT /note= "Encoded by TTG"
XX FT Misc-difference 48
XX FT /note= "Wild type leu substituted with Arg"
XX FT Misc-difference 70
XX FT /note= "Wild type asp substituted with Arg"
XX FT Misc-difference 92
XX FT /note= "Wild type Tyr substituted with Ala"
XX FT Misc-difference 157
XX FT /note= "Encoded by CTT"
XX FT Misc-difference 180
XX FT /note= "Encoded by CAG"
XX PN WO200009154-A1.
XX PD 24-FEB-2000.
XX XX 13-AUG-1998; 98WO-US016766.
XX XX 13-AUG-1998; 98WO-US016766.
XX PA (REED-) REED ARMY INST RES WALTER.
XX PI Ulrich RG, Olson MA, Bavari S;
XX DR WPI; 2000-224177/19.
XX DR N-PSDB; AA251106.
XX PT Nucleic acid encoding superantigen toxin useful as a vaccine and for
XX PT diagnosis of superantigen-associated bacterial infections.
XX PS Claim 8; Page 74-76; 118pp; English.
XX CC The present amino acid sequence is the mutant Staphylococcal enterotoxin
XX CC A (SEA), a bacterial superantigen toxin (SAG), used for the formulation
XX CC of SEA vaccine A489270P. The coding region of this SAG toxin is altered
XX CC by site directed mutagenesis, that results in disruption of binding of
XX CC the toxin to both the MHC class II or T-cell antigen receptor. This
XX CC altered SAG toxin has the leader peptide cleaved by native bacterial
XX CC enzymatic mechanism and the first residue of the mature protein is
XX CC encoded by the transcriptional start site (ATG). SEA has antibacterial
XX CC and cytostatic activity. This sequence is useful for the production of
XX CC SEA vaccines and specific antibodies. This vaccine overcomes the

CC disadvantages of the chemically inactivated toxoids and is designed to
 CC protect individuals against one or several related staphylococcal and
 CC streptococcal toxins. It is used for the diagnosis and treatment or
 CC amelioration of superantigen-associated bacterial infections
 XX
 SQ Sequence 233 AA;
 Query Match 80.1%; Score 992; DB 3; Length 233;
 Best Local Similarity 80.6%; Pred. No. 5.1e-91;
 Matches 187; Conservative 16; Mismatches 29; Indels 0; Gaps 0;
 QY 2 EKSEBINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
 Db 2 EKSEBINEKDLRKSEKOGTALGNLKOIYYNEKAITENKESHQFROHTLLFKGFTDH 61
 QY 62 PWYNDLLVDLGSKDNTNKKKKVDLYGAYGYOCAGTTPNKTCMYGVTLHNNRLTE 121
 Db 62 SWYNDLLVDFDSKDIDVRYKGGKVDLYGAYAGYOCAGTTPNKTCMYGVTLHNNRLTE 121
 QY 122 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKVQR 181
 Db 122 EKKVPINLWIDGKQNTVPLETVKTNKQNTVOELDKQARRYLQEKINLYNSDVFQGVAR 181
 QY 182 GLIVFHSSEGSTVSYDLFDAQGVPTDLRLTYRDNKTINSNHLIALYLYTT 233
 Db 182 GLIVFHTSTEPSVNYDLFGAQQYSNTLLRYRDNKTINSNMHIDIYLYTS 233
 RESULT 38
 ABU79071
 ID ABU79071 standard; protein; 258 AA.
 AC ABU79071;
 XX
 DT 18-JUN-2003 (first entry)
 XX
 DE S. aureus SED (staphylococcus enterotoxin D) protein.
 KW Superantigen; SAG; staphylococcal enterotoxin; tumour; cancer; apoptosis;
 KW Gene therapy; mammalian cell receptor; tumour associated lipid; energy;
 KW T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;
 KW APC; antitumour.
 XX
 OS Staphylococcus aureus.
 XX
 FN US2002177551-A1.
 XX
 PD 28-NOV-2002.
 XX
 PF 30-MAY-2001; 2001US-00870759.
 XX
 PR 31-MAY-2000; 2000US-0208128P.
 XX
 PA (TERM/) TERMAN D S.
 XX
 PI Terman DS;
 XX
 DR WPI; 2003-361759/34.
 DR N-PSDB; ACA64697.
 XX
 PT A mammalian cell receptor, useful in the treatment of cancer by binding
 PT to tumor associated lipids where the binding induces energy or apoptosis
 PT in T cells and antigen presenting cells.
 XX
 FS Disclosure; Page; 167pp; English.
 XX
 CC The invention relates to a mammalian cell receptor, useful in the
 CC treatment of cancer, which binds to tumour associated lipids and induces
 CC energy or apoptosis in the T cells and antigen presenting cells (APCs).
 CC Also included are a mammalian cell useful in the treatment of cancer
 CC where the receptor which binds tumour associated lipids and induces
 CC cellular inactivation or death is deleted or functionally deactivated,
 CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal

CC (by allowing tumour associated lipids to contact immunocytes in which
 CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,
 CC sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides,
 CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
 CC deleted), a construct useful in the treatment of cancer comprising a
 CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell
 CC useful in the treatment of cancer (where an adaptor protein which
 CC inhibits T cell activation by tumour associated antigens is deleted or
 CC functionally deactivated), a composition useful in the treatment of
 CC cancer (comprising a lipid raft conjugated to a superantigen), producing
 CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
 CC allowing tumour associated lipids to contact immunocytes, in which
 CC receptors for the lipids are inactivated or deleted to produce a
 CC tumouricidal immunocyte population, and administering the tumouricidal APC
 CC population ex vivo in a mammal (by allowing a tumour associated lipid to
 CC contact APCs, in which receptors for the tumour associated lipids are
 CC inactivated or deleted to produce a tumouricidally activated population,
 CC and administering APCs to the host), producing a tumouricidal T cell
 CC population ex vivo in a mammal) by allowing a tumour associated lipids to
 CC contact T cells, in which adaptor proteins, which inhibit T cell
 CC activation by tumour associated antigens, are deleted or functionally
 CC deactivated to produce a tumouricidal population of T cells, and
 CC administering the tumouricidally activated T cells to the host, or
 CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
 CC administering the tumouricidally activated T cells to the host), treating
 CC (M5) cancer in a mammal (by administering a lipid binding molecule which
 CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
 CC a tumouricidal T cell population in vivo in a mammal (by allowing a
 CC tumour associated antigen to contact immunocytes in which adaptor
 CC proteins which inhibit T cell activation by tumour associated antigens
 CC are deleted or functionally deactivated) and producing (M7) a
 CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
 CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
 CC receptors, methods and compositions are useful for treating cancers and
 CC tumours. Bacterial superantigens are co-administered or administered as
 CC fusion constructs with anti-tumour proteins or motifs. The present
 CC sequence represents a bacterial superantigen protein (e.g. a
 CC staphylococcal enterotoxin). Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format from the US patent office website at
 CC "seqdata.uspto.gov/sequence.html?docID=20020177551"
 XX
 SQ Sequence 258 AA;
 Query Match 53.6%; Score 663; DB 6; Length 258;
 Best Local Similarity 55.0%; Pred. No. 6.4e-58;
 Matches 127; Conservative 33; Mismatches 71; Indels 0; Gaps 0;
 QY 1 SEKSEBINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTTG 60
 Db 26 NENIDSVKEKELHKKSELSSTALNNMKHSYADKNPIIGENKSTGQFLENTLLYKKFFTD 85
 QY 61 HPWYNDLLVDLGSKDNTNKKKKVDLYGAYGYOCAGTTPNKTCMYGVTLHNNRLT 120
 Db 86 LINFEDLLINFNSKEVAHQFKSNVDVPEIRYSINCYGGEIDRTACTGYGVTPHEGNK 145
 QY 121 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKVQ 180
 Db 146 ERKIPINLWINGVQKESVLSLDKVDTKNVTVOELDAQARRYLQDKLYNNDTLGGKIQ 205
 QY 181 RGLIVFHSSEGSTVSYDLFDAQGVPTDLRLTYRDNKTINSNHLIALYLY 231
 Db 206 RGIKIEPDSGSKVSYDLFQVDFKGFPEKQIRIYSNDKNTLSTHLHIDIYLY 256
 RESULT 39
 AAR45013
 ID AAR45013 standard; protein; 228 AA.
 XX
 AC AAR45013;
 XX
 DT 25-MAR-2003 (revised)

PN US2002051765-A1.
XX 02-MAY-2002.
XX 19-DEC-2000; 2000US-00741503.
XX 03-OCT-1989; 89US-00416530.
XX 17-JAN-1990; 90US-00466577.
XX 17-JAN-1991; 91WO-US000342.
XX 01-JUN-1992; 92US-00891718.
XX 02-MAR-1993; 93US-00025144.
XX 31-JAN-1994; 94US-00089424.
XX 19-JUN-1995; 95US-00491746.
XX (TERM/) TERMAN D S.
XX Terman DS;
XX WPI; 2002-415198/44.
XX Reagent for treating cancer without the need for e.g. radiotherapy,
XX comprises a specific V beta subset of T cells sensitized to a growing
XX tumor and stimulated with superantigens.
XX Disclosure; Fig 2; 17pp; English.
XX The present sequence is the protein sequence of enterotoxin D (SED) of
XX Staphylococcus aureus. Similarity is shown, in several stretches of
XX sequence, between staphylococcal enterotoxins, streptococcal pyrogenic
XX exotoxins and staphylococcal exfoliative toxins (see ABB76234-44). In the
XX present invention, synthetic polypeptides useful in tumour therapy and in
XX blocking or destroying autoreactive T and B lymphocyte populations are
XX characterised by substantial structural homology to staphylococcal
XX enterotoxin A and enterotoxin B, and to streptococcal pyrogenic
XX exotoxins, with statistically significant sequence homology and
XX similarity (Z value of Lipman and Pearson algorithm in Monte Carlo
XX analysis exceeding 6) to include alignment of cysteine residues and
XX similar hydropathy profiles. These superantigens are used to treat solid
XX tumours, including their metastases, without radiation, surgery or
XX standard chemotherapeutic agents. A claimed method of human cancer
XX treatment involves contacting haematopoietic cells from a patient with
XX one or more superantigens ex vivo to generate stimulated cells, selecting
XX a specific V beta subset of cells, and reintroducing these cells into the
XX patient to induce an in vivo therapeutic, tumoricidal reaction
XX
SQ Sequence 228 AA;
Query Match 53.1%; Score 657; DB 5; Length 228;
Best Local Similarity 56.0%; Pred. No. 2.2e-57;
Matches 126; Conservative 31; Mismatches 68; Indels 0; Gaps 0;
QY 7 INEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGHPWYND 66
Db 2 VKEKELHKKSLSSTALNNMKHSYADKNPIIGENKSTGQFLENTLLYKKFFTDLINFED 61
QY 67 LLVDLGSKDATNKYKGVLDYGYVGYOCAGGTPNKTACMYGGVTLHDNNRLTEKKVP 126
Db 62 LLINFSKEMAQHFKSNVDVPIRYSINCYGGEIDRTACTYGGVTPHEGNLKERKKIP 121
QY 127 INLWIDGKQTTVPIDKVKTSKKEVTQVELDQARHYLHGKFGLYNSDSFGKVGQRLIVF 186
Db 122 INLWINGVQKEVSLDKVQTDKKNVTQVELDAQRRYLQKDLKLYNNDTLGGKIQRGKIEF 181
QY 187 HSSEGSTVSVDLFDAGQGYPTLLRIYRDNKNTINSENHIALYLY 231
Db 182 DSSDGSKVSVDLFDVKGFPEKQRIYSNDKTLSTELHLDIYLY 226
RESULT 42
AAR13205
XX AAR13205 standard; protein; 228 AA.
AC AAR13205;

XX 15-OCT-1991 (first entry)
XX Staphylococcal enterotoxin D.
XX SED; cancer treatment; pyrogen; tumouricide.
XX Staphylococcus aureus.
XX WO9110680-A.
XX 25-JUL-1991.
XX 17-JAN-1990; 90US-00466577.
XX 17-JAN-1990; 90US-00466577.
XX (TERM/) TERMAN D S.
XX Terman DS;
XX WPI; 1991-237984/32.
XX Treating cancer with enterotoxin from Staphylococcus aureus -
XX administered by IV injection, having same tumoricidal activity as
XX Staphylococcal protein A without potential toxic reactions.
XX Disclosure; Fig 1; 74pp; English.
XX SED was isolated and purified from S.aureus. It can be used for treating
XX cancer, activating cytokine mediators and procoagulant systems,
XX augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be
XX administered intravenously, optionally with ibuprofen to attenuate toxic
XX reaction to SED. Synthetic polypeptides having structural homology to
XX Staphylococcal exotoxins are claimed, provided the homology includes
XX statistically significant sequence homology, alignment of Cysteine
XX residues and similar hydropathy profiles. See AAR13203-R13211
XX
SQ Sequence 228 AA;
Query Match 52.4%; Score 649; DB 2; Length 228;
Best Local Similarity 55.6%; Pred. No. 1.4e-56;
Matches 125; Conservative 31; Mismatches 69; Indels 0; Gaps 0;
QY 7 INEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGHPWYND 66
Db 2 VKEKELHKKSLSSTALNNMKHSYADKNPIIGENKSTGQFLENTLLYKKFFTDLINFED 61
QY 67 LLVDLGSKDATNKYKGVLDYGYVGYOCAGGTPNKTACMYGGVTLHDNNRLTEKKVP 126
Db 62 LLINFSKEMAQHFKSNVDVPIRYSINCYGGEIDRTACTYGGVTPHEGNLKERKKIP 121
QY 127 INLWIDGKQTTVPIDKVKTSKKEVTQVELDQARHYLHGKFGLYNSDSFGKVGQRLIVF 186
Db 122 INLWINGVQKEVSLDKVQTDKKNVTQVELDAQRRYLQKDLKLYNNDTLGGKIQRGKIEF 181
QY 187 HSSEGSTVSVDLFDAGQGYPTLLRIYRDNKNTINSENHIALYLY 231
Db 182 DSSDGSKVSVDLFDVKGFPEKQRIYSNDKTLSTELHLDIYLY 226
RESULT 43
ABP58459
XX ABP58459 standard; protein; 203 AA.
AC ABP58459;
XX 14-APR-2003 (first entry)
XX Staphylococcal enterotoxin D.
XX Superantigen; staphylococcal enterotoxin D; antibody; cancer; tumour;
XX cytostatic; vaccine.

XX OS Staphylococcus sp.
XX PN WC2003002143-A1.
XX PD 09-JAN-2003.
XX PF 19-JUN-2002; 2002WO-SE001188.
XX PR 28-JUN-2001; 2001SE-00002327.
XX PA (ACTI-) ACTIVE BIOTECH AB.
XX PI Forsberg G, Erlandsson E, Antonsson P, Walse B;
XX PN WPI; 2003-201467/19.
XX DR Conjugate for therapy, has bacterial superantigen with a region in T-cell
XX PT receptor and four regions to determine binding to class II major
XX PT histocompatibility complex, antibody to cancer associated cell surface
XX PT structure.
XX PS Example 3; Fig 3; 102pp; English.
XX CC The present sequence is the protein sequence of staphylococcal
XX CC enterotoxin D (SED). The invention provides novel conjugates (see
XX CC ABP58454) for human cancer therapy. These comprise an engineered
XX CC bacterial superantigen, such as novel SEA/E-120 (see ABP58455), and an
XX CC antibody moiety, such as tumour reactive antibody 5T4. Bacterial
XX CC enterotoxins such as SEA, SED, and SEH were used in the molecular
XX CC modelling of the engineered superantigens. The superantigens were
XX CC engineered to reduce seroreactivity whilst maintaining biological
XX CC activity and production levels. The novel conjugates were designed to
XX CC target and destroy cancer cells, including cancer of the lung, breast,
XX CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
XX CC Sequence 203 AA;
XX
Query Match 42.2%; Score 523; DB 6; Length 203;
Best Local Similarity 50.0%; Pred. No. 5.2e-44;
Matches 110; Conservative 23; Mismatches 67; Indels 20; Gaps 3;
QY 12 LRKSLQGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTGHVWINDLLVDL 71
DB 2 LHKSELSSTALNMKHSVADANPIGANKSTGQFLENTLLYKAPF-----LLINF 53
QY 72 GSKDATNKYKGVLDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTEKKVPINLWI 131
DB 54 NSAEQAQHFESKNDVVYAIRYAAAC-----RTACTYGGVTPHAGNALRKARKKIPINLWI 107
QY 132 DGKQTTVPIDKVTSKKVTQVQLDLOARHYLHGKFGLYNSDSFGKGVORGLIVFHSSEG 191
DB 108 IGQVKEVSLDKVTDKQNVTVQELDQAARYLOKDLKLYNA-----IORGKLEFDSAAA 161
QY 192 STVSYDLFDAGQGYPTLLIYRDNKTINSENLIHIALYLY 231
DB 162 SKVSYDLFDVAGDFPEKQLRIYSDNKTLSLHLDIYLY 201
RESULT 44
ID ABM70958
XX ABM70958 standard; protein; 250 AA.
XX AC ABM70958;
XX XX
XX 20-NOV-2003 (first entry)
XX DE Staphylococcus aureus protein #198.
XX KW Antibacterial; vaccine, gene therapy; infection; sepsis; diagnosis;
XX KW enzymatic assay; antibiotic target.
XX OS Staphylococcus aureus.

XX PN WO200294868-A2.
XX PD 28-NOV-2002.
XX PF 27-MAR-2002; 2002WO-IB002637.
XX PR 27-MAR-2001; 2001GB-00007661.
XX PA (CHIR-) CHIRON SPA.
XX PI Masignani V, Mora M, Scarselli M;
XX PN WPI; 2003-120786/11.
XX DR N-ESDB; ACF72519.
XX CC New Staphylococcus aureus protein, useful as a vaccine for treating or
XX PT preventing Staphylococcal infection, specifically an infection caused by
XX PT S. aureus, e.g. sepsis.
XX PS Claim 1; SEQ ID NO 396; 49pp; English.
XX CC The invention relates to novel genes and encoded proteins from
XX CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
XX CC nucleic acid encoding the protein, or an antibody to the protein, is
XX CC useful as a pharmaceutical, particularly as a vaccine for treating or
XX CC preventing infection due to Staphylococcus bacteria, specifically an
XX CC infection caused by S. aureus. The composition is particularly useful for
XX CC treating or preventing sepsis in a patient. The composition can also be
XX CC used for diagnostics. The protein is also used in an assay for enzymatic
XX CC studies and as a target for antibiotics. This sequence represents one of
XX CC the novel S. aureus proteins of the invention
XX CC Sequence 250 AA;
XX
Query Match 39.1%; Score 483.5; DB 6; Length 250;
Best Local Similarity 39.4%; Pred. No. 6.5e-40;
Matches 91; Conservative 47; Mismatches 88; Indels 5; Gaps 3;
QY 1 SEKSEENEDLRKSKELQGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
DB 23 TNSASALEYSDLHHKSKFDSKRISNAK-MSFINPTQL-ENKINDRLKDLHDFHMFVN 80
QY 61 HPWYNDDLVDLIGSKDATNKYKGVLDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 120
DB 81 DDWKKDFKVEFENEALSCKKFKINDIDIFAGNYGVGCHGGATNKTQCSYGGVTLSDNNKYD 140
QY 121 BEKKVPINLWIDGKQTTVPIDKVTSKKVTQVQLDLOARHYLHGKFGLYNSDSFGKQV 180
DB 141 DYKNIPCNLWIDGKQTTVPIDKVTSKKVTQVQLDLOARHYLHGKFGLYNSDSFGKQV 197
QY 181 RGLVHFSSSGSTVSYDLFDAGQGYPTLLIYRDNKTINSENLIHIALYLY 231
DB 198 KGYVYNDDEQNVDFYNLNGEYGREVLKMWADNKTINSDKLHLDIYLYF 248
RESULT 45
ID ABU10091
XX ABU10091 standard; protein; 82 AA.
XX AC ABU10091;
XX XX
XX 11-AUG-2003 (first entry)
XX DE Bacterial superantigen toxin SEB.
XX XX Superantigen-associated bacterial infection; superantigen toxin; vaccine;
XX KW SEB.
XX OS Unidentified.
XX PN US2003009015-A1.
XX XX

PD 09-JAN-2003.
 XX
 XX 25-JUN-1997; 97US-00882431.
 XX
 XX 25-JUN-1997; 97US-00882431.
 XX
 XX (ULRI/) ULRICH R G.
 PA (OLSO/) OLSON M A.
 PA (BAVA/) BAVARI S.
 XX
 XX ULRICH RG, Olson MA, Bavari S;
 XX
 XX WPI; 2003-401542/38.
 DR
 XX
 XX New superantigen toxin and/or DNA fragment with an altered binding of the
 PT encoded altered toxin to either MHC class II or T cell antigen receptor,
 PT useful for treating or ameliorating superantigen-associated bacterial
 PT infection.
 XX
 XX Example 1; Page 36; 50pp; English.
 PS
 XX The invention relates to an isolated and purified superantigen toxin
 CC and/or DNA fragment, which has been altered so that the binding of the
 CC encoded toxin to either major histocompatibility complex (MHC) class II
 CC or T cell antigen receptor is altered. The superantigen toxins, DNA
 CC fragments, and vaccines are useful for treating or ameliorating
 CC superantigen-associated bacterial infection. The DNA fragments are
 CC particularly useful for producing vaccine against superantigen toxin
 CC infections. The transformed host cells are useful for analysing the
 CC effectiveness of drugs and agents that affect the binding of
 CC superantigens to MHC class II or T-cell antigen receptors. The present
 CC sequence represents the amino acid sequence of the bacterial superantigen
 CC toxin SEE
 XX
 XX Sequence 82 AA;
 SQ

Query Match 36.9%; Score 457; DB 6; Length 82;
 Best Local Similarity 100.0%; Pred. No. 6.1e-38;
 Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 SDDQFLENTLLFKGFTGHPWYNDLLVGLSKDATNKYKGVLDYGYGYOCAGGTPN 102
 DB 1 SDDQFLENTLLFKGFTGHPWYNDLLVGLSKDATNKYKGVLDYGYGYOCAGGTPN 60
 QY 103 KTACMYGGVTLHDNNRLTEKK 124
 DB 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 46
 ABU62338
 ID ABU62338 standard; protein; 82 AA.
 XX
 XX AC ABU62338;
 XX
 XX DT 27-AUG-2003 (first entry)
 XX
 XX DE S. aureus enterotoxin E, SEE, MHC binding region.
 XX
 XX KW SEE; staphylococcal enterotoxin E; vaccine; superantigen toxin; MHC;
 XX KW superantigen-associated bacterial infection; bacterial infection;
 XX KW antibacterial.
 XX
 XX OS Staphylococcus aureus.
 XX
 XX PN US2003036644-A1.
 XX
 XX PD 20-FEB-2003.
 XX
 XX PF 26-NOV-2001; 2001US-00002784.
 XX
 XX PR 25-JUN-1997; 97US-00882431.
 XX PR 01-SEP-1996; 98US-00144776.
 PR

XX (ULRI/) ULRICH R G.
 XX Ulrich RG;
 XX WPI; 2003-492125/46.
 XX
 XX New superantigen toxin DNA fragment, useful for preparing a composition
 PT for treating or preventing bacterial infection.
 XX
 XX Disclosure; Fig 3; 68pp; English.
 XX
 XX The invention relates to an isolated and purified superantigen toxin DNA
 CC fragment is altered so that binding of the encoded altered toxin to
 CC either the MHC class II or T cell antigen receptor is altered. Also
 CC included are a recombinant DNA construct (comprising a vector and an
 CC isolated and purified altered superantigen toxin DNA fragment), a host
 CC cell transformed with the recombinant DNA construct, producing altered
 CC superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
 CC superantigen toxin peptide, diagnosing superantigen-associated bacterial
 CC infection, a vaccine (comprising an altered superantigen toxin for
 CC producing antigenic and immunogenic response resulting in the protection
 CC of a mammal against superantigen-associated bacterial infection),
 CC treating/ameliorating a superantigen-associated bacterial infection, an
 CC antiserum isolated from individuals immunised with one or more altered
 CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-
 CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
 CC SEB, SEC) and streptococcal pyrogenic enterotoxin a and b (SPEa and
 CC SEB). The superantigen toxin DNA fragment is useful for preparing a
 CC composition for treating or preventing bacterial infection. The present
 CC sequence represents the S. aureus enterotoxin E, SEE, MHC binding region
 XX
 XX Sequence 82 AA;
 SQ

Query Match 36.9%; Score 457; DB 7; Length 82;
 Best Local Similarity 100.0%; Pred. No. 6.1e-38;
 Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 SDDQFLENTLLFKGFTGHPWYNDLLVGLSKDATNKYKGVLDYGYGYOCAGGTPN 102
 DB 1 SDDQFLENTLLFKGFTGHPWYNDLLVGLSKDATNKYKGVLDYGYGYOCAGGTPN 60
 QY 103 KTACMYGGVTLHDNNRLTEKK 124
 DB 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 47
 ABU10089
 ID ABU10089 standard; protein; 82 AA.
 XX
 XX AC ABU10089;
 XX
 XX DT 11-AUG-2003 (first entry)
 XX
 XX DE Bacterial superantigen toxin SEA.
 XX
 XX KW Superantigen-associated bacterial infection; superantigen toxin; vaccine;
 XX KW SEA.
 XX
 XX OS Unidentified.
 XX
 XX PN US2003009015-A1.
 XX
 XX PD 09-JAN-2003.
 XX
 XX PF 25-JUN-1997; 97US-00882431.
 XX
 XX PR 25-JUN-1997; 97US-00882431.
 XX
 XX PA (ULRI/) ULRICH R G.
 XX PA (OLSO/) OLSON M A.
 XX PA (BAVA/) BAVARI S.
 PA

```

XX PI Ulrich RG, Olson MA, Bavari S;
XX DR WPI; 2003-401542/38.
XX CC
XX CC New superantigen toxin and/or DNA fragment with an altered binding of the
XX PT encoded altered toxin to either MHC class II or T cell antigen receptor,
XX PT useful for treating or ameliorating superantigen-associated bacterial
XX PT infection.
XX CC
XX PS Example 1; Page 35; 50pp; English.
XX CC
XX CC The invention relates to an isolated and purified superantigen toxin
XX CC and/or DNA fragment, which has been altered so that the binding of the
XX CC encoded toxin to either major histocompatibility complex (MHC) class II
XX CC or T cell antigen receptor is altered. The superantigen toxins, DNA
XX CC fragments, and vaccines are useful for treating or ameliorating
XX CC superantigen-associated bacterial infection. The DNA fragments are
XX CC particularly useful for producing vaccine against superantigen toxin
XX CC infections. The transformed host cells are useful for analysing the
XX CC effectiveness of drugs and agents that affect the binding of
XX CC superantigens to MHC class II or T-cell antigen receptors. The present
XX CC sequence represents the amino acid sequence of the bacterial superantigen
XX CC toxin SEA
XX CC
XX SQ Sequence 82 AA;
XX CC
XX CC Query Match 32.2%; Score 399; DB 6; Length 82;
XX CC Best Local Similarity 86.6%; Pred. No. 4.1e-32;
XX CC Matches 71; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
XX CC
XX QY 43 SDQFLNTLLFKGFFTGHPWYNDLLVLDLGSKDATNKYKGVLDLYGAYYGQCAGGTPN 102
XX DB 1 SHDQFLQHTILFKGFFTDHSHWYNDLLVDPDSKDIDVKYKGVLDLYGAYYGQCAGGTPN 60
XX CC
XX QY 103 KTACMYGGVTLHDNNRLTEKK 124
XX DB 61 KTACMYGGVTLHDNNRLTEKK 82
XX CC
XX RESULT 48
XX ABU62336
XX ID ABU62336 standard; protein; 82 AA.
XX AC
XX AC ABU62336;
XX DT
XX DT 27-AUG-2003 (first entry)
XX DE
XX DE S. aureus enterotoxin A, SEA, MHC binding region.
XX KW SEA; staphylococcal enterotoxin A; vaccine; superantigen toxin; MHC;
XX KW superantigen-associated bacterial infection; bacterial infection;
XX KW antibacterial.
XX OS
XX OS Staphylococcus aureus.
XX PH
XX PH US2003036644-A1.
XX FT
XX FT 20-FEB-2003.
XX PN
XX PN 26-NOV-2001; 2001US-00002784.
XX PD
XX PD 25-JUN-1997; 97US-00882431.
XX PF
XX PF 01-SEP-1996; 98US-00144776.
XX PR
XX PR (ULRI/) ULRICH R G.
XX PA
XX PA Ulrich RG;
XX PI
XX PI WPI; 2003-492125/45.
XX DR
XX DR New superantigen toxin DNA fragment, useful for preparing a composition
XX PT for treating or preventing bacterial infection.

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XX PS Disclosure; Fig 3; 68pp; English.
XX CC
XX CC The invention relates to an isolated and purified superantigen toxin DNA
XX CC fragment is altered so that binding of the encoded altered toxin to
XX CC either the MHC class II or T cell antigen receptor is altered. Also
XX CC included are a recombinant DNA construct (comprising a vector and an
XX CC isolated and purified altered superantigen toxin DNA fragment), a host
XX CC cell transformed with the recombinant DNA construct, producing altered
XX CC superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
XX CC superantigen toxin peptide, diagnosing superantigen-associated bacterial
XX CC infection, a vaccine (comprising an altered superantigen toxin for
XX CC producing antigenic and immunogenic response resulting in the protection
XX CC of a mammal against superantigen-associated bacterial infection),
XX CC treating/ameliorating a superantigen-associated bacterial infection, an
XX CC antiserum isolated from individuals immunised with one or more altered
XX CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-
XX CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
XX CC SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and
XX CC SPEb). The superantigen toxin DNA fragment is useful for preparing a
XX CC composition for treating or preventing bacterial infection. The present
XX CC sequence represents the S. aureus enterotoxin A, SEA, MHC binding region
XX CC
XX SQ Sequence 82 AA;
XX CC
XX CC Query Match 32.2%; Score 399; DB 7; Length 82;
XX CC Best Local Similarity 86.6%; Pred. No. 4.1e-32;
XX CC Matches 71; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
XX CC
XX QY 43 SDDQFLNTLLFKGFFTGHPWYNDLLVLDLGSKDATNKYKGVLDLYGAYYGQCAGGTPN 102
XX DB 1 SHDQFLQHTILFKGFFTDHSHWYNDLLVDPDSKDIDVKYKGVLDLYGAYYGQCAGGTPN 60
XX CC
XX QY 103 KTACMYGGVTLHDNNRLTEKK 124
XX DB 61 KTACMYGGVTLHDNNRLTEKK 82
XX CC
XX RESULT 49
XX AAW24299
XX ID AAW24299 standard; protein; 91 AA.
XX AC
XX AC AAW24299;
XX DT
XX DT 14-APR-1998 (first entry)
XX DE
XX DE Staphylococcus aureus Gene #5 polypeptide sequence 2.
XX KW Staphylococcus aureus WCUH 29; antagonist; antibacterial; immunogen;
XX KW vaccine; disease; protection; isolation.
XX OS
XX OS Staphylococcus aureus.
XX PH
XX PH Key Location/Qualifiers
XX FT
XX FT Misc-difference 29 /note= "Unspecified amino acid"
XX PN
XX PN WO9731114-A2.
XX PD
XX PD 28-AUG-1997.
XX PF
XX PF 25-FEB-1997; 97WO-GB000524.
XX XX
XX XX 26-FEB-1996; 96GB-00004045.
XX PR
XX PR (SMIX ) SMITHKLINE BEECHAM PLC.
XX PA
XX PA Burnham MKR, Hodgson JE;
XX PI
XX PI WPI; 1997-435166/40.
XX DR
XX DR N-PSDB; AAV01865.
XX XX
XX XX New Staphylococcus aureus polynucleotide and polypeptide(s) - for

```

PT isolating antagonist of the polypeptide(s) useful as anti-bacterials.
 XX Claim 11; Page 33; 117pp; English.
 XX
 CC The present sequence represents a novel polypeptide, which is optionally
 CC expressed in NCIMB 40771. The polypeptide, and polynucleotide encoding
 CC it, are derived from *Staphylococcus aureus*. Cells expressing ligands
 CC binding the polypeptide can be used to isolated candidate compounds that
 CC bind and inhibit the activity of the polypeptide. Such compounds can be
 CC used as anti-bacterial compounds. The polypeptide may also be used as an
 CC immunogen to vaccinate an animal for protection against *Staphylococcus*
 CC *aureus* caused disease
 XX
 SQ Sequence 91 AA;
 Query Match 29.9%; Score 370; DB 2; Length 91;
 Best Local Similarity 76.9%; Pred. No. 3.8e-29;
 Matches 70; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
 QY 107 MYGGVTLHNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTQVQLDQARHYLHGK 166
 Db 1 MYGGVTLHNNRLTEKKVPINLWIDGKXNTVPLETVKTNKNTVQVQLDQARRYLQEK 60
 QY 167 FGLYNSDFGGKVGQGLIVFPHSSSGSTVSYD 197
 Db 61 YNLVNSDFGKVGQGLIVFHTSTPVSVDY 91
 RESULT 50
 ID ABP58460
 AC ABP58460 standard; protein; 217 AA.
 XX
 DT 14-APR-2003 (first entry)
 DE Staphylococcal enterotoxin H.
 KW Superantigen; staphylococcal enterotoxin H; antibody; cancer; tumour;
 KW cytostatic; vaccine.
 XX
 OS Staphylococcus sp.
 XX
 PN WO200302143-A1.
 XX
 PD 09-JAN-2003.
 XX
 PF 19-JUN-2002; 2002WO-SE001189.
 XX
 PR 28-JUN-2001; 2001SE-00002327.
 XX
 PA (ACTI-) ACTIVE BIOTECH AB.
 XX
 PI Forsberg G, Erlandsson E, Antonsson P, Walse B;
 XX
 DR WPI; 2003-201467/19.
 XX
 CC Conjugate for therapy, has bacterial superantigen with a region in T-cell
 CC receptor and four regions to determine binding to class II major
 CC histocompatibility complex, antibody to cancer associated cell surface
 CC structure.
 XX
 PS Example 3; Fig 3; 102pp; English.
 XX
 CC The present sequence is the protein sequence of staphylococcal
 CC enterotoxin D (SED). The invention provides novel conjugates (see
 CC ABP58454) for human cancer therapy. These comprise an engineered
 CC bacterial superantigen, such as novel SEA/E-120 (see ABP58455), and an
 CC antibody moiety, such as tumour reactive antibody 574. Bacterial
 CC enterotoxins such as SEA, SED, SEB and SEH were used in the molecular
 CC modelling of the engineered superantigens. The superantigens were
 CC engineered to reduce seroreactivity whilst maintaining biological
 CC activity and production levels. The novel conjugates were designed to

CC target and destroy cancer cells, including cancer of the lung, breast,
 CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
 XX
 SQ Sequence 217 AA;
 Query Match 29.1%; Score 360; DB 6; Length 217;
 Best Local Similarity 37.5%; Pred. No. 1.3e-27;
 Matches 84; Conservative 45; Mismatches 83; Indels 12; Gaps 7;
 QY 10 KDLRKSELOQPALGNLKOIYYNEKAITENKESDDQFLENTLFFKGGFTGHPWYNDLLV 69
 Db 1 EDLHDKSELTDIALAN--AYGQYHNPFIKENIKSDEISGEKDLIFRN--QGDSCGNDLRV 55
 QY 70 DLGSDATNKYKGVKVDLYGAYGVQCAGGTPNKTACWYGGVTLHNNRLTEKKVPINL 129
 Db 56 KFAADLAQKFNKNDIYGASFYKKEKISENISECLYGGTIL--NSEKLAQERVIGANV 114
 QY 130 WIDGKQTTVPIDKVKTSKEVTQVQLDQARHYLHGKFGLYNSDFGKVGQGLIVFPHSS 189
 Db 115 WVDGKQKTEL--INTNKNVTLOELDIKIRKILSDKYKIYKDS--EISKGLIEPDMK 169
 QY 190 ESGTSVSYDLFAQGVQPTLRLIYRDKNKTINSENL--HIALVLYT 232
 Db 170 TPRDYSFDIYDLKGENYEDIKIYEDNKTLSKSDIISHIDVNLVLT 213
 RESULT 51
 ID ABP29357
 AC ABP29357 standard; protein; 259 AA.
 XX
 DT 02-JUL-2002 (first entry)
 DE Streptococcus polypeptide SEQ ID NO 7890.
 KW Streptococcus; GAS; group B streptococcus; Streptococcus agalactiae;
 KW group A streptococcus; Streptococcus pyogenes; antibacterial;
 KW antiinflammatory; infection; vaccine; meningitis; gene therapy.
 XX
 OS Streptococcus pyogenes.
 XX
 PN WO200234771-A2.
 XX
 PD 02-MAY-2002.
 XX
 PF 29-OCT-2001; 2001WO-GB004789.
 XX
 PR 27-OCT-2000; 2000GB-00026333.
 PR 24-NOV-2000; 2000GB-00028727.
 PR 07-MAR-2001; 2001GB-00005640.
 XX
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Telford J, Masignani V, Margarit Y Rosi, Grandi G, Fraser C;
 PI Tettelin H;
 XX
 DR WPI; 2002-352536/38.
 DR N-PSDB; ABN69988.
 XX
 PT New Streptococcus protein for the treatment or prevention of infection or
 PT disease caused by Streptococcus bacteria, such as meningitis, and for
 PT detecting a compound that binds to the protein.
 XX
 CC Claim 1; Page 3920; 4525pp; English.
 XX
 CC The invention relates to a protein (ABP25413-ABP30895) from group B
 CC streptococcus/GAS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (SI), given in
 CC the specification. The proteins have antibacterial and antiinflammatory
 CC activity. (I), nucleic acids encoding (I), ABN6044-ABN71526 and
 CC antibodies that bind (I) are used in the manufacture of medicaments for

CC	Typically, the modification involves deletions within the disulfide loop
CC	region of SEC (see AA06261). The modified toxins retain useful
CC	biological properties, such as the ability to induce cytokine production,
CC	but have substantially reduced toxicity compared to the corresponding
CC	unmodified native toxin. Emetic response inducing activity and fever
CC	inducing activity are typically decreased by at least about 100-fold,
CC	while LD50 (in Dutch belted rabbits) is at least 100-fold higher than the
CC	native toxin
XX	
XX	
SQ	Sequence 239 AA;
	Query Match 25.1%; Score 310.5; DB 2; Length 239;
	Best Local Similarity 35.0%; Pred. No. 1.4e-22;
	Matches 82; Conservative 46; Mismatches 87; Indels 19; Gaps 9;
QY	11 DLRKSELGQTALGNLKHQIYYVNEKAITENK-BSDQOFTENTLLFKGPTGHFVNDLLV 69
Db	: : : : : : : : : : : : : :
QY	10 DLHKSSEFTGT-MGNMK--LYLDHYVSATPKVKSVDKFLAHLIDININDKLNNYDKVKT 66
Db	: : : : : : : : : : : : :
QY	70 DLGSKDATNKKYGGKVPLYGAYTYGQC-----AGTPTNKTCMVGGYTLHDNRLTBE 122
Db	67 ELLNEDLANKYDEBWDVYGSVNYVCYPSSKNVGVKTSCKTKCYGGITKEGHNHFDNG 126
QY	123 --KKVPNLMTDGGQTTPVTDKVTYSKETVQELDLQARHVILHGFGVLNSDSFGVKVQ 180
Db	127 NLQWLVLRV-ENKRVTSIFE-VQTDKKSVTAGELDIKARNFLINKNLIYEFS--SPVE 182
QY	181 RGLIVFHSSSGSTSVSYDLFDAQGYPD--TLRLRYRDNTKIINSNLHIALYLT 232
Db	183 TGYIKFTESNGTFWYDMMPAPGKFQDSKYLMIYKDNPQWDSKSVKIEVHLT 236
	: : : : : : : : : : : : :

[illegible]

XX The invention relates to a modified pyrogenic toxin derived from a native
 CC disulphide loop-containing pyrogenic toxin where the modified toxin
 CC comprises a disulphide loop having no more than 10 amino acids. The
 CC modified toxin has a fever-inducing activity or an emetic response-
 CC inducing activity decreased by about 100-fold in comparison to a native
 CC toxin. The modified pyrogenic toxin, that is a staphylococcal
 CC enterotoxin, is useful for non-specifically enhancing an immune function
 CC and for vaccination against diseases such as toxic shock syndrome and
 CC food poisoning. This sequence represents the staphylococcal enterotoxin,
 CC SEC3-FRI99

XX SQ Sequence 240 AA;
 Query Match 25.1%; Score 310.5; DB 6; Length 240;
 Best Local Similarity 35.0%; Pred. No. 1.4e-22;
 Matches 82; Conservative 46; Mismatches 87; Indels 19; Gaps 9;
 QY 11 DLKXSELOQTALGNLKIYYNEKAITENK-ESDDOFLNTLLFKGFFTHPWYNDLLV 69
 Db 10 DLKXSEFTGT-MGNMK--YLYDDHYVSATKVSVDKFLAHLIYNINDKLNNDYDKVT 66
 QY 70 DLGSKDATNKYKGVLDLYGAYGYQC-----AGGTPNKTCMYGGVTLHDNNRLTEE 122
 Db 67 ELLNEDLANKYKDEVVDVYGSVYVNCYFSSKDNVGVTSKTCMYGGITKHEGNHFDNG 126
 QY 123 --KKVPINLWIDGKQTTVPIDKVKTSKEVTQVQLDQARHYLHGKFLYNSDSFGGKVQ 180
 Db 127 NLQNVLRVY-ENKRNITISFE-VQTDKSVTAQELDIKARNFLINKNLYEFNS--SPYE 182
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPD--TLIRYRDNKTINSENHIALYLYT 232
 Db 183 TGYIKFIESNGNTFWYDMMPAGPKFDQSKYLMYTKNMYDSKSVKIEVHLTT 236

RESULT 54
 AAY06253
 ID AAY06253 standard; protein; 239 AA.
 AC AAY06253;
 XX
 XX 23-AUG-1999 (first entry)
 DE Staphylococcal group C enterotoxin SEC3-FRI913.
 XX Enterotoxin; SEC3-FRI913; toxin; disulphide loop; protein engineering.
 KW
 XX Staphylococcus aureus.
 OS
 XX
 XX Key Location/Qualifiers
 FH Disulfide-bond 93..110
 FT
 XX WO9927889-A2.
 XX 10-JUN-1999.
 XX 01-DEC-1998; 98WO-US025107.
 XX 02-DEC-1997; 97US-0067357P.
 XX (IDAH-) IDAHO RES FOUND INC.
 XX Bohach GI;
 XX WPI; 1999-358008/30.
 DR
 XX Non-toxic modified staphylococcal enterotoxins.
 PT
 XX Disclosure; Page 17; 25pp; English.
 PS
 XX This protein represents the Staphylococcus aureus type C enterotoxin SEC3
 CC -FRI913. The invention relates to pyrogenic toxins, such as
 CC staphylococcal enterotoxins, modified in the disulfide loop region.

CC Typically, the modification involves deletions within the disulfide loop
 CC region of SEC (see AAY06261). The modified toxins retain useful
 CC biological properties, such as the ability to induce cytokine production,
 CC but have substantially reduced toxicity compared to the corresponding
 CC unmodified native toxin. Emetic response inducing activity and fever
 CC inducing activity are typically decreased by at least about 100-fold,
 CC while LD50 (in Dutch Belted rabbits) is at least 100-fold higher than the
 CC native toxin
 XX
 SQ Sequence 239 AA;

Query Match 24.7%; Score 305.5; DB 2; Length 239;
 Best Local Similarity 33.8%; Pred. No. 4.5e-22;
 Matches 79; Conservative 47; Mismatches 89; Indels 19; Gaps 9;
 QY 11 DLKXSELOQTALGNLKIYYNEKAITENK-ESDDOFLNTLLFKGFFTHPWYNDLLV 69
 Db 10 DLKXSEFTGT-MGNMK--YLYDDHYVSATKVSVDKFLAHLIYNISDKLKNYDKVT 66
 QY 70 DLGSKDATNKYKGVLDLYGAYGYQC-----AGGTPNKTCMYGGVTLHDNNRLTEE 122
 Db 67 ELLNEDLANKYKDEVVDVYGSVYVNCYFSSKDNVGVTSKTCMYGGITKHEGNHFDNG 126
 QY 123 --KKVPINLWIDGKQTTVPIDKVKTSKEVTQVQLDQARHYLHGKFLYNSDSFGGKVQ 180
 Db 127 NLQNVLRVY-ENKRNITISFE-VQTDKSVTAQELDIKARNFLINKNLYEFNS--SPYE 182
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPD--TLIRYRDNKTINSENHIALYLYT 232
 Db 183 TGYIKFIENNGNTFQDMMPAGPKFDQSKYLMYNDNKTVDKSVKIEVHLTT 236

RESULT 55
 ABG71369
 ID ABG71369 standard; protein; 240 AA.
 AC ABG71369;
 XX
 XX 29-JAN-2003 (first entry)
 DE Staphylococcal enterotoxin SEC3-FRI913.
 XX Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
 KW emetic response-inducing activity; staphylococcal enterotoxin;
 KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
 KW SEC3-FRI913.
 XX
 XX Staphylococcus aureus.
 OS
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 240 /label= unknown
 FT
 XX WO200283169-A1.
 XX 24-OCT-2002.
 XX 11-APR-2002; 2002WO-US011619.
 XX 13-APR-2001; 2001US-0283720P.
 XX (IDAH-) IDAHO RES FOUND INC.
 XX Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
 XX WPI; 2003-058608/05.
 DR
 XX New modified staphylococcal enterotoxin derived from a native disulfide
 PT loop-containing pyrogenic toxin, useful for non-specifically enhancing an
 PT immune function and as a vaccine against toxic shock syndrome or food
 PT poisoning.
 PS Disclosure; Fig 15; 67pp; English.

XX The invention relates to a modified pyrogenic toxin derived from a native
 CC disulphide loop-containing pyrogenic toxin where the modified toxin
 CC comprises a disulphide loop having no more than 10 amino acids. The
 CC modified toxin has a fever-inducing activity or an emetic response-
 CC inducing activity decreased by about 100-fold in comparison to a native
 CC toxin. The modified pyrogenic toxin, that is a staphylococcal
 CC enterotoxin, is useful for non-specifically enhancing an immune function
 CC and for vaccination against diseases such as toxic shock syndrome and
 CC food poisoning. This sequence represents the staphylococcal enterotoxin,
 CC SEC3-FR1913
 XX
 SQ Sequence 240 AA;

Query Match 24.7%; Score 305.5; DB 6; Length 240;
 Best Local Similarity 33.8%; Pred. No. 4.6e-22;
 Matches 79; Conservative 47; Mismatches 89; Indels 19; Gaps 9;

QY 11 DLKKSSELTGALGNLQIYYNEKAITENK-ESDQFLENTLLFKGFTGHPWYNDLLV 69
 DB 10 DLKKSSEFTGT-MGNMK--YLYDDHYVSATKVSVDKFLAHLDIYINISDKLXNDYDKVKT 66
 QY 70 DLGSKDATNKYKGVLDLYGAYGYQC-----AGSTPNKTACMYGGVTLHDNNRLTEE 122
 DB 67 ELLNEDLAKYKDEVVDVYGSNYVNCYFSSKDNVGVKVTGCTMYGGITKEGHNFDNG 126
 QY 123 --KKVPINLWIDGKQITVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 DB 127 NLQNLVLRVY-ENKRNITISFE-VQTDKKSVTAEQELDIKARNFLINKKNLYEFS--SPYE 182
 QY 181 RGLIVFHSSSGSVSYDLFDAQGYPD--TLRIYRDNKTINSENHLIALYLT 232
 DB 183 TGYIKFIENNGNTFYDMPAPGDKFDQSKYLMYNDNKTVDKSKVIEVHLTT 236

RESULT 56
 AAY06256
 ID AAY06256 standard; protein; 239 AA.
 AC AAY06256;
 XX
 DT 23-AUG-1999 (first entry)
 XX
 DE Staphylococcal group C enterotoxin SEC-4446.
 XX
 KW Enterotoxin; SEC-4446; toxin; disulfide loop; protein engineering.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 93..110
 XX
 PN WO9927889-A2.
 XX
 PD 10-JUN-1999.
 XX
 PF 01-DEC-1998; 98WO-US025107.
 XX
 PR 02-DEC-1997; 97US-0067357P.
 XX
 PA (IDAH-) IDAHO RES FOUND INC.
 XX
 PI Bohach GI;
 XX
 DR WPI; 1999-358008/30.
 XX
 PT Non-toxic modified staphylococcal enterotoxins.
 XX
 PS Disclosure; Page 17; 25pp; English.
 XX
 CC This protein represents the Staphylococcus aureus type C enterotoxin SEC-
 CC 4446. The invention relates to pyrogenic toxins, such as staphylococcal
 CC enterotoxins, modified in the disulfide loop region. Typically, the

CC modification involves deletions within the disulfide loop region of SEC
 CC (see AAY06261). The modified toxins retain useful biological properties,
 CC such as the ability to induce cytokine production, but have substantially
 CC reduced toxicity compared to the corresponding unmodified native toxin.
 CC Emetic response inducing activity and fever inducing activity are
 CC typically decreased by at least about 100-fold, while LD50 (in Dutch
 CC Belted rabbits) is at least 100-fold higher than the native toxin
 XX
 SQ Sequence 239 AA;

Query Match 24.6%; Score 304.5; DB 2; Length 239;
 Best Local Similarity 33.8%; Pred. No. 5.7e-22;
 Matches 79; Conservative 46; Mismatches 90; Indels 19; Gaps 9;

QY 11 DLKKSSELTGALGNLQIYYNEKAITENK-ESDQFLENTLLFKGFTGHPWYNDLLV 69
 DB 10 DLKKSSEFTGT-MGNMK--YLYDDHYVSATKVSVDKFLAHLDIYINISDKLXNDYDKVKT 66
 QY 70 DLGSKDATNKYKGVLDLYGAYGYQC-----AGSTPNKTACMYGGVTLHDNNRLTEE 122
 DB 67 ELLNEDLAKYKDEVVDVYGSNYVNCYFSSKDNVGVKVTGCTMYGGITKEGHNFDNG 126
 QY 123 --KKVPINLWIDGKQITVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 DB 127 NLQNLVLRVY-ENKRNITISFE-VQTDKKSVTAEQELDIKARNFLINKKNLYEFS--SPYE 182
 QY 181 RGLIVFHSSSGSVSYDLFDAQGYPD--TLRIYRDNKTINSENHLIALYLT 232
 DB 183 TGYIKFIENNGNTFYDMPAPGDKFDQSKYLMYNDNKTVDKSKVIEVHLTT 236

RESULT 57
 ABG71372
 ID ABG71372 standard; protein; 240 AA.
 AC ABG71372;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Staphylococcal enterotoxin SEC-4446.
 XX
 KW Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
 KW emetic response-inducing activity; staphylococcal enterotoxin;
 KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
 KW SEC-4446.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 240
 XX /label= unknown
 FT
 PN WO200283169-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 11-APR-2002; 2002WO-US011619.
 XX
 PR 13-APR-2001; 2001US-0283720P.
 XX
 PA (IDAH-) IDAHO RES FOUND INC.
 XX
 PI Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
 XX
 DR WPI; 2003-058608/05.
 XX
 PT New modified staphylococcal enterotoxin derived from a native disulfide
 PT loop-containing pyrogenic toxin, useful for non-specifically enhancing an
 PT immune function and as a vaccine against toxic shock syndrome or food
 PT poisoning.
 XX
 PS Disclosure; Fig 15; 67pp; English.
 XX

Db 260 YLTT 263

RESULT S9
AAW64647
ID AAW64647 standard; peptide; 239 AA.
AC AAW64647;
DT 23-OCT-1998 (first entry)
XX Synthetic SEB protein fragment.
DE Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KW therapeutic; vaccine; food poisoning.
XX
OS Synthetic.
OS Staphylococcus aureus.
PN WO9829444-A1.
XX
PD 09-JUL-1998.
XX
PF 30-DEC-1997; 97WO-IL000438.
XX
PR 30-DEC-1996; 96IL-00119938.
XX
PA (YISS) YISSUM RES & DEV CO.
XX
PI Kaempfer R, Arad G;
XX
DR WPI; 1998-388042/33.
XX
XX New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s).
XX
PS Example 8; Page 41; 68pp; English.
XX
AAW64636-M64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by
CC PET or by a mixture of PETs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by *il-2*, *il-6* or *il-1*
CC beta genes. The peptides may be used to prepare therapeutics or vaccines
CC for the treatment of prophylaxis of toxin-mediated activation of T cells
CC and eliciting protective immunity against toxic shock induced by PETs.
CC They can also be used for the treatment of harmful effects (especially
CC food poisoning) and toxic shock caused by PET. Antiserum to the peptides
CC can also be used for alleviating toxic shock induced by PET
XX
SQ Sequence 239 AA;

Query Match 24.5%; Score 303.5; DB 2; Length 239;
Best Local Similarity 34.6%; Pred. No. 7.2e-22;
Matches 84; Conservative 44; Mismatches 96; Indels 19; Gaps 8;

QY 2 EKSEINEKDLRKXSELOGTALGNLKOIYYNEKAITENKESDDOFLNTLLPKGFTTGH 61
Db 1 ESQDPKPEDEHLKSKFTG-LMENKRVLYDDNHVSAL-NVKSIDQFLYFDLIYSIKDTKL 58
QY 62 PWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTKACMYGGV 111
Db 59 GNYDNRVFEFNKDLADKYKVDVFGANYYYQCVFSKKTNDINSHQTDKRTKTCMYGGV 118
QY 112 TLHDNRLTEKKYVPINLWDGKQTVPIDKVTSKKEVTVOELDLQARHYLHGKFLYN 171
Db 119 TEHNGNQLDKVRSITRVFEDCK-NLLSFD-VQTNKKKVTQAQELDLTRHYLVKSKLYE 176
QY 172 SDSFGGKVGQRLIVFHSESGTGVSYDLFDAQGVDP--TLRLIYRNKNTINSENHLIALY 229

Db 177 FNN--SPYETGYIKFIENENS-FWYDMFAPGDKFDQSKYLMAQYNDNKKVDSKVKIEVY 233

QY 230 LYT 232
Db 234 LTT 236

RESULT 60
AAB67341
ID AAB67341 standard; peptide; 239 AA.
XX
AC AAB67341;
XX
DT 23-APR-2001 (first entry)
XX Staphylococcus aureus enterotoxin B protein.
DE Tumour; cancer; immune; enterotoxin.
XX
OS Staphylococcus aureus.
PN US6180097-B1.
XX
PD 30-JAN-2001.
XX
PF 30-OCT-1998; 98US-00183437.
XX
PR 03-OCT-1989; 89US-00416530.
PR 17-JAN-1990; 90US-00466577.
PR 17-JAN-1991; 91WO-US000342.
PR 01-JUN-1992; 92US-00691718.
PR 02-MAR-1993; 93US-00025144.
PR 31-JAN-1994; 94US-00189424.
PR 19-JUN-1995; 95US-00491746.
XX
XX (TERM/) Terman D S.
XX
PI Terman DS;
XX
DR WPI; 2001-158657/16.
XX
XX Tumor cell capable of stimulating antitumor immune reactivity in vitro or
PT in vivo comprises exogenous nucleic acids encoding a superantigen and a
PT costimulatory molecule.
XX
PS Disclosure; Fig 2; 16pp; English.
XX
XX The present invention relates to a tumour cell capable of stimulating
CC antitumor immune reactivity in vitro or in vivo contains and expresses an
CC exogenous nucleic acid molecule encoding a superantigen or its active
CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
CC molecule that activates T cells in conjunction with an antigenic
CC stimulus. The invention may be used for cancer therapy by stimulating an
CC anticancer immune response in vivo or ex vivo
XX
SQ Sequence 239 AA;

Query Match 24.5%; Score 303.5; DB 4; Length 239;
Best Local Similarity 34.6%; Pred. No. 7.2e-22;
Matches 84; Conservative 44; Mismatches 96; Indels 19; Gaps 8;

QY 2 EKSEINEKDLRKXSELOGTALGNLKOIYYNEKAITENKESDDOFLNTLLPKGFTTGH 61
Db 1 ESQDPKPEDEHLKSKFTG-LMENKRVLYDDNHVSAL-NVKSIDQFLYFDLIYSIKDTKL 58
QY 62 PWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTKACMYGGV 111
Db 59 GNYDNRVFEFNKDLADKYKVDVFGANYYYQCVFSKKTNDINSHQTDKRTKTCMYGGV 118
QY 112 TLHDNRLTEKKYVPINLWDGKQTVPIDKVTSKKEVTVOELDLQARHYLHGKFLYN 171
Db 119 TEHNGNQLDKVRSITRVFEDCK-NLLSFD-VQTNKKKVTQAQELDLTRHYLVKSKLYE 176

QY 172 SDSFGKVGORGLIVPHSSEGSTVSYDLFDAQGYPD--TLRIYRDNKTINSENHLIALY 229
DB 177 FNN--SPYETGYIKFIENENS-FWYDMMPAPGDKPDQSKYLLMYNDNKNVDSKDVKIEVY 233
QY 230 LYT 232
DB 234 LTT 236

RESULT 61
AAW06737
ID AAW06737 standard; protein; 255 AA.
XX
AC AAW06737;
XX
DT 08-MAR-1997 (first entry)
XX
DE Staphylococcus enterotoxin B.
XX
KW Enterotoxin B; superantigen; antigen; cytokine; chemokine; T cell;
KW lymphocyte; monocyte; natural killer cell; gene therapy; cancer; vaccine;
KW adjuvant.
XX
OS Staphylococcus sp.
XX
FH Key Location/Qualifiers
FT Peptide 1..15
FT /label= Sig_peptide
XX
PN W09636366-Al.
XX
PD 21-NOV-1996.
XX
PF 20-MAY-1996; 96WO-US007432.
XX
PR 18-MAY-1995; 95US-00446918.
XX
PR 29-DEC-1995; 95US-00580806.
XX
PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
XX
PI Dow SW, Elmslie RE, Potter TR;
XX
DR WPI; 1997-011857/01.
DR N-PSDB; AAT45698.
XX
PT Recombinant molecule encoding super:antigen and opt. cytokine or
PT chemokine - controls activity of effector cells (T cells, monocytes,
PT natural killer cells), used for gene therapy of cancer.
XX
PS Example 1; Page 96-97; 131pp; English.

XX
CC A cDNA clone (AAT45698) codes for staphylococcal enterotoxin B (AAW06737)
CC superantigen. Nucleic acids encoding superantigens (see also AAW06738-
CC 39), esp. truncated forms of the superantigen lacking the leader peptide,
CC can be utilised in the gene therapy of cancer, infectious diseases and
CC immunological disorders. The nucleic acid, optionally in combination with
CC cytokine or chemokine nucleic acids, is delivered to an animal using e.g.
CC liposomes. It acts by controlling the activity of effector cells, such as
CC T-cells, macrophages, monocytes and/or natural killer cells. Localised
CC prodn. of an effective but non-toxic amount of encoded proteins allows
CC safe treatment of the animal
XX
SQ Sequence 255 AA;

Query Match 24.5%; Score 303.5; DB 2; Length 255;
Best Local Similarity 34.6%; Pred. No. 7.9e-22;
Matches 84; Conservative 44; Mismatches 96; Indels 19; Gaps 8;

QY 2 EKSEINEKDLKKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTGH 61
DB 17 ESQDPKPPDELKSKSKFTG-LMENMKVLYDDNHVSAL-NVKSIDQFLYFDLIYSIKOTRL 74
QY 62 PWYNLLVDLGSKDATNKYKGGKVDLYGAYGVQC-----AGGTPNKTACWGGV 111

DB 75 GNYDNVRFVFFKKDLADKYKVDVFGANYYYQCYFSSKKTNDINSHQTDKRTCWYGGV 134
QY 112 TLHNNRLTEEEKVPIINLWIDKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLYN 171
DB 135 TEHNGNQLDKYRSITVRVFDGK-NLLSPD-VQTNKKKYTAQELDYLTRHYLVKNKKLYE 192
QY 172 SDSFGKVGORGLIVPHSSEGSTVSYDLFDAQGYPD--TLRIYRDNKTINSENHLIALY 229
DB 193 FNN--SPYETGYIKFIENENS-FWYDMMPAPGDKPDQSKYLLMYNDNKNVDSKDVKIEVY 249
QY 230 LYT 232
DB 250 LTT 252

RESULT 62
AAW06255
ID AAW06255 standard; protein; 239 AA.
XX
AC AAW06255;
XX
DT 23-AUG-1999 (first entry)
XX
DE Staphylococcal group C enterotoxin SEC-MNCopeland.
XX
KW Enterotoxin; SEC-MNCopeland; toxin; disulfide loop; protein engineering.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT Disulfide-bond 93..110
XX
PN W09927889-A2.
XX
PD 10-JUN-1999.
XX
PF 01-DEC-1998; 98WO-US025107.
XX
PR 02-DEC-1997; 97US-0067357P.
XX
PA (IDAH-) IDAHO RES FOUND INC.
XX
PI Bohach GI;
XX
DR WPI; 1999-358008/30.
XX
PT Non-toxic modified staphylococcal enterotoxins.
XX
PS Disclosure; Page 17; 25pp; English.

XX
CC This protein represents the Staphylococcus aureus type C enterotoxin SEC-
CC MNCopeland. The invention relates to pyrogenic toxins, such as
CC staphylococcal enterotoxins, modified in the disulfide loop region.
CC Typically, the modification involves deletions within the disulfide loop
CC region of SEC (see AAW06261). The modified toxins retain useful
CC biological properties, such as the ability to induce cytokine production,
CC but have substantially reduced toxicity compared to the corresponding
CC unmodified native toxin. Emetic response inducing activity and fever
CC inducing activity are typically decreased by at least about 100-fold,
CC while LD50 (in Dutch belted rabbits) is at least 100-fold higher than the
CC native toxin
XX
SQ Sequence 239 AA;

Query Match 24.4%; Score 302.5; DB 2; Length 239;
Best Local Similarity 32.9%; Pred. No. 9.1e-22;
Matches 80; Conservative 47; Mismatches 97; Indels 19; Gaps 9;

QY 2 EKSEINEKDLKKSELOQTALGNLKOIYYNEKAITENK-ESDDQFLENTLLFKGFFTG 60
DB 1 ESQDPDDELKSKSEFTGT-MGNMK--YLYDDHYVSATKSVKDFLADLIYNISDKK 57

QY 61 HPWNDDLLVLSKADATNKYKGVLDLYGAYGYQC-----AGTTPNKATCMYGGVTL 113
 Db 58 LKNYDKVKTLLNEDLAKYKDEVVDVYGSYVNCYFSSKDNVGVTKTCMYGGITK 117
 QY 114 HDNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYN 171
 Db 118 HEGNHFNGNLQNVLRVY-ENKNTISFE-VQTDKSVTAQELDIKARNFLINKKNLYE 175
 QY 172 SDSFGKVQRLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKNTINSENHIALY 229
 Db 176 FNS--SPYETGYIKFIENNGNTFOYDMMPAPGDKFDQSKYLMYNDNKTVDSEKRVKIEVH 233
 QY 230 LYT 232
 Db 234 LTT 236

RESULT 63
 ABG71371
 ID ABG71371 standard; protein; 240 AA.
 XX
 AC ABG71371;
 XX
 DT 29-JAN-2003 (first entry)
 XX
 DE Staphylococcal enterotoxin SEC-MNCopeland.
 XX
 KW Modified pyrogenic toxin; disulphide loop; fever-inducing activity;
 KW emetic response-inducing activity; staphylococcal enterotoxin;
 KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
 KW SEC-MNCopeland.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 240
 FT /label= unknown
 XX
 PN WO200283169-A1.
 XX
 PD 24-OCT-2002.
 XX
 PF 11-APR-2002; 2002WO-US011619.
 XX
 PR 13-APR-2001; 2001US-0283720P.
 XX
 PA (IDAH-) IDAHO RES FOUND INC.
 XX
 PI Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
 XX
 DR WPI; 2003-058608/05.
 XX
 PT New modified staphylococcal enterotoxin derived from a native disulphide
 PT loop-containing pyrogenic toxin, useful for non-specifically enhancing an
 PT immune function and as a vaccine against toxic shock syndrome or food
 PT poisoning.
 XX
 PS Disclosure; Fig 15; 67pp; English.
 XX
 CC The invention relates to a modified pyrogenic toxin derived from a native
 CC disulphide loop-containing pyrogenic toxin where the modified toxin
 CC comprises a disulphide loop having no more than 10 amino acids. The
 CC modified toxin has a fever-inducing activity or an emetic response-
 CC inducing activity decreased by about 100-fold in comparison to a native
 CC toxin. The modified pyrogenic toxin, that is a staphylococcal
 CC enterotoxin, is useful for non-specifically enhancing an immune function
 CC and for vaccination against diseases such as toxic shock syndrome and
 CC food poisoning. This sequence represents the staphylococcal enterotoxin,
 CC SEC-MNCopeland
 XX
 SQ Sequence 240 AA;

Query Match 24.4%; Score 302.5; DB 6; Length 240;

Best Local Similarity 32.9%; Pred. No. 9.1e-22;
 Matches 80; Conservative 47; Mismatches 97; Indels 19; Gaps 9;

QY 2 EKSEINEKDLRKKESELOQTALGNLKOIYYNKAITENK-ESDDQFLENTLLPFKGFFTG 60
 Db 1 ESQPDPTDELHKSEFTGT-MGNWK--LYDDHYVSATKVKSVDKFLAHDLIYNISDKK 57
 QY 61 HPWNDDLLVLSKADATNKYKGVLDLYGAYGYQC-----AGTTPNKATCMYGGVTL 113
 Db 58 LKNYDKVKTLLNEDLAKYKDEVVDVYGSYVNCYFSSKDNVGVTKTCMYGGITK 117
 QY 114 HDNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYN 171
 Db 118 HEGNHFNGNLQNVLRVY-ENKNTISFE-VQTDKSVTAQELDIKARNFLINKKNLYE 175
 QY 172 SDSFGKVQRLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKNTINSENHIALY 229
 Db 176 FNS--SPYETGYIKFIENNGNTFOYDMMPAPGDKFDQSKYLMYNDNKTVDSEKRVKIEVH 233
 QY 230 LYT 232
 Db 234 LTT 236

RESULT 64
 AAY06252
 ID AAY06252 standard; protein; 239 AA.
 XX
 AC AAY06252;
 XX
 DT 23-AUG-1999 (first entry)
 XX
 DE Staphylococcal group C enterotoxin SEC2.
 XX
 KW Enterotoxin; SEC2; toxin; disulphide loop; protein engineering.
 XX
 OS Staphylococcus aureus.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 93..110
 XX
 PN WO9927889-A2.
 XX
 PD 10-JUN-1999.
 XX
 PF 01-DEC-1998; 98WO-US025107.
 XX
 PR 02-DEC-1997; 97US-0067357P.
 XX
 PA (IDAH-) IDAHO RES FOUND INC.
 XX
 PI Bohach GI;
 XX
 PT WPI; 1999-358008/30.
 XX
 PT Non-toxic modified staphylococcal enterotoxins.
 XX
 PS Disclosure; Page 17; 25pp; English.
 XX
 CC This protein represents the Staphylococcus aureus type C enterotoxin
 CC SEC2. The invention relates to pyrogenic toxins, such as staphylococcal
 CC enterotoxins, modified in the disulfide loop region. Typically, the
 CC modification involves deletions within the disulfide loop region of SEC
 CC (see AAY06261). The modified toxins retain useful biological properties,
 CC such as the ability to induce cytokine production, but have substantially
 CC reduced toxicity compared to the corresponding unmodified native toxin.
 CC Emetic response inducing activity and fever inducing activity are
 CC typically decreased by at least about 100-fold, while LD50 (in Dutch
 CC Belted rabbits) is at least 100-fold higher than the native toxin
 XX
 SQ Sequence 239 AA;

Query Match 24.3%; Score 300.5; DB 2; Length 239;

Best Local Similarity	32.9%;	Pred. NO. 1.4e-21;	
Matches	80;	Conservative	47; Mismatches 97; Indels 19; Gaps 9;
Qy	2	EKSEINEKDLRKSELOQTALGNLQIYYNEKAITENK-ESDDQFLENLTLFKGFTG	60
Db	1	ESQDPPTDELHKSSEFTGT-MGNMK--LYDDHVVSAATKWSVDKFLAHLDIYNISDKK	57
Qy	61	HPWYNLLVDLGSKDATNKYKGGKVLDLYGAYGYQC-----AGGTPNKTAQWYGVTL	113
Db	58	LKNYDKVKTEUNLDELAKYKDEVDVVGNSYYNCFSSKNDYKGVTKGTCMYGGITK	117
Qy	114	HNNRLTEE--KKVPINLWIDCKQTVPIDKVKTSKKEVTVOELDLQARHVLHGKFGLYN	171
Db	118	HEGHNFDNGNLQNLIRVY-ENKNTISFE-VQTDKKSVAQELDIKARNFLINKMLYE	175
Qy	172	SDSFGKQVORGLIVHFSSEGTSVYDLFDAQQVDP--TLRIYRDNKTINSENHLIAY	229
Db	176	FNS--SPYETGYIKFIENNGNTFOYDMMAPAPGDXFDQSKYLMYNDNKTVDTSKVKIEVH	233
Qy	230	LYT 232	
Db	234	LTT 236	
RESULT	65		
ABG71368			
ID	ABG71368	standard; protein; 240 AA.	
XX			
AC	ABG71368;		
XX			
DT	29-JAN-2003	(first entry)	
XX			
XX	Staphylococcal enterotoxin SEC2.		
KW	Modified pyrogenic toxin; disulphide loop; fever-inducing activity;		
KW	emetic response-inducing activity; staphylococcal enterotoxin; SEC2;		
KW	toxic shock syndrome; food poisoning; immunostimulant; antibacterial.		
XX			
OS	Staphylococcus aureus.		
XX			
FH	Key	Location/Qualifiers	
FT	Misc-difference 240		
FT		/label= unknown	
XX			
PN	W0200283169-A1.		
XX			
PD	24-OCT-2002.		
XX			
PF	11-APR-2002; 2002WO-US011619.		
XX			
PR	13-APR-2001; 2001US-0283720P.		
XX			
PA	(IDAH-) IDAHO RES FOUND INC.		
XX			
PI	Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;		
XX			
XX	WPI; 2003-058608/05.		
DR			
XX			
PT	New modified staphylococcal enterotoxin derived from a native disulfide		
PT	loop-containing pyrogenic toxin, useful for non-specifically enhancing an		
PT	immune function and as a vaccine against toxic shock syndrome or food		
PT	poisoning.		
XX			
PS	Disclosure; Fig 15; 67pp; English.		
XX			
CC	The invention relates to a modified pyrogenic toxin derived from a native		
CC	disulphide loop-containing pyrogenic toxin where the modified toxin		
CC	comprise a disulphide loop having no more than 10 amino acids. The		
CC	modified toxin has a fever-inducing activity or an emetic response-		
CC	inducing activity decreased by about 100-fold in comparison to a native		
CC	toxin. The modified pyrogenic toxin, that is a staphylococcal		
CC	enterotoxin, is useful for non-specifically enhancing an immune function		
CC	and for vaccination against diseases such as toxic shock syndrome and		

PS	XX	Example 3; Page; 68pp; English.
CC	XX	The invention relates to an isolated and purified superantigen toxin DNA
CC	CC	fragment is altered so that binding of the encoded altered toxin to
CC	CC	either the MHC class II or T cell antigen receptor is altered. Also
CC	CC	included are a recombinant DNA construct (comprising a vector and an
CC	CC	isolated and purified altered superantigen toxin DNA fragment), a host
CC	CC	cell transformed with the recombinant DNA construct, producing altered
CC	CC	superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
CC	CC	superantigen toxin peptide, diagnosing superantigen-associated bacterial
CC	CC	infection, a vaccine (comprising an altered superantigen toxin for
CC	CC	producing antigenic and immunogenic response resulting in the protection
CC	CC	of a mammal against superantigen-associated bacterial infection),
CC	CC	treatment/ameliorating a superantigen-associated bacterial infection, an
CC	CC	antisera isolated from individuals immunised with one or more altered
CC	CC	TSST-1 superantigen toxin and an antibody which recognises altered TSST-
CC	CC	1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
CC	CC	SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPeA and
CC	CC	SPeB). The superantigen toxin DNA fragment is useful for preparing a
CC	CC	composition for treating or preventing bacterial infection. The present
CC	CC	sequence represents the f94A (with reference to the mature protein
CC	CC	sequence) mutant of SEB. Note: The present sequence is not shown in the
CC	CC	specification but was created by the indexer using the wild-type sequence
CC	CC	and the information in the specification
XX	XX	Sequence 266 AA;
SQ	XX	Query Match 24.3%; Score 300.5; DB 7; Length 266;
		Best Local Similarity 34.0%; Pred. No. 1.7e-21;
		Matches 83; Conservative 45; Mismatches 97; Indels 19; Gaps 8;
QY	1	SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFRGFTG 60
DB	27	ABSQPKPDELKSKFTG-LMEDMKVLYDDNHVSAL-NVKSIDQFLYFDLIYSIKDTK 84
QY	61	HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGG-----TPNKTACMYGG 110
DB	85	LGDYDNVRVEFNKDLADKYKVDVFGANYYYQCAFESKNTDINSHQTDKRTKCMYGG 144
QY	111	VTLDHNNRLTEERKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLY 170
DB	145	VTEHNGQLDKYRSITVRVEDGK-NLSSFD-VQTNKKVTAQELDYLTRHVLVKNKLY 202
QY	171	NSDSFGGKVQRLIVFHSSSGSTVSYDLFDAQGG--YPTLLRIYRDNKNTINSENHLIAL 228
DB	203	EFNN--SPYETGYIKFIENENS-FWIDMMPAPGDKFPAQSKYLMYNDNKNQVDSKDVKIEV 259
QY	229	YLVT 232
DB	260	YLTT 263
		RESULT 67
		AAR45016
ID		AAR45016 standard; protein; 238 AA.
XX		AC AAR45016;
XX		25-MAR-2003 (revised)
DT		08-JUN-1994 (first entry)
XX		Staphylococcal enterotoxin SEC3.
XX		Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
KW		autoimmune disease; toxicity; Protein A; perfusion system.
XX		Staphylococcus aureus.
XX		WO9324136-A1.
XX		09-DEC-1993.
XX		01-JUN-1993; 93WO-US005213.
PF		
XX		01-JUN-1992; 92US-00891718.
XX		(TERM/) TERMAN D S.
PA		(STON/) STONE J L.
XX		Terman DS, Stone JL;
PI		WPI; 1993-405418/50.
XX		Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
XX		in a patient or for the treatment of auto-immune diseases.
PT		Disclosure; Fig 1; 90pp; English.
XX		The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
CC		which may be used in the methods of the invention for treating cancer in
CC		a patient. These SEs, and homologues of them, can be used as tumouricidal
CC		agents for treating cancers and autoimmune disease. They exhibit
CC		tumouricidal activity and toxicity identical to that observed for the
CC		Protein A perfusion system. They may be administered by i.v. injection.
CC		(Updated on 25-MAR-2003 to correct PN field.)
CC		Sequence 238 AA;
SQ		Query Match 24.1%; Score 298.5; DB 2; Length 238;
		Best Local Similarity 34.2%; Pred. No. 2.3e-21;
		Matches 80; Conservative 45; Mismatches 90; Indels 19; Gaps 9;
QY	11	DLRKSLQGTALGNLKOIYYNEKAITENK-ESDDQFLENTLLFRGFTGHFWYNDLJV 69
DB	9	ELHKSSEFTGT-MGNVK--LYDDHYVSATKWSVDKFLAHDLIYNSDKLKNYDKVKT 65
QY	70	DLGSKDATNKYKGGKVDLYGAYGYQC-----AGTPNKTACMYGGVTLHDNNRLTEE 122
DB	66	ELLNEDLAKYKDEVDVVGSNYYVNCYFSSKDNVKGVTGKTCMYGKITKEGHNFDNG 125
QY	123	--KKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB	126	NLQWNLIRVY-ENKRNITISFE-VQTDKKSVAQELDKARFNLINKNLYEFNS--SPYE 181
QY	181	RGLIVFHSSSGSTVSYDLFDAQGGYD--TLLRIYRDNKNTINSENHLIALYLT 232
DB	182	TGYIKFIENNGTWFYDLMPAPGDKFQSKYLMYNDNKTVDKSVKIEVHLAT 235
		RESULT 68
		AAB67343
ID		AAB67343 standard; peptide; 238 AA.
XX		AC AAB67343;
XX		23-APR-2001 (first entry)
DT		Staphylococcus aureus enterotoxin C3 protein.
XX		Tumour; cancer; immune; enterotoxin.
XX		Staphylococcus aureus.
OS		US6180097-B1.
XX		30-JAN-2001.
XX		30-OCT-1998; 98US-00183437.
XX		03-OCT-1989; 89US-00416530.
XX		17-JAN-1990; 90US-00466577.
XX		17-JAN-1991; 91WO-US000342.
XX		01-JUN-1992; 92US-00891718.
XX		02-MAR-1993; 93US-00025144.
XX		31-JAN-1994; 94US-00189424.
XX		19-JUN-1995; 95US-00491746.


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XX (TERM/) TERMAN D S.
XX Terman DS;
XX WPI; 2001-158657/16.
XX Tumor cell capable of stimulating antitumor immune reactivity in vitro or
XX in vivo comprises exogenous nucleic acids encoding a superantigen and a
XX costimulatory molecule.
XX Disclosure; Fig 2; 16pp; English.
XX The present invention relates to a tumour cell capable of stimulating
XX antitumor immune reactivity in vitro or in vivo contains and expresses an
XX exogenous nucleic acid molecule encoding a superantigen or its active
XX fragment and an exogenous nucleic acid molecule encoding a costimulatory
XX molecule that activates T cells in conjunction with an antigenic
XX stimulus. The invention may be used for cancer therapy by stimulating an
XX anticancer immune response in vivo or ex vivo
XX Sequence 238 AA;
XX
XX Query Match. 23.9%; Score 296.5; DB 4; Length 238;
XX Best Local Similarity 33.8%; Pred. No. 3.6e-21;
XX Matches 79; Conservative 46; Mismatches 90; Indels 19; Gaps 9;
XX
XX QY 11 DLKKSELOGTALGNLKOIYYNKAITENK--ESDDOFLNTLLFKGFFTGHPWYNDLLV 69
XX DB 9 ELHKSSEFTGT-MGNMK--LYDDHYVSATKVMVDRLAHLIYINISDKLKNYDKVKT 65
XX
XX QY 70 DLGSKDATNKYGGKVDLYGAYGYQC-----AGGTPNKTCACMYGGVTLHDNNRLTEE 122
XX DB 66 ELLNEDLAKKYKDEVDVYGSNYVNCYFSSKDNVGVTKGTCMYGGITKEGHNHFDNG 125
XX
XX QY 123 --KKVPINLWDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGGKVQ 180
XX DB 126 NLQNVLIIRVY-ENKRNITISFE-VQTDKKSVAQELDIKARNFLNKKNLIEFNS--SPYE 181
XX
XX QY 181 RGLIVFHSSEGSTVSVDLFDAGQGVDP--TLRIYRDNKTINSENHIALYLYT 232
XX DB 182 TGYIKFIENNGNTFYDWMAPAGDKFQSKYLMYNDNKTVDKSKVIEVHLTT 235
XX
XX RESULT 69
XX ABB76239
XX ID ABB76239 standard; protein; 238 AA.
XX AC ABB76239;
XX
XX XX 09-AUG-2002 (first entry)
XX DE Staphylococcus aureus enterotoxin C3.
XX KW Enterotoxin C3; SEC3; superantigen; antigen; tumour; cancer; antitumour;
XX therapy.
XX
XX XX Staphylococcus aureus.
XX OS
XX FH Key Location/Qualifiers
XX FT Misc-difference 208
XX FT /note= "given as 'O' in the specification"
XX
XX PN US2002051765-A1.
XX
XX XX 02-MAY-2002.
XX
XX XX 19-DEC-2000; 2000US-00741503.
XX
XX XX 03-OCT-1989; 89US-00416530.
XX PR 17-JAN-1990; 90US-00466577.
XX PR 17-JAN-1991; 91WO-US0000342.
XX PR 01-JUN-1992; 92US-00891718.

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PR 02-MAR-1993; 93US-00025144.
PR 31-JAN-1994; 94US-00189424.
PR 19-JUN-1995; 95US-00491746.
XX
XX PA (TERM/) TERMAN D S.
XX PI Terman DS;
XX
XX XX WPI; 2002-415198/44.
XX
XX PT Reagent for treating cancer without the need for e.g. radiotherapy,
XX comprises a specific V beta subset of T cells sensitized to a growing
XX tumor and stimulated with superantigens.
XX
XX PS Disclosure; Fig 2; 17pp; English.
XX
XX CC The present sequence is the protein sequence of enterotoxin C3 (SEC3) of
XX Staphylococcus aureus. Similarity is shown, in several stretches of
XX sequence, between staphylococcal enterotoxins, streptococcal pyrogenic
XX exotoxins and staphylococcal exfoliative toxins (see ABB76234-44). In the
XX present invention, synthetic polypeptides useful in tumour therapy and in
XX blocking or destroying autoreactive T and B lymphocyte populations are
XX characterised by substantial structural homology to staphylococcal
XX enterotoxin A and enterotoxin B, and to streptococcal pyrogenic
XX exotoxins, with statistically significant sequence homology and
XX similarity (Z value of Lipman and Pearson algorithm in Monte Carlo
XX analysis exceeding 6) to include alignment of cysteine residues and
XX similar hydrophathy profiles. These superantigens are used to treat solid
XX tumours, including their metastases, without radiation, surgery or
XX standard chemotherapeutic agents. A claimed method of human cancer
XX treatment involves contacting haematopoietic cells from a patient with
XX one or more superantigens ex vivo to generate stimulated cells, selecting
XX a specific V beta subset of cells, and reintroducing these cells into the
XX patient to induce an in vivo therapeutic, tumouricidal reaction
XX
XX SQ Sequence 238 AA;
XX
XX Query Match 23.9%; Score 296.5; DB 5; Length 238;
XX Best Local Similarity 33.8%; Pred. No. 3.6e-21;
XX Matches 79; Conservative 45; Mismatches 91; Indels 19; Gaps 9;
XX
XX QY 11 DLKKSELOGTALGNLKOIYYNKAITENK--ESDDOFLNTLLFKGFFTGHPWYNDLLV 69
XX DB 9 ELHKSSEFTGT-MGNMK--LYDDHYVSATKVMVDRLAHLIYINISDKLKNYDKVKT 65
XX
XX QY 70 DLGSKDATNKYGGKVDLYGAYGYQC-----AGGTPNKTCACMYGGVTLHDNNRLTEE 122
XX DB 66 ELLNEDLAKKYKDEVDVYGSNYVNCYFSSKDNVGVTKGTCMYGGITKEGHNHFDNG 125
XX
XX QY 123 --KKVPINLWDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGGKVQ 180
XX DB 126 NLQNVLIIRVY-ENKRNITISFE-VQTDKKSVAQELDIKARNFLNKKNLIEFNS--SPYE 181
XX
XX QY 181 RGLIVFHSSEGSTVSVDLFDAGQGVDP--TLRIYRDNKTINSENHIALYLYT 232
XX DB 182 TGYIKFIENNGNTFYDWMAPAGDKFQSKYLMYNDNKTVDKSKVIEVHLTT 235
XX
XX RESULT 70
XX AARI3206
XX ID AARI3206 standard; protein; 239 AA.
XX AC AARI3206;
XX
XX XX 15-OCT-1991 (first entry)
XX DE Staphylococcal enterotoxin B.
XX KW SEB; cancer treatment; pyrogen; tumouricide.
XX
XX OS Staphylococcus aureus.
XX XX WO9110680-A.

```

XX PD 25-JUL-1991.
 XX PF 17-JAN-1990; 90US-00466577.
 XX PR 17-JAN-1990; 90US-00466577.
 XX PA (TERM/) TERMAN D S.
 XX PI Terman DS;
 XX DR WPI; 1991-237984/32.
 XX PT Treating cancer with enterotoxin from *Staphylococcus aureus* -
 PT administered by IV injection, having same tumoricidal activity as
 PT Staphylococcal protein A without potential toxic reactions.
 XX PS Disclosure; Fig 1; 74pp; English.
 XX CC SEB was isolated and purified from *S. aureus*. It can be used for treating
 CC cancer, activating cytokine mediators and procoagulant systems,
 CC augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be
 CC administered intravenously, optionally with ibuprofen to attenuate toxic
 CC reaction to SEB. Synthetic polypeptides having structural homology to
 CC Staphylococcal exotoxins are claimed, provided the homology includes
 CC statistically significant sequence homology, alignment of Cysteine
 CC residues and similar hydrophathy profiles. See AAR13203-R13211
 XX SQ Sequence 239 AA;
 Query Match 23.9%; Score 296.5; DB 2; Length 239;
 Best Local Similarity 34.9%; Pred. No. 3.6e-21;
 Matches 84; Conservative 42; Mismatches 96; Indels 19; Gaps 8;
 QY 2 EKSEINEKDLRKKSELQGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTGH 61
 Db 1 ESQDPKPDELHKSSKFTG-LMENMKVLYDDNHVSAL-NVKSIDQFLYFLDIYSIKDTKL 58
 QY 62 PWYNDLVLGLSKDATNKYKGVLDLYGAYGYQC-----AGGTPNKTCMVGCV 111
 Db 59 GNYDNVRFVKKDLADKYKVDVFGANYYYQCYFSKKTNDINSHQTDKRTKCMYGV 118
 QY 112 TLHDNNRLTEKKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHLYHGKGLYN 171
 Db 119 TEHNGQLDKYRSLTVRVFEDGK-NLLSFD-VQTNKKKVTQAQELDYLRHLYLVKNKKLYE 176
 QY 172 SDSFGKVGQGLIVFHSSEGSTVSYDLFDAQGYPD--TLRIYRDNKTINSENHLIALY 229
 Db 177 FNN--SPYETGYIKFIENENS-FWYDLPAPGDKFDQSKYLMYNDNKNKVDKVKIEVY 233
 QY 230 L 230
 Db 234 L 234
 RESULT 71
 AAR45014
 ID AAR45014 standard; protein; 239 AA.
 XX AC AAR45014;
 XX AC AAR45014;
 DT 25-MAR-2003 (revised)
 DT 08-JUN-1994 (first entry)
 XX DE Staphylococcal enterotoxin SEB.
 XX DE Staphylococcal enterotoxin; SE; cancer; tumoricidal agent;
 KW autoimmune disease; toxicity; Protein A; perfusion system.
 XX OS Staphylococcus aureus.
 XX PN WO9324136-A1.
 XX XX

PD 09-DEC-1993.
 XX 01-JUN-1993; 93WO-US005213.
 XX 01-JUN-1992; 92US-00891718.
 XX PA (TERM/) TERMAN D S.
 XX PI (STON/) STONE J L.
 XX Terman DS, Stone JL;
 XX WPI; 1993-405418/50.
 XX PT Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
 PT in a patient or for the treatment of auto-immune diseases.
 XX PS Disclosure; Fig 1; 90pp; English.
 XX CC The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer in
 CC a patient. These SEs, and homologues of them, can be used as tumoricidal
 CC agents for treating cancers and autoimmune disease. They exhibit
 CC tumoricidal activity and toxicity identical to that observed for the
 CC Protein A perfusion system. They may be administered by i.v. injection.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX SQ Sequence 239 AA;
 Query Match 23.9%; Score 296.5; DB 2; Length 239;
 Best Local Similarity 34.9%; Pred. No. 3.6e-21;
 Matches 84; Conservative 42; Mismatches 96; Indels 19; Gaps 8;
 QY 2 EKSEINEKDLRKKSELQGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTGH 61
 Db 1 ESQDPKPDELHKSSKFTG-LMENMKVLYDDNHVSAL-NVKSIDQFLYFLDIYSIKDTKL 58
 QY 62 PWYNDLVLGLSKDATNKYKGVLDLYGAYGYQC-----AGGTPNKTCMVGCV 111
 Db 59 GNYDNVRFVKKDLADKYKVDVFGANYYYQCYFSKKTNDINSHQTDKRTKCMYGV 118
 QY 112 TLHDNNRLTEKKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHLYHGKGLYN 171
 Db 119 TEHNGQLDKYRSLTVRVFEDGK-NLLSFD-VQTNKKKVTQAQELDYLRHLYLVKNKKLYE 176
 QY 172 SDSFGKVGQGLIVFHSSEGSTVSYDLFDAQGYPD--TLRIYRDNKTINSENHLIALY 229
 Db 177 FNN--SPYETGYIKFIENENS-FWYDLPAPGDKFDQSKYLMYNDNKNKVDKVKIEVY 233
 QY 230 L 230
 Db 234 L 234
 RESULT 72
 AAR452319
 ID AAR452319 standard; protein; 266 AA.
 XX AC AAR452319;
 XX AC AAR452319;
 DT 10-AUG-2000 (first entry)
 XX DE Plant-optimized mutant staphylococcal enterotoxin B.
 XX DE Rep; replicase; rescue; replication; vector; gene expression;
 KW recombinant protein production; plant; intronless; enterotoxin B.
 XX OS Staphylococcus sp.
 XX OS Synthetic.
 XX PN WO200020557-A2.
 XX PD 13-APR-2000.
 XX XX

PF 07-OCT-1999; 99WO-US023520.
 XX
 PR 07-OCT-1998; 98US-0103352P.
 XX
 PA (UTCO-) UNIV CORNELL BOYCE INST PLANT RES.
 XX
 PI Mason HS, Palmer KE, Mor TS, Hefferon KL, Arntzen C;
 XX
 DR WPI; 2000-303756/26.
 DR N-PSDB; AAA09240.
 XX
 PT Nucleic acids comprising a portion of a long intergenic region of a
 PT geminivirus genome and a sequence comprising a geminiviral replicase
 PT gene, useful for amplifying a gene of interest and overproducing a
 PT protein of interest in plants.
 XX
 PS Example 17; Fig 36; 12pp; English.
 XX
 CC A pair of nucleic acids comprising a portion of a long intergenic region
 CC (LIR) of a geminivirus genome lacking a sequence encoding a geminiviral
 CC coat protein, and a nucleic acid comprising a geminiviral replicase gene
 CC linked to a fruit ripening-dependent promoter, are new. Strains of
 CC Escherichia coli and Agrobacterium tumefaciens transfected with an
 CC expression vector containing the nucleic acids and a gene of interest are
 CC useful for the production of transgenic plants (or cells). The sequences
 CC and methods are useful for amplifying a gene of interest and
 CC overproducing a protein of interest in recombinant plants
 XX
 SQ Sequence 266 AA;
 Query Match 23.9%; Score 296.5; DB 3; Length 266;
 Best Local Similarity 34.0%; Pred. No. 4.2e-21;
 Matches 83; Conservative 45; Mismatches 97; Indels 19; Gaps 8;
 QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYVNEKAITENKESDDQFLENTLLFKGFFTG 60
 DB 27 AESQDPKPELHKSKFTG-LMENMKVLYDDNHVSAI-NVKSIDQSLYFDLIYSIKDTK 84
 QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCMYGG 110
 DB 85 LGYDNRVFEFNKDLADKYDKYVDVFGANYVYQCYFESKKTNDINSHQTDKRKTCMYGG 144
 QY 111 VTLHDNRRLTEKKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLY 170
 DB 145 VTEHNGQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAELDYLTRHYLVKNKKLY 202
 QY 171 NSDSFGGKQVQGLIVFHSSEGSTSVSYDLFDAQGGPD--TLLRIYRDNKNTINSENLIHAL 228
 DB 203 EFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFDQSKYLMYNDNKNVDSKDKVIEV 259
 QY 229 YLYT 232
 DB 260 YLTT 263
 RESULT 73
 ID ABB79503
 XX ABB79503 standard; protein; 266 AA.
 AC ABB79503;
 XX
 DT 23-SEP-2002 (first entry)
 XX
 DE Staphylococcal enterotoxin B vaccine (B42360210).
 XX
 KW Enterotoxin B; superantigen; antigen; toxin; vaccine; B42360210;
 XX attenuation.
 OS Staphylococcus sp.
 XX
 PN US6399332-B1.
 XX
 PD 04-JUN-2002.

XX 01-SEP-1998; 98US-00144776.
 XX
 PR 25-JUN-1997; 97US-00882431.
 XX
 PA (USSA) US SEC OF ARMY.
 XX
 PI Ulrich RG, Olson MA, Bavari S;
 XX
 DR WPI; 2002-546281/58.
 DR N-PSDB; ABN84224.
 XX
 PT Novel isolated and purified superantigen toxin DNA fragment which has
 PT been genetically altered, useful for producing vaccine for treatment of
 PT superantigen toxin-associated bacterial diseases.
 XX
 PS Disclosure; Col 41-43; 46pp; English.
 XX
 CC The present sequence is the protein sequence of staphylococcal
 CC enterotoxin B (SEB) vaccine B42360210. The invention relates to a vaccine
 CC against superantigen toxin-associated bacterial diseases. Superantigen
 CC vaccines were developed by engineering changes in the receptor-binding
 CC portions of superantigen toxins such as SEB to reduce receptor-binding
 CC affinities and toxicity while maintaining antigenicity. In examples from
 CC the invention, attenuated superantigen toxins were shown to protect
 CC animals against challenge with wild-type toxin. Methods of producing and
 CC using the altered superantigen toxins as vaccines, and in diagnosis and
 CC therapy, are provided. A multivalent vaccine consisting of altered
 CC superantigen toxins from SEA, SEB, SEC-1, TST-1 and streptococcal SPEA
 CC is predicted to provide protective immunity against the majority of
 CC bacterial superantigen toxins
 XX
 SQ Sequence 266 AA;
 Query Match 23.9%; Score 296.5; DB 5; Length 266;
 Best Local Similarity 33.6%; Pred. No. 4.2e-21;
 Matches 82; Conservative 46; Mismatches 97; Indels 19; Gaps 8;
 QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYVNEKAITENKESDDQFLENTLLFKGFFTG 60
 DB 27 AESQDPKPELHKSKFTG-LMENMKVLYDDNHVSAI-NVKSIDQSLYFDLIYSIKDTK 84
 QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCMYGG 110
 DB 85 LGYDNRVFEFNKDLADKYDKYVDVFGANYVYQCYFESKKTNDINSHQTDKRKTCMYGG 144
 QY 111 VTLHDNRRLTEKKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLY 170
 DB 145 VTEHNGQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAELDYLTRHYLVKNKKLY 202
 QY 171 NSDSFGGKQVQGLIVFHSSEGSTSVSYDLFDAQGG--YPTLLRIYRDNKNTINSENLIHAL 228
 DB 203 EFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFAQSKYLMYNDNKNVDSKDKVIEV 259
 QY 229 YLYT 232
 DB 260 YLTT 263
 RESULT 74
 ID ABB10083
 XX ABB10083 standard; protein; 266 AA.
 AC ABB10083;
 XX
 DT 11-AUG-2003 (first entry)
 XX
 DE Staphylococcal enterotoxin B #1.
 XX
 KW Enterotoxin B; superantigen-associated bacterial infection; vaccine;
 XX superantigen toxin.
 OS Staphylococcus sp.

XX PN US2003009015-A1.
 XX PD 09-JAN-2003.
 XX PF 25-JUN-1997; 97US-00882431.
 XX PR 25-JUN-1997; 97US-00882431.
 XX (ULRI/) ULRICH R G.
 XX (OLSC/) OLSON M A.
 XX (BAVA/) BAVARI S.
 XX ULRICH RG, OLSON MA, Bavari S;
 XX WPI; 2003-401542/38.
 XX N-PSDB; ACA61179.
 XX New superantigen toxin and/or DNA fragment with an altered binding of the
 XX encoded altered toxin to either MHC class II or T cell antigen receptor,
 XX useful for treating or ameliorating superantigen-associated bacterial
 XX infection.
 XX Claim 12; Page 23-24; 50pp; English.
 XX The invention relates to an isolated and purified superantigen toxin
 XX and/or DNA fragment, which has been altered so that the binding of the
 XX encoded toxin to either major histocompatibility complex (MHC) class II
 XX or T cell antigen receptor is altered. The superantigen toxins, DNA
 XX fragments, and vaccines are useful for treating or ameliorating
 XX superantigen-associated bacterial infection. The DNA fragments are
 XX particularly useful for producing vaccine against superantigen toxin
 XX infections. The transformed host cells are useful for analysing the
 XX effectiveness of drugs and agents that affect the binding of
 XX superantigens to MHC class II or T-cell antigen receptors. The present
 XX sequence represents the amino acid sequence of staphylococcal enterotoxin
 XX B #1
 XX B #1
 XX Sequence 266 AA;
 Query Match 23.9%; Score 296.5; DB 6; Length 266;
 Best Local Similarity 33.6%; Pred. No. 4.2e-21;
 Matches 82; Conservative 46; Mismatches 97; Indels 19; Gaps 8;
 QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFTG 60
 Db 27 AESQDPKPDHLKSKFTG-LMEDMKVLYDDNHVSAL-NVKSIDQFLYDLYSIKDTK 84
 QY 61 HPWYNDLLVGLSKDATNKYKGVLDLYGANYGYOC-----AGTPTNKTCMYGG 110
 Db 85 LGDYDNVRVEFNKDLADKYDKYDVDFGANYGYOCYFSKNTDINSHTDKRKTCTMYGG 144
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 QY 171 NDSFGGKVQGLIVPHSSEGSTVSVDLPDAQO--YPTLLRIYRDNKTINSENHLAL 228
 Db 203 EFPN--SPYETGYIKFIENENS-FWYDMNPAPGDFAQSKLYMNYNDKNQVDSKDVLE 259
 QY 229 YLYT 232
 Db 260 YLTT 263
 RESULT 75
 ABU62326
 ID ABU62326 standard; protein; 266 AA.
 XX AC ABU62326;
 XX DT 27-AUG-2003 (first entry)
 XX

DE XX S. aureus wild-type enterotoxin B, SEB.
 KW SEB; staphylococcal enterotoxin B; vaccine; superantigen toxin; MHC;
 KW superantigen-associated bacterial infection; bacterial infection;
 XX antibacterial.
 XX Staphylococcus aureus.
 OS Key Location/Qualifiers
 PH Peptide 1..27
 FT Protein /label= Signal_peptide
 FT Protein /label= Mature_SEB
 XX US2003036644-A1.
 XX 20-FEB-2003.
 XX 26-NOV-2001; 2001US-00002784.
 XX 25-JUN-1997; 97US-00882431.
 XX 01-SEP-1998; 98US-00144776.
 XX (ULRI/) ULRICH R G.
 XX ULRICH RG;
 XX WPI; 2003-492125/46.
 XX N-PSDB; ACD28896.
 XX New superantigen toxin DNA fragment, useful for preparing a composition
 XX for treating or preventing bacterial infection.
 XX Disclosure; Page 26-27; 68pp; English.
 XX The invention relates to an isolated and purified superantigen toxin DNA
 XX fragment is altered so that binding of the encoded altered toxin to
 XX either the MHC class II or T cell antigen receptor is altered. Also
 XX included are a recombinant DNA construct (comprising a vector and an
 XX isolated and purified altered superantigen toxin DNA fragment), a host
 XX cell transformed with the recombinant DNA construct, producing altered
 XX superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
 XX superantigen toxin peptide, diagnosing superantigen-associated bacterial
 XX infection, a vaccine (comprising an altered superantigen toxin for
 XX producing antigenic and immunogenic response resulting in the protection
 XX of a mammal against superantigen-associated bacterial infection),
 XX treating/ameliorating a superantigen-associated bacterial infection,
 XX antisera isolated from individuals immunised with one or more altered
 XX TSST-1 superantigen toxin and an antibody which recognises altered TSST-
 XX SEB, SEB), and streptococcal pyrogenic enterotoxin A, B, C (SEA,
 XX SEB, SEC). The superantigen toxin DNA fragment is useful for preparing a
 XX composition for treating or preventing bacterial infection. The present
 XX sequence represents wild-type SEB
 XX Sequence 266 AA;
 Query Match 23.9%; Score 296.5; DB 7; Length 266;
 Best Local Similarity 33.6%; Pred. No. 4.2e-21;
 Matches 82; Conservative 46; Mismatches 97; Indels 19; Gaps 8;
 QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFTG 60
 Db 27 AESQDPKPDHLKSKFTG-LMEDMKVLYDDNHVSAL-NVKSIDQFLYDLYSIKDTK 84
 QY 61 HPWYNDLLVGLSKDATNKYKGVLDLYGANYGYOC-----AGTPTNKTCMYGG 110
 Db 85 LGDYDNVRVEFNKDLADKYDKYDVDFGANYGYOCYFSKNTDINSHTDKRKTCTMYGG 144
 QY 111 VTLDHNNRLTEEEKVPINLWIDGQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLY 170
 Db 145 VTEHNGNQLDKYRSITRVFEDGK-NLLSFD-VQTNKKVTAQELDYLTRHYLVKNKKLY 202

Qy 171 NSDSFGKVKQRLIVFHSSEGSTVSYDLFDAQGO--YFDTLLRIYRDNKTINSENHLIAL 228
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFPAQSKYLMYNDNKNWVDSKDVKIEV 259
Qy 229 YLYT 232
Db 260 YLTT 263

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OM protein - protein search, using sw model

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Title: US-09-900-766-3

Perfect score: 1238

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Searched: 1292805 seqs, 313927144 residues

Total number of hits satisfying chosen parameters: 1292805

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Post-processing: Minimum Match 0%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1210	97.7	257	12	US-10-267-682-112
5	1210	97.7	257	12	US-10-267-748-112
6	1168	94.3	248	9	US-09-870-759-16
7	1168	94.3	248	10	US-09-751-708A-16
8	1130	91.3	233	10	US-09-900-766-2
9	1130	91.3	672	10	US-09-900-766-4
10	1037	83.8	233	10	US-10-283-838-7
11	1037	83.8	233	14	US-10-267-682-113
12	1037	83.8	257	12	US-10-267-748-113
13	1033	83.4	233	12	US-10-354-948-4
14	1033	83.4	233	12	US-10-354-948-4
15	1024	82.7	257	9	US-09-870-759-8
					Sequence 3, Appli
					Sequence 7, Appli
					Sequence 8, Appli
					Sequence 112, App
					Sequence 112, App
					Sequence 16, Appl
					Sequence 16, Appl
					Sequence 2, Appli
					Sequence 1, Appli
					Sequence 4, Appli
					Sequence 1, Appli
					Sequence 113, App
					Sequence 113, App
					Sequence 4, Appli
					Sequence 8, Appli

16	1024	92.7	257	10	US-09-751-708A-8	Sequence 8, Appli
17	1014	91.9	257	14	US-10-002-784A-2	Sequence 2, Appli
18	1010	91.6	233	14	US-10-002-784A-4	Sequence 4, Appli
19	997	90.5	257	8	US-08-882-431-2	Sequence 2, Appli
20	992	90.1	233	8	US-08-882-431-4	Sequence 4, Appli
21	663	53.6	233	9	US-09-870-759-14	Sequence 14, Appli
22	663	53.6	258	10	US-09-751-708A-14	Sequence 14, Appli
23	523	42.2	203	10	US-09-900-766-5	Sequence 5, Appli
24	457	36.9	82	14	US-10-002-784A-34	Sequence 34, Appli
25	399	32.2	82	14	US-10-002-784A-32	Sequence 32, Appli
26	360	29.1	217	10	US-09-900-766-6	Sequence 6, Appli
27	304.5	24.6	266	9	US-09-870-759-10	Sequence 10, Appli
28	304.5	24.6	286	9	US-09-751-708A-10	Sequence 10, Appli
29	303.5	24.5	239	9	US-09-150-947B-12	Sequence 12, Appli
30	303.5	24.5	239	14	US-10-172-425B-12	Sequence 12, Appli
31	303.5	24.5	255	12	US-10-354-948-2	Sequence 2, Appli
32	296.5	23.9	266	14	US-10-002-784A-6	Sequence 6, Appli
33	296.5	23.9	266	14	US-10-151-336-8	Sequence 8, Appli
34	291.5	23.5	239	14	US-10-002-784A-10	Sequence 10, Appli
35	280.5	23.1	239	9	US-08-882-431-10	Sequence 10, Appli
36	286.5	23.1	266	14	US-10-003-784A-8	Sequence 8, Appli
37	283	22.9	265	8	US-08-882-431-6	Sequence 6, Appli
38	282.5	22.8	251	8	US-08-973-391A-13	Sequence 13, Appli
39	282.5	22.8	251	12	US-09-308-830-13	Sequence 13, Appli
40	280	22.6	265	8	US-08-882-431-8	Sequence 8, Appli
41	277.5	22.4	251	8	US-08-882-431-16	Sequence 16, Appli
42	277.5	22.4	251	14	US-10-003-784A-16	Sequence 16, Appli
43	270.5	21.8	266	9	US-09-870-759-12	Sequence 12, Appli
44	270.5	21.8	266	10	US-09-751-708A-12	Sequence 12, Appli
45	262.5	21.2	266	8	US-08-882-431-14	Sequence 14, Appli
46	262.5	21.2	266	14	US-10-002-784A-14	Sequence 14, Appli
47	244.5	19.7	220	14	US-10-002-784A-26	Sequence 26, Appli
48	244.5	19.7	468	14	US-10-002-784A-27	Sequence 27, Appli
49	234	18.9	250	9	US-09-870-759-20	Sequence 20, Appli
50	234	18.9	250	10	US-09-751-708A-20	Sequence 20, Appli
51	215	17.4	82	14	US-10-003-784A-33	Sequence 33, Appli
52	175.5	14.2	235	12	US-09-308-829-2	Sequence 2, Appli
53	175.5	14.2	235	12	US-09-336-036-2	Sequence 2, Appli
54	137.5	11.1	89	14	US-10-002-784A-35	Sequence 35, Appli
55	121	9.8	79	14	US-10-002-784A-39	Sequence 39, Appli
56	112.5	9.1	89	14	US-10-003-784A-37	Sequence 37, Appli
57	112.5	9.1	89	14	US-10-003-784A-38	Sequence 38, Appli
58	105.5	8.5	89	14	US-10-003-784A-36	Sequence 36, Appli
59	105.5	8.5	234	9	US-09-870-759-18	Sequence 18, Appli
60	105.5	8.5	234	10	US-09-751-708A-18	Sequence 18, Appli
61	105.5	8.5	234	12	US-10-267-682-111	Sequence 111, App
62	105.5	8.5	234	12	US-10-267-748-111	Sequence 111, App
63	105	8.5	233	8	US-08-882-431-12	Sequence 12, Appli
64	104.5	8.4	232	12	US-10-282-122A-70242	Sequence 70242, A
65	104.5	8.4	234	14	US-10-002-784A-12	Sequence 12, Appli
66	103.5	8.4	194	10	US-09-465-714-3	Sequence 3, Appli
67	103.5	8.4	194	12	US-10-354-948-6	Sequence 6, Appli
68	103.5	8.4	234	12	US-10-282-122A-70241	Sequence 70241, A
69	103.5	8.4	238	10	US-09-465-714-1	Sequence 1, Appli
70	101	8.2	1634	15	US-10-435-766-23	Sequence 23, Appli
71	100	8.1	226	9	US-09-815-242-5900	Sequence 5900, Ap
72	100	8.1	226	9	US-09-815-242-13156	Sequence 13156, A
73	99	8.0	621	12	US-10-424-559-264720	Sequence 264720, A
74	99	8.0	621	12	US-10-425-114-57792	Sequence 57792, A
75	98.5	8.0	231	12	US-10-282-122A-70240	Sequence 70240, A
76	98	7.9	631	14	US-10-043-344-111	Sequence 111, App
77	97.5	7.7	232	12	US-10-282-122A-70241	Sequence 70241, A
78	95.5	7.7	616	15	US-10-431-273-59	Sequence 59, Appl
79	94	7.6	227	12	US-10-283-122A-70243	Sequence 70243, A
80	94	7.6	622	12	US-10-435-114-39433	Sequence 39433, A
81	94	7.6	622	12	US-10-435-114-60523	Sequence 60523, A
82	93	7.5	16	14	US-10-283-838-20	Sequence 20, Appl
83	93	7.5	306	12	US-10-425-114-54166	Sequence 54166, A
84	93	7.5	643	15	US-10-431-273-60	Sequence 60, Appl
85	93	7.5	616	12	US-10-425-114-38468	Sequence 38468, A
86	93	7.5	653	12	US-10-425-114-62449	Sequence 62449, A
87	92.5	7.5	291	12	US-10-282-122A-52208	Sequence 52208, A
88	90.5	7.3	460	12	US-10-425-114-38886	Sequence 38886, A

Sequence 489, App
Sequence 59134, A
Sequence 63660, A
Sequence 43957, A
Sequence 115, App
Sequence 19630, A
Sequence 70244, A
Sequence 5435, Ap
Sequence 173518, A
Sequence 52842, A
Sequence 50103, A
Sequence 57915, A

89 90.5 7.3 492 12 US-10-183-687-489
90 90 7.3 847 12 US-10-282-122A-59134
91 89.5 7.2 612 12 US-10-425-114-63660
92 89 7.2 226 12 US-10-282-122A-43957
93 89 7.2 631 14 US-10-043-344-115
94 89 7.2 941 15 US-10-369-493-19630
95 88.5 7.1 227 12 US-10-282-122A-70244
96 88.5 7.1 816 15 US-10-369-493-5435
97 88 7.1 611 12 US-10-424-599-173518
98 88 7.1 632 12 US-10-425-114-52842
99 88 7.1 646 12 US-10-425-114-50103
100 88 7.1 646 12 US-10-425-114-57915

ALIGNMENTS

RESULT 1
US-09-900-766-3
Sequence 3, Application US/09900766
Publication No. US20030039655A1
GENERAL INFORMATION:
APPLICANT: FORSBERG, GORAN
APPLICANT: ERLANDSSON, EVA
APPLICANT: ANTONSSON, PER
APPLICANT: WALSE, BJORN
TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
FILE REFERENCE: P02188US0;10104199
CURRENT APPLICATION NUMBER: US/09/900, 766
CURRENT FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent in version 3.0
SEQ ID NO 3
LENGTH: 233
TYPE: PRT
ORGANISM: Artificial Sequence
NAME/KEY: peptide
LOCATION: (1)..(233)
OTHER INFORMATION: Chimeric Protein
US-09-900-766-3

Query Match 100.0%; Score 1238; DB 10; Length 233;
Best Local Similarity 100.0%; Pred. No. 2.4e-115;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKKSELOQTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKKSELOQTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60

Qy 61 HPWYNDLLVGLSKDQATNKYKGVLDLYGAYGYQCAGTGNKTAACMYGGVTLHDNNRLT 120
Db 61 HPWYNDLLVGLSKDQATNKYKGVLDLYGAYGYQCAGTGNKTAACMYGGVTLHDNNRLT 120

Qy 121 EEKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 121 EEKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180

Qy 181 RGLIVFHSSEGSTVSVDLFDQAQGYPTLLRIYRDNKTINSENHLIALYLYTT 233
Db 181 RGLIVFHSSEGSTVSVDLFDQAQGYPTLLRIYRDNKTINSENHLIALYLYTT 233

RESULT 2
US-09-900-766-7
Sequence 7, Application US/09900766
Publication No. US20030039655A1
GENERAL INFORMATION:
APPLICANT: FORSBERG, GORAN
APPLICANT: ERLANDSSON, EVA
APPLICANT: ANTONSSON, PER
APPLICANT: WALSE, BJORN
TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY

Query Match 100.0%; Score 1238; DB 10; Length 233;
Best Local Similarity 100.0%; Pred. No. 2.4e-115;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

FILE REFERENCE: P02188US0;10104199
CURRENT APPLICATION NUMBER: US/09/900,766
CURRENT FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patent in version 3.0
SEQ ID NO 7
LENGTH: 233
TYPE: PRT
ORGANISM: Staphylococcus sp.
US-09-900-766-7

Query Match 97.7%; Score 1210; DB 10; Length 233;
Best Local Similarity 97.9%; Pred. No. 1.5e-112;
Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKKSELOQTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKKSELOQTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60

Qy 61 HPWYNDLLVGLSKDQATNKYKGVLDLYGAYGYQCAGTGNKTAACMYGGVTLHDNNRLT 120
Db 61 HPWYNDLLVGLSKDQATNKYKGVLDLYGAYGYQCAGTGNKTAACMYGGVTLHDNNRLT 120

Qy 121 EEKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 121 EEKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180

Qy 181 RGLIVFHSSEGSTVSVDLFDQAQGYPTLLRIYRDNKTINSENHLIALYLYTT 233
Db 181 RGLIVFHSSEGSTVSVDLFDQAQGYPTLLRIYRDNKTINSENHLIALYLYTT 233

RESULT 3
US-10-283-838-8
Sequence 8, Application US/10283838
Publication No. US20030092894A1
GENERAL INFORMATION:
APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsteden,
Johan Hansson, Terje Kalland, Lars
Abrahamson and Goran Forsberg
TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
AND THEIR USE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
STREET: 1177 West Loop South, 10th Floor
CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77027-9095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,838
FILING DATE: 30-Oct-2002
CLASSIFICATION: Unknown
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/695,692
FILING DATE: August 12, 1996
APPLICATION NUMBER: 9601245-5
FILING DATE: March 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Krieger Paul E.
REGISTRATION NUMBER: 25,886
REFERENCE/DOCKET NUMBER: 41986/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:


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/
/ LENGTH: 233 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-283-838-8

Query Match          97.7%; Score 1210; DB 14; Length 233;
Best Local Similarity 97.9%; Pred. No. 1.5e-112;
Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOCTALGNLQIYYINEKAITENKESDDQFLENTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKSELOCTALGNLQIYYINEKAITENKESDDQFLENTLLFKGFFTG 60
QY 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIALYLYTT 233
Db 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIALYLYTT 233

RESULT 4
US-10-267-682-112
; Sequence 112, Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,682
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
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/
/ LENGTH: 257 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 112:
US-10-267-682-112

Query Match          97.7%; Score 1210; DB 12; Length 257;
Best Local Similarity 97.9%; Pred. No. 1.7e-112;
Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOCTALGNLQIYYINEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELOCTALGNLQIYYINEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIALYLYTT 233
Db 205 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIALYLYTT 257

RESULT 5
US-10-267-748-112
; Sequence 112, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,748
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
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SEQUENCE CHARACTERISTICS:
 LENGTH: 257 amino acids
 TYPE: amino acid
 STRANDEDNESS: <Unknown>
 TOPOLOGY: unknown
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 112:
 US-10-267-748-112

Query Match 97.7%; Score 1210; DB 12; Length 257;
 Best Local Similarity 97.9%; Pred. No. 1.7e-112;
 Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 DB 25 SEKSEINEKDLRKKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
 QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
 DB 85 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
 QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTQVQELDLQARHYLHGKFGFLYNSDSFGGKVQ 180
 DB 145 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTQVQELDLQARHYLHGKFGFLYNSDSFGGKVQ 204
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLRIYRDNKTINSENHLALYLYTT 233
 DB 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLRIYRDNKTINSENHLIDLYLYTT 257

RESULT 6
 US-09-870-759-16
 ; Sequence 16, Application US/09870759
 ; Publication No. US20020177551A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TERMAN, David S
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 ; FILE REFERENCE: 870759
 ; CURRENT APPLICATION NUMBER: US/09/870,759
 ; CURRENT FILING DATE: 2002-01-14
 ; PRIOR APPLICATION NUMBER: US 60/208,128
 ; PRIOR FILING DATE: 2000-05-30
 ; NUMBER OF SEQ ID NOS: 166
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 16
 ; LENGTH: 248
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-870-759-16

Query Match 94.3%; Score 1168; DB 9; Length 248;
 Best Local Similarity 98.2%; Pred. No. 2.6e-108;
 Matches 220; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 DB 25 SEKSEINEKDLRKKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
 QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
 DB 85 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
 QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTQVQELDLQARHYLHGKFGFLYNSDSFGGKVQ 180
 DB 145 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTQVQELDLQARHYLHGKFGFLYNSDSFGGKVQ 204
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLRIYRDNKTINSEN 224
 DB 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLRIYRDNKTINSEN 248

RESULT 7
 US-09-751-708A-16

; Sequence 16, Application US/09751708A
 ; Publication No. US20030157113A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TERMAN, David S
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 ; FILE REFERENCE: 751708
 ; CURRENT APPLICATION NUMBER: US/09/751,708A
 ; CURRENT FILING DATE: 2002-10-15
 ; PRIOR APPLICATION NUMBER: US 60/173,371
 ; PRIOR FILING DATE: 1999-12-28
 ; NUMBER OF SEQ ID NOS: 166
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 16
 ; LENGTH: 248
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-751-708A-16

Query Match 94.3%; Score 1168; DB 10; Length 248;
 Best Local Similarity 98.2%; Pred. No. 2.6e-108;
 Matches 220; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 DB 25 SEKSEINEKDLRKKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
 QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
 DB 85 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
 QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTQVQELDLQARHYLHGKFGFLYNSDSFGGKVQ 180
 DB 145 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTQVQELDLQARHYLHGKFGFLYNSDSFGGKVQ 204
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLRIYRDNKTINSEN 224
 DB 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLRIYRDNKTINSEN 248

RESULT 8
 US-09-900-766-2
 ; Sequence 2, Application US/09900766
 ; Publication No. US20030039655A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FORSBERG, GORAN
 ; APPLICANT: ERLANDSSON, EVA
 ; APPLICANT: ANTONSSON, PER
 ; APPLICANT: WALSE, BJORN
 ; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
 ; FILE REFERENCE: P02188USO;10104199
 ; CURRENT APPLICATION NUMBER: US/09/900,766
 ; CURRENT FILING DATE: 2001-07-06
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 233
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; NAME/KEY: Peptide
 ; LOCATION: (1)..(233)
 ; OTHER INFORMATION: Chimeric Protein
 US-09-900-766-2

Query Match 91.3%; Score 1130; DB 10; Length 233;
 Best Local Similarity 91.4%; Pred. No. 1.5e-104;
 Matches 213; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 DB 1 SEKSEINEKDLRKKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120

Db 61 HPWYNDLLVLDLGSSTAAETSEYSSVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 181 RGLIVFHSSEGSTVSVDLYFDAGQGYPTDLLRIYRDNKTINSENHLIALYLYTT 233
Db 181 RGLIVFHSSEGSTVSVDLYFDAGQGYPTDLLRIYRDNKTINSENHLIALYLYTT 233

RESULT 9

US-09-900-766-1
; Sequence 1, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US010104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 672
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(672)
; OTHER INFORMATION: Conjugate protein
US-09-900-766-1

Query Match 91.3%; Score 1130; DB 10; Length 672;
Best Local Similarity 91.4%; Pred. No. 6,5e-104;
Matches 213; Conservative 9; Mismatches 11; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSQELQGTALGNLKOIYYNKEAITENKESDDQFLENTLLFKGFFTG 60
Db 226 SEKSEINEKDLRKKSQELQGTALGNLKOIYYNKEAITENKESDDQFLENTLLFKGFFTG 285
QY 61 HPWYNDLLVLDLGSSTAAETSEYSSVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120
Db 286 HPWYNDLLVLDLGSSTAAETSEYSSVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 345
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 346 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
QY 181 RGLIVFHSSEGSTVSVDLYFDAGQGYPTDLLRIYRDNKTINSENHLIALYLYTT 233
Db 406 RGLIVFHSSEGSTVSVDLYFDAGQGYPTDLLRIYRDNKTINSENHLIALYLYTT 458

RESULT 10

US-09-900-766-4
; Sequence 4, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US010104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 4
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-900-766-4
Query Match 93.8%; Score 1037; DB 10; Length 233;
Best Local Similarity 83.3%; Pred. No. 3e-95;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSQELQGTALGNLKOIYYNKEAITENKESDDQFLENTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKKSQELQGTALGNLKOIYYNKEAITENKESDDQFLENTLLFKGFFTG 60
QY 61 HPWYNDLLVLDLGSSTAAETSEYSSVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120
Db 61 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 181 RGLIVFHSSEGSTVSVDLYFDAGQGYPTDLLRIYRDNKTINSENHLIALYLYTT 233
Db 181 RGLIVFHSSEGSTVSVDLYFDAGQGYPTDLLRIYRDNKTINSENHLIALYLYTT 233

RESULT 11

US-10-283-838-7
; Sequence 7, Application US/10283838
; Publication No. US20030032894A1
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
; Johan Hansson, Terje Kalland, Lars
; Abrahamsen and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/283,838
; FILING DATE: 30-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,692
; FILING DATE: August 12, 1996
; APPLICATION NUMBER: 9601245-5
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 41986/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-10-283-838-7

Query Match 83.8%; Score 1037; DB 14; Length 233;
Best Local Similarity 83.3%; Pred. No. 3e-95;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
QY 61 HPWYNDLLVDSKDATNKYKGGKVDLYGAYGYQCAGTGNKACMYGGVTLHNNRLT 120
DB 61 HSWYNDLLVDFSKDIDVKYKGGKVDLYGAYGYQCAGTGNKACMYGGVTLHNNRLT 120
QY 121 EEKVPINLWDGKQNTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 121 EEKVPINLWDGKQNTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
QY 181 RGLIVHSSSGSVSYDLFDAQOQYPTLLRIYRDNKTINSENHLALYLYTT 233
DB 181 RGLIVHSSSGSVSYDLFDAQOQYPTLLRIYRDNKTINSENHLALYLYTT 233

RESULT 12

US-10-267-682-113
; Sequence 113, Application US/10267682
; Publication No. US2004003235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,682
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELE: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein

US-10-267-682-113

Query Match 83.8%; Score 1037; DB 12; Length 257;
Best Local Similarity 83.3%; Pred. No. 3.4e-95;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFFTG 84
QY 61 HPWYNDLLVDSKDATNKYKGGKVDLYGAYGYQCAGTGNKACMYGGVTLHNNRLT 120
DB 85 HSWYNDLLVDFSKDIDVKYKGGKVDLYGAYGYQCAGTGNKACMYGGVTLHNNRLT 144
QY 121 EEKVPINLWDGKQNTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 145 EEKVPINLWDGKQNTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 181 RGLIVHSSSGSVSYDLFDAQOQYPTLLRIYRDNKTINSENHLALYLYTT 233
DB 205 RGLIVHSSSGSVSYDLFDAQOQYPTLLRIYRDNKTINSENHLALYLYTT 257

RESULT 13

US-10-267-748-113
; Sequence 113, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,748
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELE: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown

MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 113;
US-10-267-748-113

Query Match 83.8%; Score 1037; DB 12; Length 257;
Best Local Similarity 83.3%; Pred. No. 3.4e-95;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTTG 60
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTTG 84
QY 61 HPWYNDLLVDLGSKDANKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKGLYNSDSFGKVKQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKGLYNSDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGQYPTDLRIYRDNKTINSENHIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAGQGSNTLLRIYRDNKTINSENHIDYLYTS 257

RESULT 14
US-10-354-948-4
; Sequence 4, Application US/10354948
; Publication No. US20030202962A1
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; Emslie, Robyn E.
; Potter, Terence A.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/354,948
; FILING DATE: 29-Jan-2003
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,806
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-29-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-354-948-4

Query Match 83.4%; Score 1033; DB 12; Length 233;
Best Local Similarity 83.2%; Pred. No. 7.6e-95;
Matches 193; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTTG 61
DB 2 EKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTTG 61
QY 62 PWYNDLLVDLGSKDANKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 121
DB 62 SWYNDLLVDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 121
QY 122 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKGLYNSDSFGKVKQ 181
DB 122 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKGLYNSDSFGKVKQ 181
QY 182 GLIVFHSSEGSTVSYDLFDAQGQYPTDLRIYRDNKTINSENHIALYLYTT 233
DB 182 GLIVFHTSTEPSVNYDLFGAGQGSNTLLRIYRDNKTINSENHIDYLYTS 233

RESULT 15
US-09-870-759-8
; Sequence 8, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-8

Query Match 82.7%; Score 1024; DB 9; Length 257;
Best Local Similarity 82.4%; Pred. No. 6.9e-94;
Matches 192; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTTG 60
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTTG 84
QY 61 HPWYNDLLVDLGSKDANKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKGLYNSDSFGKVKQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKGLYNSDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGQYPTDLRIYRDNKTINSENHIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAGQGSNTLLRIYRDNKTINSENHIDYLYTS 257

RESULT 16
US-09-751-708A-8
; Sequence 8, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: Patent in version 3.1

```

; SEQ ID NO 8
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-8

Query Match      82.7%; Score 1024; DB 10; Length 257;
Best Local Similarity 82.4%; Pred. No. 6.9e-94;
Matches 192; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTTG 60
DB 25 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAITENKESDDQFLOHILFKGFTN 84
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
DB 145 EEKVPINLWIDGKQTTVPLETVTKNKNVTVOELDLQARRYLQEKYLYNSDVFDFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQGYNTLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 17
US-10-002-784A-2
; Sequence 2, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 2
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin A periplasmic
US-10-002-784A-2

Query Match      81.9%; Score 1014; DB 14; Length 257;
Best Local Similarity 82.0%; Pred. No. 6.9e-93;
Matches 191; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTTG 60
DB 25 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAITENKESDDQFROHTILFKGFTD 84
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
DB 145 EEKVPINLWIDGKQTTVPLETVTKNKNVTVOELDLQARRYLQEKYLYNSDVFDFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQGYNTLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 18
US-10-002-784A-4

```

```

; Sequence 4, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 4
; LENGTH: 233
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin A cytoplasmic
US-10-002-784A-4

Query Match      81.6%; Score 1010; DB 14; Length 233;
Best Local Similarity 81.9%; Pred. No. 1.5e-92;
Matches 190; Conservative 16; Mismatches 26; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELOQTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTTG 61
DB 2 EKSEINEKDLRKSELOQTALGNLQIYYNEKAITENKESDDQFROHTILFKGFTD 61
QY 62 PWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
DB 62 SWYNDLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
QY 122 EKVPIINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 181
DB 122 EKVPIINLWIDGKQTTVPLETVTKNKNVTVOELDLQARRYLQEKYLYNSDVFDFGKVKQ 181
QY 182 GLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHIALYLYTT 233
DB 182 GLIVFHTSTEPSVNYDLFGAQGYNTLLRIYRDNKTINSENHIDIYLYTS 233

RESULT 19
US-08-882-431-2
; Sequence 2, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:

```

NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 257
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431-2

Query Match 80.5%; Score 997; DB 8; Length 257;
Best Local Similarity 81.1%; Pred. No. 3.4e-91;
Matches 189; Conservative 16; Mismatches 28; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELGQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFPTG 60
DB 25 SEKSEINEKDLRKSEKQGTALGNLKOIYYNEKAKTENKESHDPFQHTILFKGFPTD 84
QY 61 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVRFDSKDIVDKYKGVLDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLT 144
QY 121 EKKVPINLWDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFLGYNLNSDFSFGKVQ 180
DB 145 EKKVPINLWDGKQTTVPLETVKTNKXNVTVQELDLQARRYLQEKYNLNSDVFDDGKVQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNTKNTINSENHIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQGOYSNTLLRIYRDNTKNTINSENHIDIYLYTS 257

RESULT 20

US-08-882-431-4
Sequence 4, Application US/08882431
Publication No. US20030009015A1
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
TITLE OF INVENTION: Vaccines
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: John Moran
STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 233
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431-4

Query Match 80.1%; Score 992; DB 8; Length 233;
Best Local Similarity 80.6%; Pred. No. 9.5e-91;
Matches 187; Conservative 16; Mismatches 29; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELGQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFPTG 61
DB 2 EKSEINEKDLRKSEKQGTALGNLKOIYYNEKAKTENKESHDPFQHTILFKGFPTD 61
QY 62 PWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLTE 121
DB 62 SWYNDLLVRFDSKDIVDKYKGVLDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFLGYNLNSDFSFGKVQ 181
DB 122 EKKVPINLWDGKQTTVPLETVKTNKXNVTVQELDKQARYLQEKYNLNSDVFDDGKVQ 181
QY 182 GLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNTKNTINSENHIALYLYTT 233
DB 182 GLIVFHTSTEPSVNYDLFGAQGOYSNTLLRIYRDNTKNTINSENHIDIYLYTS 233

RESULT 21

US-09-870-759-14
Sequence 14, Application US/09870759
Patent No. US20020177551A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: Patent in version 3.1
SEQ ID NO 14
LENGTH: 258
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-870-759-14

Query Match 53.6%; Score 663; DB 9; Length 258;
Best Local Similarity 55.0%; Pred. No. 8.6e-58;
Matches 127; Conservative 33; Mismatches 71; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELGQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFPTG 60
DB 26 NENIDSVKEKELHKSELSSTALNNMKHSYADKNPIGENKSTGQDFLENTLLYKFFTD 85
QY 61 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLT 120
DB 86 LNFEDLLNFNSKEMAHFKSNVDVPIRYSINCYGGEIDRTACTYGVTPHEGKULK 145
QY 121 EKKVPINLWDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFLGYNLNSDFSFGKVQ 180
DB 146 ERKIPINLWINGVQKESVLDKQVTDKKNVTYQELDAQARYLQDKLYNNDTLGGKIQ 205
QY 181 RGLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNTKNTINSENHIALYLY 231
DB 206 RGLIEFDSSDGSKVSYDLFDVKGFPEKQLRIYSNKNLSTEHHLIDIYLY 256

RESULT 22

US-09-751-708A-14

[illegible]

Db 1 SHDQFLQHTLTKGFFTHSWNDLLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGTTPN 60
 QY 103 KTACMGYGVTLHDNNRLTEEXK 124
 |||||
 Db 61 KTACMGYGVTLHDNNRLTEEXK 82
 |||||

RESULT 26

US-09-900-766-6
 ; Sequence 6, Application US/09900766
 ; Publication No. US20030039655A1
 ; GENERAL INFORMATION:
 ; APPLICANT: FORSBERG, GORAN
 ; APPLICANT: ERLANDSSON, EVA
 ; APPLICANT: ANTONSSON, PER
 ; APPLICANT: WALSE, BJORN
 ; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
 ; FILE REFERENCE: P0218US0;10104199
 ; CURRENT APPLICATION NUMBER: US/09/900,766
 ; CURRENT FILING DATE: 2001-07-06
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 6
 ; LENGTH: 217
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus sp.
 US-09-900-766-6

Query Match 29.1%; Score 360; DB 10; Length 217;
 Best Local Similarity 37.5%; Pred. No. 1.3e-27;
 Matches 84; Conservative 45; Mismatches 83; Indels 12; Gaps 7;
 QY 10 KDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLNTLLPKGFFTHPWNDLLV 69
 :|||
 Db 1 EDLHDKSELTLALAN--AYQYNHFFIKENIKSEIGSKDLIFRN--QDQSG-NDLRV 55
 :|||
 QY 70 DLGSKDATNKYKGGKVDLYGAYGYQCAGTTPNKTACMGYGVTLHDNNRLTEEXKVPINL 129
 :|||
 Db 56 KFATADLAQKFKNKVDIYGASFYKCEKISENISCELYGGTTL-NSEKLAQERVIGANV 114
 :|||
 QY 130 WIDGKQTTVPIDKVKTSKEVTQVQLDQARHYLHGKGLNSDSFGKVGORGLIVFHS 189
 :|||
 Db 115 WVDGQKTELE--RTNKKNVTLQELDIKIKILSDKYYIKDS---EISKGLIEFDMK 169
 :|||
 QY 190 EGSTVSYDLFDAQGYPTLLRIYRDNKTINSNL-HIALYLT 232
 :|||
 Db 170 TPRDVSFDIYDLKGENDYEIDKIYEDNKTILKSDSDISHIDVNLVT 213
 :|||

RESULT 27

US-09-870-759-10
 ; Sequence 10, Application US/09870759
 ; Patent No. US20020177551A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TERMAN, David S
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 ; FILE REFERENCE: 870759
 ; CURRENT APPLICATION NUMBER: US/09/870,759
 ; CURRENT FILING DATE: 2002-01-14
 ; PRIOR APPLICATION NUMBER: US 60/208,128
 ; PRIOR FILING DATE: 2000-05-30
 ; NUMBER OF SEQ ID NOS: 166
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 266
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-870-759-10

Query Match 24.6%; Score 304.5; DB 9; Length 266;
 Best Local Similarity 34.4%; Pred. No. 6.2e-22;
 Matches 84; Conservative 45; Mismatches 96; Indels 19; Gaps 8;

QY 1 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLNTLLFKGFFTG 60
 :|||
 Db 27 AESQOPKPDDELHKSSKFTG-LMENMKVLYDDNHVSAL-NVKSIDQFLYDFDIYSIKDTK 84
 :|||
 QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCMYGG 110
 :|||
 Db 85 LGNYDNVRVEFFKNKDLADKYKVDVFGANYYYQCYFSSKKTNDINSHQTDKRTCTMYGG 144
 :|||
 QY 111 VTLDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTQVQLDQARHYLHGKFGLY 170
 :|||
 Db 145 VTEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKVTAQELDYLTRHYLVKNKKLY 202
 :|||
 QY 171 NSDSFGKVGORGLIVFHSSEGSTVSVDLFDACQGYPD--TLRIYRDNKTINSNLHIAL 228
 :|||
 Db 203 EFNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNKNQVDSKVKIEV 259
 :|||
 QY 229 YLYT 232
 :|||
 Db 260 YLTT 263
 :|||

RESULT 28

US-09-751-708A-10
 ; Sequence 10, Application US/09751708A
 ; Publication No. US20030157113A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TERMAN, David S
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
 ; FILE REFERENCE: 751708
 ; CURRENT APPLICATION NUMBER: US/09/751,708A
 ; CURRENT FILING DATE: 2002-10-15
 ; PRIOR APPLICATION NUMBER: US 60/173,371
 ; PRIOR FILING DATE: 1999-12-28
 ; NUMBER OF SEQ ID NOS: 166
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 266
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-751-708A-10

Query Match 24.6%; Score 304.5; DB 10; Length 266;
 Best Local Similarity 34.4%; Pred. No. 6.2e-22;
 Matches 84; Conservative 45; Mismatches 96; Indels 19; Gaps 8;

QY 1 SEKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLNTLLFKGFFTG 60
 :|||
 Db 27 AESQOPKPDDELHKSSKFTG-LMENMKVLYDDNHVSAL-NVKSIDQFLYDFDIYSIKDTK 84
 :|||
 QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCMYGG 110
 :|||
 Db 85 LGNYDNVRVEFFKNKDLADKYKVDVFGANYYYQCYFSSKKTNDINSHQTDKRTCTMYGG 144
 :|||
 QY 111 VTLDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTQVQLDQARHYLHGKFGLY 170
 :|||
 Db 145 VTEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKVTAQELDYLTRHYLVKNKKLY 202
 :|||
 QY 171 NSDSFGKVGORGLIVFHSSEGSTVSVDLFDACQGYPD--TLRIYRDNKTINSNLHIAL 228
 :|||
 Db 203 EFNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNKNQVDSKVKIEV 259
 :|||
 QY 229 YLYT 232
 :|||
 Db 260 YLTT 263
 :|||

RESULT 29

US-09-150-947B-12
 ; Sequence 12, Application US/09150947B
 ; Patent No. US20020028211A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kaempfer, Raymond
 ; APPLICANT: Arad, Gila

;; TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
;; TITLE OF INVENTION: ANTAGONISTS AND VACCINES
;; FILE REFERENCE: A31967-PCT-USA-A
;; CURRENT APPLICATION NUMBER: US/09/150,947B
;; CURRENT FILING DATE: 1998-09-10
;; PRIOR APPLICATION NUMBER: PCT/IL97/00438
;; PRIOR FILING DATE: 1997-12-30
;; PRIOR APPLICATION NUMBER: ISRAEL 119938
;; PRIOR FILING DATE: 1996-12-30
;; NUMBER OF SEQ ID NOS: 12
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 12
;; LENGTH: 239
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
US-09-150-947B-12

Query Match 24.5%; Score 303.5; DB 9; Length 239;
Best Local Similarity 34.6%; Pred. No. 6.8e-22;
Matches 84; Conservative 44; Mismatches 96; Indels 19; Gaps 8;
QY 2 EKSEINEKDLRKSKSELQGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
Db 1 ESQDPKPELHKSFKFTG-LMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
QY 62 PWNDLLVLDGSDATNKYKKVVDLYGAYGYQC-----AGGTPNKTCMYGGV 111
Db 59 GNYDNVRVEFNKDLADKYKDVDFGANYYYQCYFSKKTNDINSHETDKRKTMYGGV 118
QY 112 TLHNNRLTEKKVPINLMDIGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYN 171
Db 119 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKVTAQELDYLTRHYLVKNKKLYE 176
QY 172 SDSFGKQVQGLVHSSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKNTINSENHLIALY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMFAPGDKFDQSKYLMYNDNKWVDSKDKVIEVY 233
QY 230 LYT 232
Db 234 LTT 236

RESULT 30
US-10-172-425B-12
; Sequence 12, Application US/10172425B
; Publication No. US20030147908A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Atad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
; TITLE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
; FILE REFERENCE: A31967-PCT-USA-A 066031.0164
; CURRENT APPLICATION NUMBER: US/10/172,425B
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 09/150,947
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-172-425B-12

Query Match 24.5%; Score 303.5; DB 14; Length 239;
Best Local Similarity 34.6%; Pred. No. 6.8e-22;
Matches 84; Conservative 44; Mismatches 96; Indels 19; Gaps 8;
QY 2 EKSEINEKDLRKSKSELQGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
Db

Db 1 ESQDPKPELHKSFKFTG-LMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
QY 62 PWNDLLVLDGSDATNKYKKVVDLYGAYGYQC-----AGGTPNKTCMYGGV 111
Db 59 GNYDNVRVEFNKDLADKYKDVDFGANYYYQCYFSKKTNDINSHETDKRKTMYGGV 118
QY 112 TLHNNRLTEKKVPINLMDIGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYN 171
Db 119 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKVTAQELDYLTRHYLVKNKKLYE 176
QY 172 SDSFGKQVQGLVHSSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKNTINSENHLIALY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMFAPGDKFDQSKYLMYNDNKWVDSKDKVIEVY 233
QY 230 LYT 232
Db 234 LTT 236
RESULT 31
US-10-354-948-2
; Sequence 2, Application US/10354948
; Publication No. US20030202962A1
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; Elmalie, Robyn E.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/354,948
; FILING DATE: 29-Jan-2003
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,806
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-29-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-354-948-2

Query Match 24.5%; Score 303.5; DB 12; Length 255;
Best Local Similarity 34.6%; Pred. No. 7.4e-22;
Matches 84; Conservative 44; Mismatches 96; Indels 19; Gaps 8;
QY 2 EKSEINEKDLRKSKSELQGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
Db 17 ESQDPKPELHKSFKFTG-LMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 74

QY 62 PWYNDLLVDSKDATNKYKGGKVDLYGAYYGQC-----AGGTENKTKACMYGGV 111
Db 75 GNYDNRVFEFNKDLADKYKDYVDVFGANYYYQCYFSKKTNDINSHQTDKRTCTMYGGV 134
QY 112 TLHDNNRLTEBKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYN 171
Db 135 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLYE 192
QY 172 SDSFGGKVQGLIVFHSSEGSTVSVDLFDAGQVDP--TLRIYRDNKTINSENHLIALY 229
Db 193 FNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNMWVDSKDVKIEVY 249
QY 230 LYT 232
Db 250 LTT 252

RESULT 32
US-10-002-784A-6
; Sequence 6, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
/33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 6
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin B
US-10-002-784A-6

Query Match 23.9%; Score 296.5; DB 14; Length 266;
Best Local Similarity 33.6%; Pred. No. 3.9e-21;
Matches 82; Conservative 46; Mismatches 97; Indels 19; Gaps 8;
QY 1 SEKSEINEKDLRKXSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 27 AESQDPDPKDELHKSSKFTG-LMENKVKLYDDNHVSAL-NVKSIDQSLYFDLIYSIKDTK 84
QY 61 HPWYNDLLVDSKDATNKYKGGKVDLYGAYYGQC-----AGGTENKTKACMYGG 110
Db 85 LGYDNRVFEFNKDLADKYKDYVDVFGANYYYQCYFSKKTNDINSHQTDKRTCTMYGG 144
QY 111 VTLDHNNRLTEBKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLY 170
Db 145 VTEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLY 202
QY 171 NSDSFGGKVQGLIVFHSSEGSTVSVDLFDAGQVDP--TPDITLLRIYRDNKTINSENHLIAL 228
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMPAPGDKFQAQSKYLMYNDNMWVDSKDVKIEV 259
QY 229 LYT 232
Db 260 LTT 263

RESULT 33
US-10-151-336-8
; Sequence 8, Application US/10151336
; Publication No. US20030079248A1
; GENERAL INFORMATION:
; APPLICANT: Mason, Hugh
; APPLICANT: Palmer, Kenneth
; APPLICANT: Hefferon, Kathleen

; APPLICANT: Mor, Tsafir
; APPLICANT: Anttzen, Charles
; TITLE OF INVENTION: Gemini Virus Vectors for Gene Expression in Plants
; FILE REFERENCE: 4868/84453
; CURRENT APPLICATION NUMBER: US/10/151,336
; CURRENT FILING DATE: 2002-05-20
; PRIOR APPLICATION NUMBER: US/09/414,276
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 266
; TYPE: PRT
; ORGANISM: bean yellow dwarf virus
US-10-151-336-8

Query Match 23.9%; Score 296.5; DB 14; Length 266;
Best Local Similarity 34.0%; Pred. No. 3.9e-21;
Matches 83; Conservative 45; Mismatches 97; Indels 19; Gaps 8;
QY 1 SEKSEINEKDLRKXSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 27 AESQDPDPKDELHKSSKFTG-LMENKVKLYDDNHVSAL-NVKSIDQSLYFDLIYSIKDTK 84
QY 61 HPWYNDLLVDSKDATNKYKGGKVDLYGAYYGQC-----AGGTENKTKACMYGG 110
Db 85 LGYDNRVFEFNKDLADKYKDYVDVFGANYYYQCYFSKKTNDINSHQTDKRTCTMYGG 144
QY 111 VTLDHNNRLTEBKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLY 170
Db 145 VTEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVKNKKLY 202
QY 171 NSDSFGGKVQGLIVFHSSEGSTVSVDLFDAGQVDP--TLRIYRDNKTINSENHLIAL 228
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNMWVDSKDVKIEV 259
QY 229 LYT 232
Db 260 LTT 263

RESULT 34
US-10-002-784A-10
; Sequence 10, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
/33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 10
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin B cytoplasmic
US-10-002-784A-10

Query Match 23.5%; Score 291.5; DB 14; Length 239;
Best Local Similarity 35.0%; Pred. No. 1.1e-20;
Matches 82; Conservative 42; Mismatches 91; Indels 19; Gaps 8;
QY 11 DLKXSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVD 70
Db 10 ELKXSKFTG-LMENKVKLYDDNHVSAL-NVKSIDQFDFDIYSIKDTKLGNDNRVE 67
QY 71 LGSKDATNKYKGGKVDLYGAYYGQCAGG-----TPNKTKACMYGGVTLHDNNRLT 120

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Db 68 FKNKDLADKYKDYVDFGANAYVQCAFSSKKTNDINSHQTDKRTCMYGGVTEHNGQLD 127
QY 121 EEEKVPIINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLGFLYNSDSFGKVKQ 180
Db 128 KYRSITVRVEDGK-NLLSPD-VQTNKKVTAQELDYLTRHYLVKNNKLYEFNN--SPYE 183
QY 181 RGLIVFHSSEGSTSVSYDLFDAQOQYDP--TLRIYRDNKTINSENHLIALYLT 232
Db 184 TGYIKFIENENS-FWYDMPPAPGDKFDQSKYLMYNDNKNWDSKDVKIEVYLT 236

RESULT 35
US-08-882-431-10
; Sequence 10, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRCM-504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-10

Query Match 23.5%; Score 290.5; DB 8; Length 239;
Best Local Similarity 35.0%; Pred. No. 1.4e-20;
Matches 82; Conservative 42; Mismatches 91; Indels 19; Gaps 8;

QY 11 DLKSKSELOQTALGNLKIYYNKEAITENKESDDQFLENTLLFKGFFTHGHPYNDLLVD 70
Db 10 ELHKSSKFTG-KMENMKVLYDDNHVSAI-NVKSIDQFRYFDLIYSIKDTKLGNYDNVRVE 67
QY 71 LGSKDATNKYKGGKVDLYGAYGYQCAGG-----TPNKTACMYGGVTLHNNRLT 120
Db 68 FKNKDLADKYKDYVDFGANAYVQCAFSSKKTNDINSHQTDKRTCMYGGVTEHNGQLD 127
QY 121 EEEKVPIINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLGFLYNSDSFGKVKQ 180
Db 128 KYRSITVRVEDGK-NLLSPD-VQTNKKVTAQELDYLTRHYLVKNNKLYEFNN--SPYE 183

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QY 181 RGLIVFHSSEGSTSVSYDLFDAQOQYDP--TLRIYRDNKTINSENHLIALYLT 232
Db 184 TGYIKFIENENS-FWYDMPPAPGDKFDQSKYLMYNDNKNWDSKDVKIEVYLT 236

RESULT 36
US-10-002-784A-8
; Sequence 8, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 8
; TYPE: PRT
; LENGTH: 266
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin B periplasmic
US-10-002-784A-8

Query Match 23.1%; Score 286.5; DB 14; Length 266;
Best Local Similarity 33.6%; Pred. No. 3.9e-20;
Matches 82; Conservative 44; Mismatches 99; Indels 19; Gaps 8;

QY 1 SEKSEINEKDLRKSELOQTALGNLKIYYNKEAITENKESDDQFLENTLLFKGFFTG 60
Db 27 AESQDPKPELHKSSKFTG-LMENMKVLYDDNHVSAI-NVKSIDQFRYFDLIYSIKDTK 84
QY 61 HPWYNDLLVDIGSKDATNKYKGGKVDLYGAYGYQCAGG-----TPNKTACMYGG 110
Db 85 LGNYDNVRVEFKNKDLADKYKVDVFGANAYVQCAFSSKKTNDINSHQTDKRTCMYGG 144
QY 111 VTLHNNRLTEEKVPIINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLY 170
Db 145 VTEHNGQLDKYRSITVRVEDGK-NLLSPD-VQYNKKKVTAEQELDYLTRHYLVKNNKLY 202
QY 171 NSDSFGGKVGORGLIVFHSSEGSTSVSYDLFDAQOQYDP--TLRIYRDNKTINSENHLIAL 228
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMPPAPGDKFDQSKYLMYNDNKNWDSKDVKIEV 259
QY 229 YLYT 232
Db 260 YLYT 263

RESULT 37
US-08-882-431-6
; Sequence 6, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRCM-504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
;
US-08-882-431-6

Query Match 22.9%; Score 283; DB 8; Length 265;
Best Local Similarity 32.4%; Pred. No. 8.8e-20;
Matches 79; Conservative 46; Mismatches 99; Indels 20; Gaps 8;

QY 1 SEKEINEKDLRKSELOQTALGNLKQIYYVNEKAITENKESDDOFLNTLLFKGFTG 60
DB 27 AESQDPKPELHKSSKFTG-LMEDMKVLYDDNHVSAL-NVKSIDQFLYFLIYSIKDTK 84
QY 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQC-----AGTPTNKATACMYGG 110
DB 85 LGDYDNVRVEFKNDLADKDKYVDVFGANYVYQCYFYSKTTDINSHQTDKRTOMYGG 144
QY 111 VTLHNNRLTEKKVPINLWIDGKQTTVPIDKVTSKKEVTVQBLDQARHYLHGKFGLY 170
DB 145 VTEHNGQLDKYSITRVFEDGK-NLLSFD-VQYNKKKVTQAQLDYLTRYLYVKNKLY 202
QY 171 NSDSFGGVQVGLIVFHSSEGSTVSYDLFDAQGG--YPTLLRIVRNKNTINSNLHIAL 228
DB 203 EFNN--SPYEIGYKF--LENQNFYDMNPAPGDKFAQSKYLMYNDNKVDSKDKLEV 258
QY 229 YLYT 232
DB 259 YLTT 262

RESULT 38
US-08-973-391A-13
; Sequence 13, Application US/08973391A
; Publication No. US20020054887A1
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoehr, Jennifer
; APPLICANT: Ohlendorff, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973,391A
; CURRENT FILING DATE: 1998-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 251

; MEDIUM TYPE: Streptococcus pyogenes
; ORGANISM: Streptococcus pyogenes
; US-08-973-391A-13

Query Match 22.8%; Score 282.5; DB 8; Length 251;
Best Local Similarity 33.8%; Pred. No. 9.1e-20;
Matches 80; Conservative 44; Mismatches 94; Indels 19; Gaps 10;

QY 4 SEEINEKDLRKSELOQTAL-GNLKQIYY-VNEKAIT-ENKESDDOFLNTLLFKGFTG 60
DB 25 SQEVPAAQDDPDSQLHRSSLVKNLQNTIYFLYEGDPVTHENVKSVQDLSSHLYIN---VS 81
QY 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQC-----AGTPTNKATACMYGGVTLHNNRL 119
DB 82 GPYNDKLTTELKXQEMATLFDKQNVDIYGVYTHLYCYLCENAESACIYGVGVNHEGHL 141
QY 120 TEEKVPINLWIDGKQTTVPIDKVTSKKEVTVQBLDQARHYLHGKFGLYNSDFSFGKV 179
DB 142 EIPKKIVKVSIDGIQ-SLSFD-IEINKQWVTAQELDYKVKYLTDNKQLYNGP--SKY 197
QY 180 QRGLIVFHSSEGSTVSYDLFD-----AQGYPTLLRIVRNKNTINSNLHIALYLT 232
DB 198 ETGYIKFIPKNKESFWDFPEPEFTQSKY----LMIYKDNETLDSNTSQIEVYLT 250

RESULT 39
US-09-308-830-13
; Sequence 13, Application US/09308830
; Publication No. US20020086813A1
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of Minnesota
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould P.C.
; STREET: P.O. Box 2903
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402-0903
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/308,830
; FILING DATE: 04-Aug-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/22228
; FILING DATE: 05-DEC-1997
; APPLICATION NUMBER: 60/032,930
; FILING DATE: 06-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Skoog, Mark T
; REGISTRATION NUMBER: 40,178
; REFERENCE/DOCKET NUMBER: 600.346USWO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 13:
;
US-09-308-830-13
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```

QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-AGGTPNKACMYGGVTLHDNNRL 119
Db 82 GPNYDKLKTTELKNOEMATLFDKNVDYGVVEYHLCVLCENAESACIYGGVTHGEGNHL 141
QY 120 TEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKV 179
Db 142 EIPKIVVKSIDGIQ-SLSFD-IETNKKMVTAGELDYKVKYLTDNKQLYTNGP--SKY 197
QY 180 QRGILVHSSSGSTVSVDLFD----AQGYPDTLRLIYRDNKTINSENHLIALYLT 232
Db 198 ETGYIKFIPKNKESFWDFPEPEFTQSKY----LMIYKDNETLDSNTSQIEVLYLT 250

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RESULT 42
US-10-002-784A-16
; Sequence 16, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 16
; LENGTH: 251
; TYPE: PRN
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: streptococcal pyrogenic exotoxin-A mutant
US-10-002-784A-16

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Query Match 22.4%; Score 277.5; DB 14; Length 251;
Best Local Similarity 33.3%; Pred. No. 2.9e-19; Indels 19; Gaps 10;
Matches 79; Conservative 44; Mismatches 95;
QY 4 SEINEKDLRKKSELOGTALGNLKIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
Db 25 SQEVAQDDPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYN--VS 81
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-AGGTPNKACMYGGVTLHDNNRL 119
Db 82 GPNYDKLKTTELKNOEMATLFDKNVDYGVVEYHLCVLCENAESACIYGGVTHGEGNHL 141
QY 120 TEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKV 179
Db 142 EIPKIVVKSIDGIQ-SLSFD-IETNKKMVTAGELDYKVKYLTDNKQLYTNGP--SKY 197
QY 180 QRGILVHSSSGSTVSVDLFD----AQGYPDTLRLIYRDNKTINSENHLIALYLT 232
Db 198 ETGYIKFIPKNKESFWDFPEPEFTQSKY----LMIYKDNETLDSNTSQIEVLYLT 250

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RESULT 43
US-09-870-759-12
; Sequence 12, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12

```

```

; LENGTH: 266
; TYPE: PRN
; ORGANISM: Staphylococcus aureus
US-09-870-759-12
Query Match 21.8%; Score 270.5; DB 9; Length 266;
Best Local Similarity 31.3%; Pred. No. 1.6e-18; Indels 17; Gaps 8;
Matches 76; Conservative 49; Mismatches 101;
QY 1 SEKSEINEKDLRKKSELOGTALGNLKIYY-YNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 27 AESQPDPTDELHKASKFTG-LMENMKVLYDDHYVSATKVK-SVDFLAHDLIYNISDKK 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC----AGGTPNKACMYGGVTL 113
Db 85 LKNYDKVKTELLNEGLAKYKDEVDVYGSNYVNCYFSSKDNVGVKGTGKTCMYGGITK 144
QY 114 HDNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYN 171
Db 145 HEGNHFDNGNLQNLVIRVY-ENKRNITISPE-VQTDKSVTAQELDIKARNFLINKKNLYE 202
QY 172 SDSFGGKVQGLIVFHSSEGSTVSVDLFDACQGYPD--TLLRIYRDNKTINSENHLIALY 229
Db 203 FNS--SPYETGYIKFIENNNGNTFWYDMMPAPGDKFDQSKYLLMYNDNKTVDSSKVKIEVH 260
QY 230 LYT 232
Db 261 LTT 263

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RESULT 44
US-09-751-708A-12
; Sequence 12, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 266
; TYPE: PRN
; ORGANISM: Staphylococcus aureus
US-09-751-708A-12
Query Match 21.8%; Score 270.5; DB 10; Length 266;
Best Local Similarity 31.3%; Pred. No. 1.6e-18; Indels 17; Gaps 8;
Matches 76; Conservative 49; Mismatches 101;
QY 1 SEKSEINEKDLRKKSELOGTALGNLKIYY-YNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 27 AESQPDPTDELHKASKFTG-LMENMKVLYDDHYVSATKVK-SVDFLAHDLIYNISDKK 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC----AGGTPNKACMYGGVTL 113
Db 85 LKNYDKVKTELLNEGLAKYKDEVDVYGSNYVNCYFSSKDNVGVKGTGKTCMYGGITK 144
QY 114 HDNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYN 171
Db 145 HEGNHFDNGNLQNLVIRVY-ENKRNITISPE-VQTDKSVTAQELDIKARNFLINKKNLYE 202
QY 172 SDSFGGKVQGLIVFHSSEGSTVSVDLFDACQGYPD--TLLRIYRDNKTINSENHLIALY 229
Db 203 FNS--SPYETGYIKFIENNNGNTFWYDMMPAPGDKFDQSKYLLMYNDNKTVDSSKVKIEVH 260
QY 230 LYT 232
Db 261 LTT 263

```

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RESULT 46
US-10-002-784A-14
; Sequence 14, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 14
; LENGTH: 266
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: staphylococcal enterotoxin C-1 mutant
US-10-002-784A-14

Query Match 21.2%; Score 262.5; DB 14; Length 266;
Best Local Similarity 30.9%; Pred. No. 9.9e-18;
Matches 75; Conservative 49; Mismatches 102; Indels 17; Gaps 38

QY 1 SEKSEINEKDLRKKSLOGTALGNLQIYYNKEAITENKESDDQFLENTLLFKGFFTG 60
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd AESOPDPTPELHKASKPTG-LMENMKVLYDDHYVSATKYK-SVDRFRAHDLIYNISDKK 84
QY 61 HPWYNDLLVDLGSKDATNKKYKKVLDLYGAYGYQC-----AGTTPNKTKACMYGGVTL 113
Db : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Dd 85 LKNYDKVKTELLNEGLAKKYKDEVVDYGSYNYVYFSSKDNVGVKTGKTKMYGGITK 144
QY 114 HDNRLRTEE--KKYPINLWIDGKQTTVPIDKVTSKKEVTVQBLDQARHYLHGKGLYN 171
Dd 145 HEGNHFONGNLQNLYIRVY-ENKENTISFSE-VQTDKKSSTAQBLDIKARNFLINKKNLYE 202
QY 172 SDSFGKGVORGLIVFHSSEGSTVSYDLFDAQGVDP--TLLRTRYDNKTTINSENHLIALY 229
Db 203 FNS--SFYETGYIKFIENGNFTWYDMWPAGDKFDQSKYLMYNDKNTVDSKSKVIEVH 260
QY 230 LYT 232
Db : : : : :
Dd 261 LTT 263

RESULT 47
US-10-002-784A-26
; Sequence 26, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 26
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant streptococcal pyrogenic exotoxin-A
US-10-002-784A-26

Query Match 19.7%; Score 244.5; DB 14; Length 220;
Best Local Similarity 33.3%; Pred. No. 4.8e-16;

```


Matches 75; Conservative 42; Mismatches 87; Indels 21; Gaps 12

QY 16 SELOCTAL-GNLKQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFTTGHFWYNDLLVDLG 72
Db 8 SQRHSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYN---VSGPNYDKLKTCLK 64

QY 73 SKDATNKYKGVKVDLYGAYGYQC-AGTGNKTKACMYGGVTLHDNNRLTEEEKVPIINLWI 131
Db 65 NQEMATLFPKXNIDYIGVEYVHLCVLCENAEBSACI-GGVNREGNHLBIPKKIVVKVSI 123

QY 132 DKGQTTVPIDVKYTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQVGLIVFHSSEG 191
Db 124 DGIO-SLSFD-IETNKKWMTAQELDYKVRKYLTDNKKLYTNGP--SKYETGYIKFIPKNK 179

QY 192 STVSVYDLFD---AQCQVPDTLRIYRDNKNTINSENLHIALYLT 232
Db 180 ESFWDFDFPEFTQSKY----LMIYKDNETLDS-NTQIEVILTT 219

RESULT 48
US-10-002-784A-27
; Sequence 27, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO: 27
; LENGTH: 468
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant SpeA-mutant~~a~~-SpeB fusion
US-10-002-784A-27

Query Match 19.7%; Score 244.5; DB 14; Length 468;
Best Local Similarity 33.3%; Pred. No. 1.4e-15;
Matches 75; Conservative 42; Mismatches 87; Indels 21; Gaps 12

QY 16 SELOCTAL-GNLKQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFTTGHFWYNDLLVDLG 72
Db 8 SQRHSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYN---VSGPNYDKLKTCLK 64

QY 73 SKDATNKYKGVKVDLYGAYGYQC-AGTGNKTKACMYGGVTLHDNNRLTEEEKVPIINLWI 131
Db 65 NQEMATLFPKXNIDYIGVEYVHLCVLCENAEBSACI-GGVNREGNHLBIPKKIVVKVSI 123

QY 132 DKGQTTVPIDVKYTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQVGLIVFHSSEG 191
Db 124 DGIO-SLSFD-IETNKKWMTAQELDYKVRKYLTDNKKLYTNGP--SKYETGYIKFIPKNK 179

QY 192 STVSVYDLFD---AQCQVPDTLRIYRDNKNTINSENLHIALYLT 232
Db 180 ESFWDFDFPEFTQSKY----LMIYKDNETLDS-NTQIEVILTT 219

RESULT 49
US-09-870-759-20
; Sequence 20, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14

```

US-10-002-784A-33
; Sequence 33, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 33
; LENGTH: 82
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin D
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-33

Query Match      17.4%; Score 215; DB 14; Length 82;
Best Local Similarity 51.2%; Pred. No. 1.1e-13;
Matches 41; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

Qy      45 DQLENTLLPKGFTGHPWYNDLLVLDGSKDATNKYKKVLDLYGAYGYQCAGGTENKT 104
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      3- DQLENTLLPKGFTGHPWYNDLLVLDGSKDATNKYKKVLDLYGAYGYQCAGGTENKT 104
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Qy      105 ACYGGVTLHDNNRLTEBEK 124
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      63 ACTYGGVTPHEGNKLERKK 82
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 52
US-09-308-829-2
; Sequence 2, Application US/09308829
; Publication No. US20020039585A1
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Ohlendorf, Douglas
; APPLICANT: Mitchell, David T.
; APPLICANT: Gahr, Pamela J.
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN C AND METHODS OF USE
; FILE REFERENCE: 600.347USW0
; CURRENT APPLICATION NUMBER: US/09/308,829
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: PCT/US97/22125
; PRIOR FILING DATE: 1997-12-05
; PRIOR APPLICATION NUMBER: US 60/033,251
; PRIOR FILING DATE: 1996-12-06
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-308-829-2

Query Match      14.2%; Score 175.5; DB 12; Length 235;
Best Local Similarity 25.4%; Pred. No. 4.2e-09;
Matches 60; Conservative 37; Mismatches 74; Indels 65; Gaps 11;

Qy      47 FLENTLLPKGFTGCH-----KVDLYGAYGYQCAGGTENKTACMGVTLHDNNRL 119
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      11 FIITVILISTYFTYHQSDSKDISNVKSDLLYATITPYDKRCRVNFSHTLNLDTQK 70
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      80 YKKG-----KVDLYGAYGYQCAGGTENKTACMGVTLHDNNRL 119
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      71 YRGKDYIISSEMSYEASQKFRDDHVDVFGFLYILNSHTG-----EYIYGITPAQNNKV 125
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      120 TEKKVPINLWIDGKQTTPIDKVTSKKEVTVOELDQARHYLHGKFLYNSDS--FGG 177
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      126 NH--KLLGNLFISGESQONLNKILKDIIVTFQEIIDFKIRKYLMDNYKIYDATSPYVG 183
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      178 KVORGLIVFHSSEGSTVSYDLFDA--QGQVPTDLLRIYRDNKTINSENL-HIALYL 230
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      184 RIEIG-----TKDGKHEQIDLFDSFNEGTRSDIFAK-YKONRIINMKNFHFDIYL 233
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 54
US-10-002-784A-35
; Sequence 35, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
US-10-002-784A-35

Query Match      14.2%; Score 175.5; DB 12; Length 235;
Best Local Similarity 25.4%; Pred. No. 4.2e-09;
Matches 60; Conservative 37; Mismatches 74; Indels 65; Gaps 11;

Qy      47 FLENTLLPKGFTGCH-----KVDLYGAYGYQCAGGTENKTACMGVTLHDNNRL 119
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      11 FIITVILISTYFTYHQSDSKDISNVKSDLLYATITPYDKRCRVNFSHTLNLDTQK 70
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      80 YKKG-----KVDLYGAYGYQCAGGTENKTACMGVTLHDNNRL 119
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      71 YRGKDYIISSEMSYEASQKFRDDHVDVFGFLYILNSHTG-----EYIYGITPAQNNKV 125
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      120 TEKKVPINLWIDGKQTTPIDKVTSKKEVTVOELDQARHYLHGKFLYNSDS--FGG 177
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      126 NH--KLLGNLFISGESQONLNKILKDIIVTFQEIIDFKIRKYLMDNYKIYDATSPYVG 183
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      178 KVORGLIVFHSSEGSTVSYDLFDA--QGQVPTDLLRIYRDNKTINSENL-HIALYL 230
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      184 RIEIG-----TKDGKHEQIDLFDSFNEGTRSDIFAK-YKONRIINMKNFHFDIYL 233
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 54
US-10-002-784A-35
; Sequence 35, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
US-10-002-784A-35

Query Match      14.2%; Score 175.5; DB 12; Length 235;
Best Local Similarity 25.4%; Pred. No. 4.2e-09;
Matches 60; Conservative 37; Mismatches 74; Indels 65; Gaps 11;

Qy      47 FLENTLLPKGFTGCH-----KVDLYGAYGYQCAGGTENKTACMGVTLHDNNRL 119
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      11 FIITVILISTYFTYHQSDSKDISNVKSDLLYATITPYDKRCRVNFSHTLNLDTQK 70
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      80 YKKG-----KVDLYGAYGYQCAGGTENKTACMGVTLHDNNRL 119
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      71 YRGKDYIISSEMSYEASQKFRDDHVDVFGFLYILNSHTG-----EYIYGITPAQNNKV 125
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      120 TEKKVPINLWIDGKQTTPIDKVTSKKEVTVOELDQARHYLHGKFLYNSDS--FGG 177
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      126 NH--KLLGNLFISGESQONLNKILKDIIVTFQEIIDFKIRKYLMDNYKIYDATSPYVG 183
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy      178 KVORGLIVFHSSEGSTVSYDLFDA--QGQVPTDLLRIYRDNKTINSENL-HIALYL 230
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      184 RIEIG-----TKDGKHEQIDLFDSFNEGTRSDIFAK-YKONRIINMKNFHFDIYL 233
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

```

```
; SEQ ID NO 35
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin B
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-35

Query Match          11.1%; Score 137.5; DB 14; Length 89;
Best Local Similarity 39.1%; Pred. No. 6.8e-06;
Matches 34; Conservative 14; Mismatches 28; Indels 11; Gaps 2;

QY 43 SDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGYOC----- 96
Db 1 SIDQFLYFLIYSIKDTKLGNVDYRVEFKNDLADKYDKYDVDFGANY-YQCYFSKKT 59

QY 97 ----AGTPTNKTCMYGGVTLHDNNRL 119
Db 60 NINSHQTDKRTKTCMYGGVTEHNGNQL 86

RESULT 55
US-10-002-784A-39
; Sequence 39, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 39
; LENGTH: 79
; TYPE: PRT
; ORGANISM: streptococcal pyrogenic enterotoxin a
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-39

Query Match          9.8%; Score 121; DB 14; Length 79;
Best Local Similarity 34.6%; Pred. No. 0.00026;
Matches 27; Conservative 15; Mismatches 32; Indels 4; Gaps 2;

QY 43 SDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGYOC-AGGTP 101
Db 1 SVDQLLSHLLIYN---VSGPNYDKLTKELKNQEMATLPKDKNVDLYGVEYYHLCVLCENA 57

QY 102 NKTACMYGGVTLHDNNRL 119
Db 58 ERSACIYGGVTNHEGNHL 75

RESULT 56
US-10-002-784A-37
; Sequence 37, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 37
```

```
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C2
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-37

Query Match          9.1%; Score 112.5; DB 14; Length 89;
Best Local Similarity 31.7%; Pred. No. 0.0022;
Matches 26; Conservative 14; Mismatches 35; Indels 7; Gaps 1;

QY 43 SDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGYOC----- 96
Db 1 SVDFLAHLDIYINISDKKLNKYDKVKTTELLNEDLAKKYKDEVDVYGSNYVNCYFSSKD 60

QY 97 -AGTPTNKTCMYGGVTLHDNN 117
Db 61 NVGKVTGGKTCMYGGITKHEGN 82

RESULT 57
US-10-002-784A-38
; Sequence 38, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 38
; LENGTH: 89
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C3
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-38

Query Match          9.1%; Score 112.5; DB 14; Length 89;
Best Local Similarity 31.7%; Pred. No. 0.0022;
Matches 26; Conservative 14; Mismatches 35; Indels 7; Gaps 1;

QY 43 SDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGYOC----- 96
Db 1 SVDFLAHLDIYINISDKKLNKYDKVKTTELLNEDLAKKYKDEVDVYGSNYVNCYFSSKD 60

QY 97 -AGTPTNKTCMYGGVTLHDNN 117
Db 61 NVGKVTGGKTCMYGGITKHEGN 82

RESULT 58
US-10-002-784A-36
; Sequence 36, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 36
; LENGTH: 89
```

```
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin C1
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-36

Query Match      8.5%; Score 105.5; DB 14; Length 89;
Best Local Similarity 30.5%; Pred. No. 0.011;
Matches 25; Conservative 14; Mismatches 36; Indels 7; Gaps 1;

QY 43 SDDQFLNTLLFKGFFGTHPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGYQC-----96
Db 1 SVDRFLADHLIYNISDKLKNYDKVKTTELLNEGLAKKYKDEVVDVYGSNYVNCYFSSKD 60
QY 97 -AGGTPNKTACMYGGVTLHDNN 117
Db 61 NVGKVTGGKTCMYGGITRHEGN 82

RESULT 59
US-09-870-759-18
; Sequence 18 Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION: David S
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-18

Query Match      8.5%; Score 105.5; DB 9; Length 234;
Best Local Similarity 22.6%; Pred. No. 0.041;
Matches 52; Conservative 36; Mismatches 69; Indels 73; Gaps 12;

QY 11 DLKKSBLQGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFGTHPWYNDLLVD 70
Db 58 DTFNSELVDSLGSMDR-----IKNTDGSII-SLIIFPS-----PYSPAPT- 97
QY 71 LGSKDATNKYKGGKVDL-----YGAYYGYQCAGGTENKTKACMYGGVTLHDNNR 118
Db 98 -----KGEKVDLNTKTKKSQHTSEGTYYHFQISGVT-----NTEK 133
QY 119 LTEKKVPINLWDGKQTTVPIDKVTSKKEVTVQELDQARHYLHGKFGLY-NSDSFGG 177
Db 134 LPTPIELPLKVKHGKDSPLKYGPKFDKKQLAISTLDLFEIRHQLTQIHGLYRSSDKTGG 192
QY 178 --KVQRLIVFHSSEGSTVSVDL---FDAQGYEDTLRLIYRDNKTINSE 222
Db 193 YWKIT-----MNDGSTYQSDLSKKFYEYNTKPPINI---DEIKTIEAE 232

RESULT 60
US-09-751-708A-18
; Sequence 18 Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION: David S
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
```

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-18

Query Match      8.5%; Score 105.5; DB 10; Length 234;
Best Local Similarity 22.6%; Pred. No. 0.041;
Matches 52; Conservative 36; Mismatches 69; Indels 73; Gaps 12;

QY 11 DLKKSBLQGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFGTHPWYNDLLVD 70
Db 58 DTFNSELVDSLGSMDR-----IKNTDGSII-SLIIFPS-----PYSPAPT- 97
QY 71 LGSKDATNKYKGGKVDL-----YGAYYGYQCAGGTENKTKACMYGGVTLHDNNR 118
Db 98 -----KGEKVDLNTKTKKSQHTSEGTYYHFQISGVT-----NTEK 133
QY 119 LTEKKVPINLWDGKQTTVPIDKVTSKKEVTVQELDQARHYLHGKFGLY-NSDSFGG 177
Db 134 LPTPIELPLKVKHGKDSPLKYGPKFDKKQLAISTLDLFEIRHQLTQIHGLYRSSDKTGG 192
QY 178 --KVQRLIVFHSSEGSTVSVDL---FDAQGYEDTLRLIYRDNKTINSE 222
Db 193 YWKIT-----MNDGSTYQSDLSKKFYEYNTKPPINI---DEIKTIEAE 232

RESULT 61
US-10-267-682-111
; Sequence 111 Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteaway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/10/267,682
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 111:
; SEQUENCE CHARACTERISTICS:
```

```
;
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 111:
US-10-267-682-111

Query Match      8.5%; Score 105.5; DB 12; Length 234;
Best Local Similarity 22.6%; Pred. No. 0.041;
Matches 52; Conservative 36; Mismatches 69; Indels 73; Gaps 12;

QY 11 LDRKSELOCTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTGHPWYNDLLVD 70
Db 58 DFTTNSVLNDSLGMNR-----IKNTDGSII-SLIIFPS-----PYSPAF- 97
QY 71 LGSKDATNKYKGVKVDL-----YGAYGYQCAGGTPNKTACMYGGVTLHDNNR 118
Db 98 -----KGEVDLNTKRTKKSQHTSEGTIIHFQISGVT-----NTEK 133
QY 119 LTEKKVPINLWIDKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLY-NSDSFGG 177
Db 134 LPTPIELPLKVKVHGKDSPLKYGP-KFDKKQLAISTLDPEIRHQLTQIHGLYRSDKTGG 192
QY 178 --KVQEGLVFHSSEGSTVSVDL---FDAQGOYPTDLLRIYRDNKTINSE 222
Db 193 YWKIT-----MNDGSTYQSDLSKKFYEYNTKPPINI---DEIKTIEAE 232

RESULT 62
US-10-267-748-111
; Sequence 111, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/267,748
; FILING DATE: 08-Oct-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223A
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 111:
```

```
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 111:
US-10-267-748-111

Query Match      8.5%; Score 105.5; DB 12; Length 234;
Best Local Similarity 22.6%; Pred. No. 0.041;
Matches 52; Conservative 36; Mismatches 69; Indels 73; Gaps 12;

QY 11 LDRKSELOCTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTGHPWYNDLLVD 70
Db 58 DFTTNSVLNDSLGMNR-----IKNTDGSII-SLIIFPS-----PYSPAF- 97
QY 71 LGSKDATNKYKGVKVDL-----YGAYGYQCAGGTPNKTACMYGGVTLHDNNR 118
Db 98 -----KGEVDLNTKRTKKSQHTSEGTIIHFQISGVT-----NTEK 133
QY 119 LTEKKVPINLWIDKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLY-NSDSFGG 177
Db 134 LPTPIELPLKVKVHGKDSPLKYGP-KFDKKQLAISTLDPEIRHQLTQIHGLYRSDKTGG 192
QY 178 --KVQEGLVFHSSEGSTVSVDL---FDAQGOYPTDLLRIYRDNKTINSE 222
Db 193 YWKIT-----MNDGSTYQSDLSKKFYEYNTKPPINI---DEIKTIEAE 232

RESULT 63
US-08-882-431-12
; Sequence 12, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
```

```

; MOLECULE TYPE: Peptide
US-08-882-431-12
;
Query Match      8.5%; Score 105; DB 8; Length 233;
Best Local Similarity 26.4%; Pred. No. 0.046;
Matches 42; Conservative 25; Mismatches 50; Indels 42; Gaps 8;

QY 81 KGKVDL-----YGAIVGYOCAGGTPNKTACMYGVTLDHNNRLTEKKVPINL 129
Db 98 KGEKVDLNTKTKKSQTSYTHFQISGV-----NTEKLPTEIPLK 143
QY 130 WIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLY-NSDSFGG--KVQRLIVF 186
Db 144 KVHGKDSPLKVP-KFDKKQLAISTLDFEIRHQLTQIHGLYRSSDKTGGYWKIT-----196
QY 187 HSSSEGSTVSVDL-----PDAQOQYPTLLRIYRDNKNTINSE 222
Db 197 -MNDGSTYQSDLSKKFYNTEKPPINI---DEIKTIEAE 231

RESULT 64
US-10-282-122A-70242
; Sequence 70242, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70242
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-282-122A-70242
Query Match      8.4%; Score 104.5; DB 12; Length 232;
Best Local Similarity 24.1%; Pred. No. 0.051;
Matches 61; Conservative 31; Mismatches 80; Indels 81; Gaps 14;

;
QY 10 KDLRKKSELOGTA---LGNLKOIYYVNEKAITENK---ESDDOFLENTL-----LFK 55
Db 26 KAVHAKVELDETQRYIYNMLHQ---YSEBSFESTNISVSEDIYGSNVLNFORNKTFFK 83
QY 56 GFTTGHWPYNLLVDLGSKDATNKYKGGK-----VDLYGAYYGYOCAGGTPNKT 104
Db 84 VFLLG-----DDKNKYKEKTHGLDVFAVPELIDIKGGI--YSGVGITKQNV 127
QY 105 ACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYL 164
Db 128 RSVFGFV-----SNPSLQVKV-----DAKHGFSINELFFQKEEVSLEKELDFKIRKMLV 177
QY 165 GKFGLYNSDSFGKVGQRLIVFHSSE-----GSTVSYD-LFDAOQYPTLLRIYRD 215
Db 178 EKRYLYK-----GASDKGRIVNNMKDEKKYVIDLSEKLSFDRMFDVM-----D 220
QY 216 NKTINSENHLIAL 228
Db 221 SKQI--KNIEVNL 231

RESULT 65
US-10-002-784A-12
; Sequence 12, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 12
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: toxin shock syndrome toxin-1 mutant
US-10-002-784A-12
Query Match      8.4%; Score 104.5; DB 14; Length 234;
Best Local Similarity 26.2%; Pred. No. 0.052;
Matches 42; Conservative 25; Mismatches 50; Indels 43; Gaps 8;

QY 81 KGKVDL-----YGAIVGYOCAGGTPNKTACMYGVTLDHNNRLTEKKVPIN 128
Db 98 KGEKVDLNTKTKKSQTSYTHFQISGV-----NTEKLPTEIPLK 143
QY 129 LWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLY-NSDSFGG--KVQRLIV 185
Db 144 KVHGKDSPLKVP-KFDKKQLAISTLDFEIRHQLTQIHGLYRSSDKTGGYWKIT-----197
QY 186 PHSSEGSTVSVDL-----PDAQOQYPTLLRIYRDNKNTINSE 222
Db 198 -MNDGSTYQSDLSKKFYNTEKPPINI---DEIKTIEAE 232

RESULT 66
US-09-465-714-3
; Sequence 3, Application US/09465714
; Publication No. US20030032582A1
; GENERAL INFORMATION:
; APPLICANT: Wahlsten, Jennifer L.
; APPLICANT: Ramakrishnan, S.
; APPLICANT: Schlievert, Patrick M.
; TITLE OF INVENTION: SPONTANEOUS MEMBRANE INSERTION
; FILE REFERENCE: 09531/003001
; CURRENT APPLICATION NUMBER: US/09/465,714

```

```

; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-354-948-6

Query Match      8.4%; Score 103.5; DB 12; Length 194;
Best Local Similarity 22.7%; Pred. No. 0.05;
Matches 53; Conservative 36; Mismatches 65; Indels 79; Gaps 13;

QY 11 DLRKSELOGTALGNLKQIYYNNEKAITENKESDDQFLENTLLFKGFTTGHGPMWDLVD 70
Db 18 DFTNSEVLDNLSGSMR-----IKNTDGI--SLIIFPS-----PYISAPT- 57
QY 71 LGSKDATNKYKGGKVDL-----YGAYGYQCAGGTENKTACMGVGTLDHNNR 118
Db 58 -----KGEKVDLNTKTKKSQHTSEGIYHFQISGVT-----NTEK 93
QY 119 LTEKKVPINLWDGQTTV---PIDKVTSKKEVTVQELDLQARHYLHGKFGLY-NSDS 174
Db 94 LPTPELPLKVKVHGKDSPLKYP---KFDDKKQLAISTLDPEIRHQLTQIHGLYRSSDK 149
QY 175 FCG--KVQKGLVFFHSSEGSTVSYDL---FDAQQGYPTDLLRIYRDNKTNSE 222
Db 150 TGGYWKIT-----MNDGSTVQSDLSKKFYEYNTKPPINI---DEIKTIEAE 192

RESULT 68
US-10-282-122A-70390
; Sequence 70390, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:

```

```

/ APPLICANT: Zamudio, Cheryl
/ APPLICANT: Malone, Cheryl
/ APPLICANT: Haselbeck, Robert
/ APPLICANT: Ohlsen, Kari
/ APPLICANT: Zyskind, Judith
/ APPLICANT: Wall, Daniel
/ APPLICANT: Trawick, John
/ APPLICANT: Carr, Grant
/ APPLICANT: Yamamoto, Robert
/ APPLICANT: Forsyth, R.
/ APPLICANT: Xu, H.
/ TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
/ FILE REFERENCE: ELITRA.034A
/ CURRENT APPLICATION NUMBER: US/10/282,122A
/ CURRENT FILING DATE: 2003-02-20
/ PRIOR APPLICATION NUMBER: 60/191,078
/ PRIOR FILING DATE: 2000-03-21
/ PRIOR APPLICATION NUMBER: 60/206,848
/ PRIOR FILING DATE: 2000-05-23
/ PRIOR APPLICATION NUMBER: 60/207,727
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: 60/230,335
/ PRIOR FILING DATE: 2000-09-06
/ PRIOR APPLICATION NUMBER: 60/230,347
/ PRIOR FILING DATE: 2000-09-09
/ PRIOR APPLICATION NUMBER: 60/242,578
/ PRIOR FILING DATE: 2000-10-23
/ PRIOR APPLICATION NUMBER: 60/253,625
/ PRIOR FILING DATE: 2000-11-27
/ PRIOR APPLICATION NUMBER: 60/257,931
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/267,636
/ PRIOR FILING DATE: 2001-02-09
/ PRIOR APPLICATION NUMBER: 60/269,308
/ PRIOR FILING DATE: 2001-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 78614
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 70390
/ LENGTH: 234
/ TYPE: prt
/ ORGANISM: Stanblyococcus aureus

```

US-10-282-122A-70390

Query Match	8.4%	Score 103.5;	DB 12;	Length 234;
Best Local Similarity	22.7%;	Pred. No. 0.065;		
Matches	53;	Conservative 36;	Mismatches 65;	Indels 79; Gaps 13;

QY	11	DLRKSELOGTALGNLQIYYVNEKAITENKSDQDFLENTLLPKGFFTGHPWYNLLVD	70
DB	58	DTFNSEVLNLSGSMR-----IKNTDGI--SLIIFPS-----PYSPAFI- 97	
QY	71	LGSKDATNKYKGKVDL-----YGAYGYQCAGGTPNKTACWYGVTLHDNR	118
DB	98	-----KGEKVDLNTKRKKSGHTSEGTVIHFQISGVT-----NTEK 133	
QY	119	LTEKKYPINLWIDGKQTV---PIDKVTSSKEVTQQLDLQARHYLHGKFLY-NSDS	174
DB	134	LPTPIELPQVKVHGKSDLPKYVP---KPDKKQLAISTLDFEIRHQUTQIHGLYRSDK	189
QY	175	FGG--KVQRGLIVFHSSEGSTVSYDL---FDAQGYQPDTLRIYRDNKTIINSE	222
DB	190	TGGYWKIT-----MMDGTYOSDLSSKPEYNTKEPPINI---DEIKTISAE	232

69 T.115AA

```

US-09-465-714-1
; Sequence 1, Application US/09465714
; Publication No. US20030032582A1
; GENERAL INFORMATION:
; APPLICANT: Wahlsten, Jennifer L.
; APPLICANT: Ramakrishnan, S.
; APPLICANT: Schlievert, Patrick M.
; TITLE OF INVENTION: SPONTANEOUS MEMBRANE INSERTION
; FILE REFERENCE: 09531/003001
; CURRENT APPLICATION NUMBER: US/09/465,714
; CURRENT FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/001,593
; PRIOR FILING DATE: 1998-12-31
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Hybrid containing bacterial and mammalian sequence
US-09-465-714-1

```

```

Query Match      8.4%; Score 103.5; DB 10; Length 238;
Best Local Similarity 22.7%; Pred. No. 0.067;
Matches 53; Conservative 36; Mismatches 65; Indels 79; Gaps 13;

QY      11 DLRKSELGQTALGNLKLQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVD 70
         |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
DB      18 DTFTNSEVLDNLSGR-----IKNTDGI--SLIIFPS-----PYISPAFT- 57

QY      71 LGSKDATNKKYGGKKVDL-----YGAYYGQCAGGTENKTACMGYGVTLHDNNR 118
         |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
DB      58 -----KGEKVDLNTKRTKKSQHTSBSGTVIHFQISGVT-----NTEK 93

QY      119 LTEEKKVPINLWIDGKOTTV---PIDKVTSKKEVTVQELD-QARHYLHGKFGLY-NSDS 174
         |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
DB      94 LPTPIELPLKVKVHGKUSPLKYWP---KPKKQLAISTLDFEIRHQLTQHLGYRSDK 149

QY      175 FGG--KVQRGLIVFHSSEGSTVSVDL---FDAQQYPTDLLRIYRDNKTIINSE 222
         |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||: |||:
DB      150 TGGYWKIF-----MNDGTSYSDLSKKFEYNTKPPINI---DEIKTIRAE 192

```

PECHT 70

US-10-435-766-23
; Sequence 23, Application US/10435766
; Publication No. US20030228616A1
; GENERAL INFORMATION:

```

1  APPLICANT: Sorge, Joseph A
2  APPLICANT: Arezi, Bahram
3  APPLICANT: Hogrefe, Holly
4  APPLICANT: Hansen, Connie J
5  TITLE OF INVENTION: DNA Polymerase Mutants with Reverse Transcript
6  FILE REFERENCE: 25436/1585C
7  CURRENT APPLICATION NUMBER: US/10/435,766
8  CURRENT FILING DATE: 2003-05-12
9  PRIOR APPLICATION NUMBER: US 10/223,650
10 PRIOR FILING DATE: 2002-08-19
11 PRIOR APPLICATION NUMBER: US 09/896,923
12 PRIOR FILING DATE: 2001-06-29
13 PRIOR APPLICATION NUMBER: US 09/698,341
14 PRIOR FILING DATE: 2000-10-27
15 PRIOR APPLICATION NUMBER: US 60/162,600
16 PRIOR FILING DATE: 1999-10-29
17 PRIOR APPLICATION NUMBER: PCT/US00/29706
18 PRIOR FILING DATE: 2000-10-27
19 NUMBER OF SEQ ID NOS: 104
20 SOFTWARE: PatentIn version 3.2
21 SEQ ID NO 23
22     LENGTH: 1634
23     TYPE: PRT
24     ORGANISM: Methanococcus jannaschii
25     FEATURE:
26     NAME/KEY: misc_feature
27     LOCATION: (382)..(382)
28     OTHER INFORMATION: Xaa can be any naturally occurring amino acid
29     US-10-435-766-23

```

Query Match	8.2%;	Score 101;	DB 15;	Length 1634;
Best Local Similarity	22.9%;	Pred. No. 1.7;		
Matches 53;	Conservative 33;	Mismatches 79;	Indels 66;	
QY	12	LRKGELOGTALGNLQIYYNEXAKTENKESDQFLENTLLRFGPFTGHPWYND		
Db	614	VARKGKTATILGCAKDYLKIEELKCKE--KYLPNAIL-RGFFEGDGYVNT		
QY	72	GSKDATNRYKGGK-----VDLYGAYYQCAGGTGPNKTACMYGGVTLDHNNRLTE		
Db	670	VVNQGTNNYDKIFETASLLDLRGIKYSF-----YTYSYBERGKKK		
QY	127	INLWIDGRQTTVPIDKVKTS-----KKEVTVQELDLQARHYLHGKFGLYNSD		
Db	714	EIFSKG-----DLIKFSLLISFISRRKNLNEIRQKTLKIGDYGFYDL		
QY	174	-----SFGKV-----QRGLIVFHSSEGS-TVSYDLFDAQCGQVPDTL 209		
Db	767	IESYGEVVDLTLEGRYPFYANGILTNLSYPSIIISYNI-----SPDTL 811		

```

RESULT 71
US-09-815-242-5900
; Sequence 5900, Application US/09815242
; Patent No. US20020061589A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011a
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; CURRENT APPLICATION NUMBER: 60/206,848

```



```
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 1410
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5900
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5900

Query Match
Best Local Similarity 24.1%; Score 100; DB 9; Length 226;
Matches 48; Conservative 42; Mismatches 79; Indels 30; Gaps 8;

QY 8 NEKLRKKSELOQTALGNLKQIYYNE-----KAITENKESDD--QFLENTLLFKGFTG 60
Db 24 NVQSVQAKAEVKQOSESELK--HYNKPILERKNVTGFKYTDEGKHYLEVT----- 73
QY 61 HPWYNDLLVDLGS-KDATNKYKGGKVDLYGAYGYQCAGGTGPNKTCMYGGVTLHDNNRL 119
Db 74 -GQHSRITLLGSDKDKFKDGENSNIDVF-----ILREGDSRCATNYSIGVTKNSVQY 127
QY 120 TEKKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFLYNSDSFGGKV 179
Db 128 IDYINTPI-LEIKKDNEDVLKDFYISKEDISLKELDYLRERAIKQHGLYSNG----- 181
QY 180 QRGGLIVFHSSEGSTVSVDL 198
Db 182 KQGQITITMNDGTTHTIDL 200

RESULT 72
US-09-815-242-13156
; Sequence 13156, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 1410
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13156
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-13156

Query Match
Best Local Similarity 24.1%; Score 100; DB 9; Length 226;
Matches 48; Conservative 42; Mismatches 79; Indels 30; Gaps 8;

QY 8 NEKLRKKSELOQTALGNLKQIYYNE-----KAITENKESDD--QFLENTLLFKGFTG 60
Db 24 NVQSVQAKAEVKQOSESELK--HYNKPILERKNVTGFKYTDEGKHYLEVT----- 73
QY 61 HPWYNDLLVDLGS-KDATNKYKGGKVDLYGAYGYQCAGGTGPNKTCMYGGVTLHDNNRL 119
Db 74 -GQHSRITLLGSDKDKFKDGENSNIDVF-----ILREGDSRCATNYSIGVTKNSVQY 127
QY 120 TEKKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFLYNSDSFGGKV 179
Db 128 IDYINTPI-LEIKKDNEDVLKDFYISKEDISLKELDYLRERAIKQHGLYSNG----- 181
QY 180 QRGGLIVFHSSEGSTVSVDL 198
Db 182 KQGQITITMNDGTTHTIDL 200

RESULT 73
US-10-424-599-264720
; Sequence 264720, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 264720
; LENGTH: 621
; TYPE: PRT
; ORGANISM: Glycine max
; OTHER INFORMATION: Clone ID: PAT_MRT3847_81062C.1.pap
US-10-424-599-264720

Query Match
Best Local Similarity 22.8%; Score 99; DB 12; Length 621;
Matches 50; Conservative 40; Mismatches 77; Indels 52; Gaps 11;

QY 24 GNLKQIYYN--EKAITEN-KESDDQFLENTLLFKGFTGHPWYNDLLVDLGSKDATNK 79
Db 155 GNGTDVYQKGDSSSTLTDSEESDSSVNN---YSGFSRNG---SDLGINRRIMELETE 208
QY 80 YKGGKVDLYGAYGYQCAGGTGPNKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVP 139
Db 209 LREVKELWQEEHA-----DGSSTRGRNENTEDVYTKINAY---EQELMT 252
QY 140 I-DKVTKSKKEVTVQELDLQARHYLHGKFLYNSDSFGGKVQRLIVFHSSEGST----- 193
Db 253 VNEKRLSEBEITKQKIELQ-----KYRLFNTENLEAGFESSLTKKHINEGGEAHKMI 305
QY 194 -----VSDYDFDAQQYFDTILLRIYRDNKTKINSEN 224
Db 306 EVEGSDIGVDKELFDQNGEI-ETLARELR-----ITKENL 339

RESULT 74
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US-10-425-114-57792
; Sequence 57792, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 57792
; LENGTH: 628
; TYPE: PRT
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: UC-GMROPI0107B05_FLI.pep
US-10-425-114-57792

Query Match      8.0%; Score 99; DB 12; Length 628;
Best Local Similarity 22.8%; Pred. No. 0.72;
Matches 50; Conservative 40; Mismatches 77; Indels 52; Gaps 11;

QY 24 GNLKQIYYYN---EKAITEN-KESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNK 79
DB 162 GNGTDVQKGDSESTLTDSEESDDSVNN---YSGFSRNG---SDLGINRIMELETE 215
QY 80 YGKKVDLYGAYGYQCAGGTPNKTCWYGVTLHNNRLTEKKVPINLWIDGKQTTVP 139
DB 216 LREVEKELMQEBEHA-----DGSTRGSRNENTEDLYTKINAY---EQELMT 259
QY 140 I-DKVTSKKEVTVOEQLDQARVHLHGKFGLYNSDSPGGKVQVORGLIVFHSSEGST---- 193
DB 260 VNEKRLUSEEITKQKIELQ-----KYRLFNTENLEAGFESLTKKHINEGEAHKMI 312
QY 194 -----VSYDLFDAOGQYPTDLLRIYRDNKNTINSEN 224
DB 313 EVEGSDGVDKELFDQNGEI-ETLARELR-----ITKENL 346

RESULT 75
US-10-282-122A-70240
; Sequence 70240, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
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; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 70240
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-282-122A-70240

Query Match      8.0%; Score 98.5; DB 12; Length 231;
Best Local Similarity 23.6%; Pred. No. 0.2;
Matches 55; Conservative 29; Mismatches 96; Indels 53; Gaps 10;

QY 2 EKSEBINE---KDLRKSELOQTALGNL--KQIYYNEKAITENKESDDQFLENTLLFK 55
DB 32 EKQERVQHLVDIKOLYRYYSSEFEFNSGKVENYNGSNVVRFNQEK-----QNHQLF- 85
QY 56 GFETGHPWYNDLLVDLGSKDATNKYK---GKKYVDLYGAYGYQCAGGTPNKTCMYGV 111
DB 86 -----LLGKD-KDKYKKGLEQNVVVKELI-----DPNGRLSTVGV 122
QY 112 TLHDNNRLTEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOEQLDQARVHLHGKFGLYN 171
DB 123 TKKNNKSETNTHLFVNK-VYGGNLDASIDSFLINKBEVSLKELDFKIRKOLVEKGYLK 181
QY 172 SDSFGKQVQVORGLIVFHSSEGSTVSYDLFDAOGQYPTDLLRIYRDNKNTINSEN 224
DB 182 -----GTTKYGKITINLKDEKKEVIDLGDK-----LQFERMGDVNLNSKI 221

Search completed: August 12, 2004, 13:46:23
Job time : 27.7742 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 12, 2004, 13:27:15 ; Search time 9.21353 Seconds

(without alignments)
1305.563 Million cell updates/sec

Title: US-09-900-766-3

Perfect score: 1238

Sequence: 1 SEKSEINERDLRKKSELOQ.....RDKNKTINSENHIALYLYTT 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA.**

1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep.*

2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep.*

3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep.*

4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep.*

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6: /cgn2_6/ptodata/2/iaa/backfiles.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1210	97.7	233	4	US-08-695-692B-8
2	1210	97.7	257	3	US-08-486-0399-112
3	1210	97.7	257	3	US-08-360-107A-122
4	1210	97.7	257	3	US-08-484-223B-112
5	1210	97.7	257	3	US-08-919-597-112
6	1210	97.7	257	3	US-08-475-668A-112
7	1210	97.7	257	3	US-08-485-551A-112
8	1210	97.7	257	3	US-08-471-913A-112
9	1210	97.7	257	3	US-08-485-264A-112
10	1210	97.7	257	4	US-08-474-349A-112
11	1210	97.7	257	4	US-08-470-896-112
12	1210	97.7	257	4	US-08-485-546A-112
13	1143	92.3	226	3	US-08-896-933-24
14	1143	92.3	226	4	US-09-314-235-24
15	1037	83.8	233	4	US-08-695-692B-7
16	1037	83.8	257	3	US-08-486-0399-113
17	1037	83.8	257	3	US-08-360-107A-123
18	1037	83.8	257	3	US-08-484-223B-113
19	1037	83.8	257	3	US-08-919-597-113
20	1037	83.8	257	3	US-08-475-668A-113
21	1037	83.8	257	3	US-08-485-551A-113
22	1037	83.8	257	3	US-08-471-913A-113
23	1037	83.8	257	3	US-08-485-264A-113
24	1037	83.8	257	4	US-08-474-349A-113
25	1037	83.8	257	4	US-08-470-896-113
26	1037	83.8	257	4	US-08-485-546A-113
27	1033	83.4	233	1	US-08-446-918A-4

28	1033	83.4	233	2	US-08-580-806-4	Sequence 4, Appli
29	1017.5	82.2	232	3	US-08-896-933-23	Sequence 23, Appl
30	1017.5	82.2	232	4	US-09-314-235-23	Sequence 23, Appl
31	1014	81.9	237	4	US-09-144-776B-2	Sequence 2, Appli
32	1010	81.6	233	4	US-09-144-776B-4	Sequence 4, Appli
33	657	53.1	228	3	US-08-896-933-25	Sequence 25, Appl
34	657	53.1	228	4	US-09-314-235-25	Sequence 25, Appl
35	457	36.9	82	4	US-09-144-776B-19	Sequence 19, Appl
36	399	32.2	82	4	US-09-144-776B-17	Sequence 17, Appl
37	303.5	24.5	255	1	US-08-446-918A-2	Sequence 17, Appl
38	303.5	24.5	255	2	US-08-580-806-2	Sequence 2, Appli
39	298.5	24.1	238	3	US-08-896-933-28	Sequence 28, Appl
40	298.5	24.1	238	4	US-09-314-235-28	Sequence 28, Appl
41	296.5	23.9	239	3	US-08-896-933-26	Sequence 26, Appl
42	296.5	23.9	239	4	US-09-314-235-26	Sequence 26, Appl
43	296.5	23.9	266	4	US-09-144-776B-6	Sequence 6, Appli
44	296.5	23.9	266	4	US-09-144-776B-10	Sequence 10, Appl
45	291.5	23.1	239	4	US-09-144-776B-8	Sequence 8, Appli
46	286.5	23.1	266	4	US-08-896-933-29	Sequence 29, Appl
47	284.5	23.0	221	3	US-08-896-933-29	Sequence 29, Appl
48	284.5	23.0	221	4	US-09-314-235-29	Sequence 29, Appl
49	282.5	22.8	251	4	US-08-973-391C-13	Sequence 13, Appl
50	279.5	22.6	251	4	US-08-973-391C-14	Sequence 14, Appl
51	277.5	22.4	251	4	US-09-144-776B-16	Sequence 16, Appl
52	271.5	21.9	239	3	US-08-896-933-27	Sequence 27, Appl
53	271.5	21.9	239	4	US-09-314-235-27	Sequence 27, Appl
54	264.5	21.4	239	3	US-08-896-933-21	Sequence 21, Appl
55	264.5	21.4	239	4	US-09-314-235-21	Sequence 21, Appl
56	262.5	21.2	266	4	US-09-144-776B-14	Sequence 14, Appl
57	234	18.9	220	3	US-08-896-933-20	Sequence 20, Appl
58	234	18.9	220	4	US-09-314-235-20	Sequence 20, Appl
59	215	17.4	82	4	US-09-144-776B-18	Sequence 18, Appl
60	213	17.2	45	1	US-08-220-378-1	Sequence 1, Appli
61	213	17.2	45	2	US-08-696-012-1	Sequence 1, Appli
62	173.5	14.0	208	3	US-08-896-933-30	Sequence 30, Appl
63	173.5	14.0	208	4	US-09-314-235-30	Sequence 30, Appl
64	137.5	11.1	89	4	US-09-144-776B-20	Sequence 20, Appl
65	131	10.6	27	3	US-08-896-933-34	Sequence 34, Appl
66	131	10.6	27	4	US-09-314-235-34	Sequence 34, Appl
67	129	10.4	28	1	US-08-220-378-2	Sequence 2, Appli
68	129	10.4	28	2	US-08-696-012-2	Sequence 2, Appli
69	127	10.3	24	3	US-08-838-413A-22	Sequence 22, Appl
70	126	10.2	23	1	US-08-220-378-5	Sequence 5, Appli
71	126	10.2	23	2	US-08-696-012-5	Sequence 5, Appli
72	124	10.0	29	1	US-08-220-378-6	Sequence 6, Appli
73	124	10.0	29	2	US-08-696-012-6	Sequence 6, Appli
74	121	9.8	79	4	US-09-144-776B-24	Sequence 24, Appl
75	120	9.7	22	1	US-08-220-378-4	Sequence 4, Appli
76	120	9.7	22	2	US-08-696-012-4	Sequence 4, Appli
77	112.5	9.1	89	4	US-09-144-776B-22	Sequence 22, Appl
78	112.5	9.1	89	4	US-09-144-776B-23	Sequence 23, Appl
79	110.5	8.9	444	4	US-09-134-001C-4346	Sequence 4346, Ap
80	107	8.6	193	3	US-08-896-933-31	Sequence 31, Appl
81	107	8.6	193	4	US-09-314-235-31	Sequence 31, Appl
82	106.5	8.6	29	1	US-08-220-378-9	Sequence 9, Appli
83	106.5	8.6	29	2	US-08-696-012-9	Sequence 9, Appli
84	106	8.6	28	1	US-08-220-378-7	Sequence 7, Appli
85	106	8.6	28	2	US-08-696-012-7	Sequence 7, Appli
86	105.5	8.5	89	4	US-09-144-776B-21	Sequence 21, Appl
87	105.5	8.5	234	3	US-08-486-099-111	Sequence 111, App
88	105.5	8.5	234	3	US-08-360-107A-121	Sequence 121, App
89	105.5	8.5	234	3	US-08-471-913A-111	Sequence 111, App
90	105.5	8.5	234	3	US-08-485-551A-111	Sequence 111, App
91	105.5	8.5	234	3	US-08-471-913A-111	Sequence 111, App
92	105.5	8.5	234	3	US-08-485-264A-111	Sequence 111, App
93	105.5	8.5	234	3	US-08-485-264A-111	Sequence 111, App
94	105.5	8.5	234	4	US-08-474-349A-111	Sequence 111, App
95	105.5	8.5	234	4	US-08-470-896-111	Sequence 111, App
96	105.5	8.5	234	4	US-08-485-546A-111	Sequence 111, App
97	105.5	8.5	234	4	US-08-485-546A-111	Sequence 111, App
98	105	8.5	25	1	US-08-220-378-3	Sequence 3, Appli
99	105	8.5	25	2	US-08-696-012-3	Sequence 3, Appli
100	104.5	8.4	234	4	US-09-144-776B-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-08-695-692B-8
; Sequence 8, Application US/08695692B
; Patent No. 6514498
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
; APPLICANT: Johan Hansson, Terje Kalland, Lars
; APPLICANT: Abrahamson and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; TITLE OF INVENTION: AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: August 12, 1996
; APPLICATION NUMBER: US/08/695,692B
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9601245-5
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 41986/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-695-692B-8

Query Match 97.7%; Score 1210; DB 4; Length 233;
Best Local Similarity 97.9%; Pred. No. 4.6e-117;
Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTKACMYGGVTLHDNNRLT 120
DB 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTKACMYGGVTLHDNNRLT 120
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 181 RGLIVFHSSSGSVSYDLFDAQCYPTLLRIYRDKNKTINSENHLIALYLYTT 233
DB 181 RGLIVFHSSSGSVSYDLFDAQCYPTLLRIYRDKNKTINSENHLIALYLYTT 233

RESULT 2
US-08-486-099-112

; Sequence 112, Application US/08486099
; Patent No. 6013263
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
; TITLE OF INVENTION: B VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,099
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-486-099-112

Query Match 97.7%; Score 1210; DB 3; Length 257;
Best Local Similarity 97.9%; Pred. No. 5.3e-117;
Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOQTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTKACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTKACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSSGSVSYDLFDAQCYPTLLRIYRDKNKTINSENHLIALYLYTT 233
DB 205 RGLIVFHSSSGSVSYDLFDAQCYPTLLRIYRDKNKTINSENHLIALYLYTT 257

RESULT 3
US-08-360-107A-122
; Sequence 122, Application US/08360107A
; Patent No. 6017536
; GENERAL INFORMATION:

APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Pettaway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360.107A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-360-107A-122

Query Match 97.7%; Score 1210; DB 3; Length 257;
Best Local Similarity 97.9%; Pred. No. 5.3e-117;
Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLPKGFTG 60
Db 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLPKGFTG 84
Qy 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 120
Db 85 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 144
Qy 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
Db 145 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 204
Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHIALYLYTT 233
Db 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHIALYLYTT 257

RESULT 4
US-08-484-223B-112
Sequence 112, Application US/08484223B
Patent No. 6020459
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.

APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Pettaway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 245
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-223B-112

Query Match 97.7%; Score 1210; DB 3; Length 257;
Best Local Similarity 97.9%; Pred. No. 5.3e-117;
Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Qy 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLPKGFTG 60
Db 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLPKGFTG 84
Qy 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 120
Db 85 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 144
Qy 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
Db 145 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 204
Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHIALYLYTT 233
Db 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSENHIALYLYTT 257

RESULT 5
US-08-919-597-112
Sequence 112, Application US/08919597
Patent No. 6054265
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Pettaway, Stephen R.

```

; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/919,597
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,896
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Cortuzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 780-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-919-597-112

Query Match 97.7%; Score 1210; DB 3; Length 257;
Best Local Similarity 97.9%; Pred. No. 5.3e-117;
Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELOQTALGNLKIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDANKYKGVKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVDLGSKDANKYKGVKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDQAQGYPTLLRIYRDNKTINSENHLIALYLYTT 233
Db 205 RGLIVFHSSEGSTVSVDLFDQAQGYPTLLRIYRDNKTINSENHLIALYLYTT 257

RESULT 6
US-08-475-668A-112
; Sequence 112, Application US/08475668A
; Patent No. 6060065
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION

```

```

; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,668A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Cortuzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 780-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-475-668A-112

Query Match 97.7%; Score 1210; DB 3; Length 257;
Best Local Similarity 97.9%; Pred. No. 5.3e-117;
Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOQTALGNLKIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELOQTALGNLKIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDANKYKGVKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVDLGSKDANKYKGVKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDQAQGYPTLLRIYRDNKTINSENHLIALYLYTT 233
Db 205 RGLIVFHSSEGSTVSVDLFDQAQGYPTLLRIYRDNKTINSENHLIALYLYTT 257

RESULT 7
US-08-485-551A-112
; Sequence 112, Application US/08485551A
; Patent No. 6068973
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP

```

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485.551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-551A-112

Query Match 97.7%; Score 1210; DB 3; Length 257;

Best Local Similarity 97.9%; Pred. No. 5.3e-117;

Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKXSELQGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKXSELQGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYOCAGTGNKACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYOCAGTGNKACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVTSKKVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHIALYLYTT 233
DB 205 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHIALYLYTT 257

RESULT 8

US-08-471-913A-112

; Sequence 112, Application US/08471913A

; Patent No. 6093794

; GENERAL INFORMATION:

; APPLICANT: Bolognesi, Dani P.

; APPLICANT: Matthews, Thomas J.

; APPLICANT: Wild, Carl T.

; APPLICANT: Barney, Shawn O.

; APPLICANT: Lambert, Dennis M.

; APPLICANT: Pettaway, Stephen R.

; APPLICANT: Langlois, Alphonse J.

; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE

; FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS

; TRANSMISSION

; NUMBER OF SEQUENCES: 214

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-471-913A-112

Query Match 97.7%; Score 1210; DB 3; Length 257;

Best Local Similarity 97.9%; Pred. No. 5.3e-117;

Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKXSELQGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKXSELQGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYOCAGTGNKACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYOCAGTGNKACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVTSKKVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHIALYLYTT 233
DB 205 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHIALYLYTT 257

RESULT 9

US-08-485-264A-112

; Sequence 112, Application US/08485264A

; Patent No. 6228983

; GENERAL INFORMATION:

; APPLICANT: Bolognesi, Dani P.

; APPLICANT: Matthews, Thomas J.

; APPLICANT: Wild, Carl T.

; APPLICANT: Barney, Shawn O.

; APPLICANT: Lambert, Dennis M.

; APPLICANT: Pettaway, Stephen R.

; APPLICANT: Langlois, Alphonse J.

; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF

; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING

; RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION

; NUMBER OF SEQUENCES: 232

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds LLP

; STREET: 1155 Avenue of the Americas

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10036-2711

; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,264A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-021
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-264A-112

Query Match 97.7%; Score 1210; DB 3; Length 257;
Best Local Similarity 97.9%; Pred. No. 5.3e-117;
Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSELOQTALGNLKQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSELOQTALGNLKQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVLDGSKDATNKYKKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 120
DB 85 HPWYNDLLVLDGSKDATNKYKKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 144
QY 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHVLHGKFLGFLYNSDSFGKVKQ 180
DB 145 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHVLHGKFLGFLYNSDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDQAQGYPTDLLRIYRDNKTINSENLHIALYLYTT 233
DB 205 RGLIVFHSSEGSTVSVDLFDQAQGYPTDLLRIYRDNKTINSENLHIALYLYTT 257

RESULT 10
US-08-474-349A-112
Sequence 112, Application US/08/474349A
Patent No. 633395
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
TITLE OF INVENTION: VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 517
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,349A
FILING DATE: 07-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-024
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-474-349A-112
Query Match 97.7%; Score 1210; DB 4; Length 257;
Best Local Similarity 97.9%; Pred. No. 5.3e-117;
Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKKSELOQTALGNLKQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSELOQTALGNLKQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVLDGSKDATNKYKKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 120
DB 85 HPWYNDLLVLDGSKDATNKYKKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHNNRLT 144
QY 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHVLHGKFLGFLYNSDSFGKVKQ 180
DB 145 EEKVPINLWIDGKQTTPIDKVKTSKEVTVOELDLQARHVLHGKFLGFLYNSDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDQAQGYPTDLLRIYRDNKTINSENLHIALYLYTT 233
DB 205 RGLIVFHSSEGSTVSVDLFDQAQGYPTDLLRIYRDNKTINSENLHIALYLYTT 257

RESULT 11
US-08-470-896-112
Sequence 112, Application US/08470896
Patent No. 647955
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,896


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; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-470-896-112

Query Match 97.7%; Score 1210; DB 4; Length 257;
Best Local Similarity 97.9%; Pred. No. 5.3e-117;
Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTTG 60
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTTG 84
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGTGNKACMYGGVTLHNNRLT 120
DB 85 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGTGNKACMYGGVTLHNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNKTINSENHLIALYLYTT 233
DB 205 RGLIVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNKTINSENHLIALYLYTT 257

RESULT 12
US-08-485-546A-112
; Sequence 112, Application US/08485546A
; Patent No. 6518013
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Pettaway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,546A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
```

```
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-485-546A-112

Query Match 97.7%; Score 1210; DB 4; Length 257;
Best Local Similarity 97.9%; Pred. No. 5.3e-117;
Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTTG 60
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTTG 84
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGTGNKACMYGGVTLHNNRLT 120
DB 85 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGTGNKACMYGGVTLHNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNKTINSENHLIALYLYTT 233
DB 205 RGLIVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNKTINSENHLIALYLYTT 257

RESULT 13
US-08-896-933-24
; Sequence 24, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-08-896-933-24

Query Match 92.3%; Score 1143; DB 3; Length 226;
Best Local Similarity 93.5%; Pred. No. 3.7e-110;
Matches 215; Conservative 5; Mismatches 6; Indels 4; Gaps 1;

QY 4 SESEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTTGHPW 63
DB 1 SESEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTTGHPW 60
QY 64 YNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGTGNKACMYGGVTLHNNRLTEEX 123
DB 61 YNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGTGNKACMYGGVTLHNNRLTEE - 119
QY 124 KVPINLWIDGKQTTVPIDKVTSKKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQ 183
DB 120 ---VBKWIDGKQTTVPIDKVTSKKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQ 176
```

QY 184 IVFHSSEGSTVSYDLFDAQGYPTLRIYRDNKTINSENHIALYLYTT 233
 Db 177 IVFHSSEGSTVSYDLFDAQGYPTLRIYRDNKTINSENHIALYLYTT 226

RESULT 14

US-09-314-235-24
 ; Sequence 24, Application US/09314235
 ; Patent No. 6338845
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 ; SUPERANTIGENS, AND RELATED COMPOUNDS
 ; FILE REFERENCE: 09628/005004
 ; CURRENT APPLICATION NUMBER: US/09/314,235
 ; CURRENT FILING DATE: 1999-05-18
 ; EARLIER APPLICATION NUMBER: 08/896,933
 ; EARLIER FILING DATE: 1997-07-18
 ; EARLIER APPLICATION NUMBER: 08/252,978
 ; EARLIER FILING DATE: 1994-06-02
 ; EARLIER APPLICATION NUMBER: 07/891,718
 ; EARLIER FILING DATE: 1992-06-01
 ; EARLIER APPLICATION NUMBER: US91/00342
 ; EARLIER FILING DATE: 1991-01-17
 ; EARLIER APPLICATION NUMBER: 07/466,577
 ; EARLIER FILING DATE: 1990-01-17
 ; EARLIER APPLICATION NUMBER: 07/416,530
 ; EARLIER FILING DATE: 1989-10-03
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 24
 ; LENGTH: 226
 ; TYPE: PRP
 ; ORGANISM: Staphylococcus aureus
 US-09-314-235-24

Query Match 92.3%; Score 1143; DB 4; Length 226;
 Best Local Similarity 93.5%; Pred. No. 3.7e-110;
 Matches 215; Conservative 5; Mismatches 6; Indels 4; Gaps 1;
 QY 4 SEBINEKDLRKSELOGTALGNLQKIYYNEKAITENKESDDQFLENTLLFKGFTGHPW 63
 Db 1 SEBINEKDLRKSELOGTALGNLQKIYYNEKAITENKESDDQFLENTLLFKGFTGHPW 60
 QY 64 YNDLLVDLGSKDATNKYKGVLDLYGAYGYQACAGTGNKTCMYGGVTLHDNNRLTEK 123
 Db 61 YNDLLVDLGSKDATNKYKGVLDLYGAYGYQACAGTGNKTCMYGGVTLHDNNRLTEB 119
 QY 124 KVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRL 183
 Db 120 ---VBKWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRL 176
 QY 184 IVFHSSEGSTVSYDLFDAQGYPTLRIYRDNKTINSENHIALYLYTT 233
 Db 177 IVFHSSEGSTVSYDLFDAQGYPTLRIYRDNKTINSENHIALYLYTT 226

RESULT 15

US-08-695-692B-7
 ; Sequence 7, Application US/08695692B
 ; Patent No. 6514498
 ; GENERAL INFORMATION:
 ; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
 ; APPLICANT: Johan Hansson, Terje Kalland, Lars
 ; APPLICANT: Abrahamson and Goran Forsberg
 ; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
 ; TITLE OF INVENTION: AND THEIR USE
 ; NUMBER OF SEQUENCES: 24
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
 ; STREET: 1177 West Loop South, 10th Floor
 ; CITY: Houston

STATE: TX
 COUNTRY: USA
 ZIP: 77027-9095
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/695,692B
 FILING DATE: August 12, 1996
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 9601245-5
 FILING DATE: March 29, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Krieger, Paul E.
 REGISTRATION NUMBER: 25,886
 REFERENCE/DOCKET NUMBER: 41986/1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 713-850-0909
 TELEFAX: 713-850-0165
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 233 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-695-692B-7

Query Match 83.8%; Score 1037; DB 4; Length 233;
 Best Local Similarity 83.3%; Pred. No. 3.5e-99;
 Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOGTALGNLQKIYYNEKAITENKESDDQFLENTLLFKGFTG 60
 Db 1 SEKSEINEKDLRKSELOGTALGNLQKIYYNEKAITENKESDDQFLENTLLFKGFTG 60
 QY 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQACAGTGNKTCMYGGVTLHDNNRLT 120
 Db 61 HSWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQACAGTGNKTCMYGGVTLHDNNRLT 120
 QY 121 EEKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVG 180
 Db 121 EEKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKVG 180
 QY 181 RGLIVFHTSTEPSVYDLFDAQGYPTLRIYRDNKTINSENHIALYLYTT 233
 Db 181 RGLIVFHTSTEPSVYDLFDAQGYPTLRIYRDNKTINSENHIALYLYTT 233

RESULT 16

US-08-486-099-113
 ; Sequence 113, Application US/08486099
 ; Patent No. 6013263
 ; GENERAL INFORMATION:
 ; APPLICANT: Bolognesi, Dani P.
 ; APPLICANT: Matthews, Thomas J.
 ; APPLICANT: Wild, Carl T.
 ; APPLICANT: Barney, Shawn O.
 ; APPLICANT: Lambert, Dennis M.
 ; APPLICANT: Petteway, Stephen R.
 ; APPLICANT: Langlois, Alphonse J.
 ; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
 ; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
 ; TITLE OF INVENTION: B VIRUS TRANSMISSION
 ; NUMBER OF SEQUENCES: 209
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA

ZIP: 10036-2711
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741/8864
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-486-099-113

Query Match 83.8%; Score 1037; DB 3; Length 257;
Best Local Similarity 83.3%; Pred. No. 4.1e-99;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESDDQFLENTLLPKGFTTG 60
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESDDQFLENTLLPKGFTTG 84
QY 61 HPWYNDLLVLDGSKDATNKYKGVVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIDYKGVKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENHLIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQQGYSTNLLRIYRDNKTINSENHDIYLYTS 257

RESULT 17
US-08-360-107A-123
Sequence 123, Application US/08360107A
Patent No. 6017536
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741/8864
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-360-107A-123

Query Match 83.8%; Score 1037; DB 3; Length 257;
Best Local Similarity 83.3%; Pred. No. 4.1e-99;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESDDQFLENTLLPKGFTTG 60
DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAKTENKESDDQFLENTLLPKGFTTG 84
QY 61 HPWYNDLLVLDGSKDATNKYKGVVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIDYKGVKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENHLIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQQGYSTNLLRIYRDNKTINSENHDIYLYTS 257

RESULT 18
US-08-484-223B-113
Sequence 113, Application US/08484223B
Patent No. 6020459
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 245
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

```
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/484,223B
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7872-029
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 113:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 257 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ US-08-484-223B-113

Query Match 83.8%; Score 1037; DB 3; Length 257;
Best Local Similarity 83.3%; Pred. No. 4.1e-99;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKXSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLPKGFFTG 60
Db 25 SEKSEINEKDLRKXSELOGTALGNLKOIYYNEKAKTENKESHDOFLOHTILFKGFFD 84
QY 61 HPWYNDLLVDLGSKDANKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGQTTVPIDKVKTSKKEVTVOELDQARHYLHGFGYNSDSFGKVKQ 180
Db 145 EEKVPINLWIDGQNTVPLETVTKTKKNVTVOELDQARRYLQEKYLYNSDVFQKVKQ 204
QY 181 RGLIVFHSSEGSVSYDLFDQAQGYPTDLLRIYRDNKTINSENHLIALYLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFQAQGYSNLRLIYRDNKTINSENHIDIYLYTS 257

RESULT 19
US-08-919-597-113
; Sequence 113, Application US/08919597
; Patent No. 6054265
; GENERAL INFORMATION:
; APPLICANT: Biocognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/919,597
; FILING DATE:

/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/470,896
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A.
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7872-020
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 113:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 257 amino acids
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: unknown
/ MOLECULE TYPE: protein
/ US-08-919-597-113

Query Match 83.8%; Score 1037; DB 3; Length 257;
Best Local Similarity 83.3%; Pred. No. 4.1e-99;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKXSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLPKGFFTG 60
Db 25 SEKSEINEKDLRKXSELOGTALGNLKOIYYNEKAKTENKESHDOFLOHTILFKGFFD 84
QY 61 HPWYNDLLVDLGSKDANKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDIYDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGQTTVPIDKVKTSKKEVTVOELDQARHYLHGFGYNSDSFGKVKQ 180
Db 145 EEKVPINLWIDGQNTVPLETVTKTKKNVTVOELDQARRYLQEKYLYNSDVFQKVKQ 204
QY 181 RGLIVFHSSEGSVSYDLFDQAQGYPTDLLRIYRDNKTINSENHLIALYLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFQAQGYSNLRLIYRDNKTINSENHIDIYLYTS 257

RESULT 20
US-08-475-668A-113
; Sequence 113, Application US/08475668A
; Patent No. 6060065
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,668A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
```

REFERENCE/DOCKET NUMBER: 7872-026
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-475-668A-113

Query Match 83.8%; Score 1037; DB 3; Length 257;
Best Local Similarity 83.3%; Pred. No. 4.1e-99;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSELGQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSELGQTALGNLKOIYYNEKAITENKESHDOFLOHTILFKGFFTD 84
QY 61 HPWYNDLLVDSKDATNKYKGGKVDLYGAYGYQCAGGTGPNKTACMYGGVTLHNNRLT 120
DB 85 HSWYNDLLVDFSKDIDVTKYKGGKVDLYGAYGYQCAGGTGPNKTACMYGGVTLHNNRLT 144
QY 121 EEKKVPINLWIDGKQTPIDKVTSKKEVTVOELDQARHYLHGKFLYNSDGFSGKVQ 180
DB 145 EEKKVPINLWIDGKQTPLETVTKNKNVTVOELDQARHYLHGKFLYNSDGFSGKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNDLFGAQGYNTLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 21
US-08-485-551A-113
Sequence 113, Application US/0848551A
Patent No. 6068973
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090

TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-551A-113

Query Match 83.8%; Score 1037; DB 3; Length 257;
Best Local Similarity 83.3%; Pred. No. 4.1e-99;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSELGQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSELGQTALGNLKOIYYNEKAITENKESHDOFLOHTILFKGFFTD 84
QY 61 HPWYNDLLVDSKDATNKYKGGKVDLYGAYGYQCAGGTGPNKTACMYGGVTLHNNRLT 120
DB 85 HSWYNDLLVDFSKDIDVTKYKGGKVDLYGAYGYQCAGGTGPNKTACMYGGVTLHNNRLT 144
QY 121 EEKKVPINLWIDGKQTPIDKVTSKKEVTVOELDQARHYLHGKFLYNSDGFSGKVQ 180
DB 145 EEKKVPINLWIDGKQTPLETVTKNKNVTVOELDQARHYLHGKFLYNSDGFSGKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNKTINSENHIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNDLFGAQGYNTLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 22
US-08-471-913A-113
Sequence 113, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,913A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-030
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 113:

```
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; MOLECULE TYPE: protein
; US-08-471-913A-113

Query Match      83.8%; Score 1037; DB 3; Length 257;
Best Local Similarity 83.3%; Pred. No. 4.1e-99;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEETNEKDLRKSELOQTALGNLQKIIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEETNEKDLRKSELOQTALGNLQKIIYYNEKAKTENKESHDFLOHTILLFKGFFTD 84
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDI VDKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWLDGKQNTVPLETVKTKNKNVTVOELDLQARHYLQEKYLNYSVDFGKVQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHLIALYLYTT 233
Db 145 EEKVPINLWLDGKQNTVPLETVKTKNKNVTVOELDLQARHYLQEKYLNYSVDFGKVQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHLIALYLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQGYSTLLRIYRDNKTINSENHDIYLYTS 257

RESULT 24
US-08-474-349A-113
; Sequence 113, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
; TITLE OF INVENTION: VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-471-913A-113

Query Match      83.8%; Score 1037; DB 3; Length 257;
Best Local Similarity 83.3%; Pred. No. 4.1e-99;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEETNEKDLRKSELOQTALGNLQKIIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEETNEKDLRKSELOQTALGNLQKIIYYNEKAKTENKESHDFLOHTILLFKGFFTD 84
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDI VDKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWLDGKQNTVPLETVKTKNKNVTVOELDLQARHYLQEKYLNYSVDFGKVQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHLIALYLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQGYSTLLRIYRDNKTINSENHDIYLYTS 257

RESULT 23
US-08-485-264A-113
; Sequence 113, Application US/08485264A
; Patent No. 6228983
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,264A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
```

US-08-474-349A-113

Query Match
Best Local Similarity 83.8%; Score 1037; DB 4; Length 257;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKXSELOQTALGNLKQIYYNEKAITENKESDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKXSELOQTALGNLKQIYYNEKAITENKESHDFLOHTILFKGFFTD 84

QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTACMGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFPSKDIYDKYKGGKVDLYGAYGYOCAGGTPNKTACMGVTLHDNNRLT 144

QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGYNSDSFGGKVQ 180
DB 145 BEKKVPINLWLDGKQNTVPLETVKTNKKNVTVOELDLQARYLQKYNLYNSDVDFGKVQ 204

QY 181 RGLIVFHSSSEGSVSYDLFDAQOQYPTLLRIYRDNKTINSENHLIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFQAQOQYNTLLRIYRDNKTINSENMHIDIYLYTS 257

RESULT 25
US-08-470-896-113
; Sequence 113, Application US/08470896
; Patent No. 6479055
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; NUMBER OF SEQUENCES: 273
; TITLE OF INVENTION: TRANSMISSION
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/470,896
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-470-896-113

Query Match 83.8%; Score 1037; DB 4; Length 257;

Best Local Similarity 83.3%; Pred. No. 4.1e-99;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKXSELOQTALGNLKQIYYNEKAITENKESDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKXSELOQTALGNLKQIYYNEKAITENKESHDFLOHTILFKGFFTD 84

QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTACMGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFPSKDIYDKYKGGKVDLYGAYGYOCAGGTPNKTACMGVTLHDNNRLT 144

QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGYNSDSFGGKVQ 180
DB 145 BEKKVPINLWLDGKQNTVPLETVKTNKKNVTVOELDLQARYLQKYNLYNSDVDFGKVQ 204

QY 181 RGLIVFHSSSEGSVSYDLFDAQOQYPTLLRIYRDNKTINSENHLIALYLYTT 233
DB 205 RGLIVFHTSTEPSVNYDLFQAQOQYNTLLRIYRDNKTINSENMHIDIYLYTS 257

RESULT 26
US-08-485-546A-113
; Sequence 113, Application US/08485546A
; Patent No. 6518013
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION NUMBER: US/08/485,546A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-485-546A-113

Query Match 83.8%; Score 1037; DB 4; Length 257;
Best Local Similarity 83.3%; Pred. No. 4.1e-99;
Matches 194; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSELOQTALGNLKIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSELOQTALGNLKIYYNEKAITENKESHQDQLQHTILFKGFFTD 84
QY 61 HPWYNDLLVDLGSKDATNKKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIIVDKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 145 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 204
QY 181 RGLIVHSSSGSTVSYDLFDAQGQVPTLLRIYRDNKTINSENHLIALYLYTT 233
DB 205 RGLIVHSTEPSVNYDLFGAQQYSNTLLRIYRDNKTINSENMHIDIYLYTS 257

RESULT 27
US-08-446-918A-4
; Sequence 4, Application US/08446918A
; Patent No. 5705151
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmali, Robyn E.
; TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/446,918A
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 552
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-29
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-918A-4

Query Match 83.4%; Score 1033; DB 1; Length 233;
Best Local Similarity 83.2%; Pred. No. 9.1e-99;
Matches 193; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKKSELOQTALGNLKIYYNEKAITENKESDDQFLENTLLFKGFFTG 61
DB 2 EKSEINEKDLRKKSELOQTALGNLKIYYNEKAITENKESHQDQLQHTILFKGFFTDH 61
QY 62 PWYNDLLVDLGSKDATNKKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
DB 62 SWYNDLLVDFDSKDIIVDKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 181
DB 122 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 181
QY 181 RGLIVHSSSGSTVSYDLFDAQGQVPTLLRIYRDNKTINSENHLIALYLYTT 233
DB 205 RGLIVHSTEPSVNYDLFGAQQYSNTLLRIYRDNKTINSENMHIDIYLYTS 233

QY 182 GLIVFHSSSGSTVSYDLFDAQGQVPTLLRIYRDNKTINSENHLIALYLYTT 233
DB 182 GLIVHSTEPSVNYDLFGAQQYSNTLLRIYRDNKTINSENMHIDIYLYTS 233

RESULT 28
US-08-580-806-4
; Sequence 4, Application US/08580806
; Patent No. 5935568
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmali, Robyn E.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/08/580,806
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Concell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-29-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-580-806-4

Query Match 83.4%; Score 1033; DB 2; Length 233;
Best Local Similarity 83.2%; Pred. No. 9.1e-99;
Matches 193; Conservative 16; Mismatches 23; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKKSELOQTALGNLKIYYNEKAITENKESDDQFLENTLLFKGFFTG 61
DB 2 EKSEINEKDLRKKSELOQTALGNLKIYYNEKAITENKESHQDQLQHTILFKGFFTDH 61
QY 62 PWYNDLLVDLGSKDATNKKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
DB 62 SWYNDLLVDFDSKDIIVDKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 181
DB 122 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 181
QY 182 GLIVFHSSSGSTVSYDLFDAQGQVPTLLRIYRDNKTINSENHLIALYLYTT 233
DB 182 GLIVHSTEPSVNYDLFGAQQYSNTLLRIYRDNKTINSENMHIDIYLYTS 233

RESULT 29
US-08-896-933-23
; Sequence 23, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.

; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 ; FILE REFERENCE: 09629/005002
 ; CURRENT APPLICATION NUMBER: US/08/896,933
 ; CURRENT FILING DATE: 1997-07-18
 ; EARLIER FILING DATE: 1994-06-02
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO 23
 ; LENGTH: 232
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-08-896-933-23

Query Match 82.2%; Score 1017.5; DB 3; Length 232;
 Best Local Similarity 82.8%; Pred. No. 3.6e-97;
 Matches 193; Conservative 15; Mismatches 24; Indels 1; Gaps 1;
 QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFTG 60
 DB 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDOFL-HTILFKGFTD 59
 QY 61 HPWYNDLLVLDGSKDATNKYKGVVDLYGAYGYOCAGTGNKTKACMYGGVTLHDNNRLT 120
 DB 60 HSWYNDLLVDFSKDIYDKYKGVVDLYGAYGYOCAGTGNKTKACMYGGVTLHDNNRLT 119
 QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 DB 120 EEKVPINLWLDGKQNTVPLETKNKVTVQELDPQARRYLQEKYNLYNSDVDFGKVQ 179
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNTKINSENHLIYLYTT 233
 DB 180 RGLIVFHTSTEPSVNYDLFGAQGYSTNLLRIYRDNTKINSENHDIYLYTS 232

RESULT 30
 US-09-314-235-23
 ; Sequence 23, Application US/09314235
 ; Patent No. 6338845
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 ; FILE REFERENCE: 09629/005004
 ; CURRENT APPLICATION NUMBER: US/09/314,235
 ; CURRENT FILING DATE: 1999-05-18
 ; EARLIER FILING DATE: 1997-07-18
 ; EARLIER FILING DATE: 1997-07-18
 ; EARLIER FILING DATE: 1994-06-02
 ; EARLIER FILING DATE: 1992-06-01
 ; EARLIER FILING DATE: 1991-01-17
 ; EARLIER FILING DATE: 1991-01-17
 ; EARLIER FILING DATE: 1990-01-17
 ; EARLIER FILING DATE: 1989-10-03
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO 23
 ; LENGTH: 232
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 US-09-314-235-23

Query Match 82.2%; Score 1017.5; DB 4; Length 232;
 Best Local Similarity 82.8%; Pred. No. 3.6e-97;
 Matches 193; Conservative 15; Mismatches 24; Indels 1; Gaps 1;
 QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFTG 60

DB 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDOFL-HTILFKGFTD 59
 QY 61 HPWYNDLLVLDGSKDATNKYKGVVDLYGAYGYOCAGTGNKTKACMYGGVTLHDNNRLT 120
 DB 60 HSWYNDLLVDFSKDIYDKYKGVVDLYGAYGYOCAGTGNKTKACMYGGVTLHDNNRLT 119
 QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 DB 120 EEKVPINLWLDGKQNTVPLETKNKVTVQELDPQARRYLQEKYNLYNSDVDFGKVQ 179
 QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTLLRIYRDNTKINSENHLIYLYTT 233
 DB 180 RGLIVFHTSTEPSVNYDLFGAQGYSTNLLRIYRDNTKINSENHDIYLYTS 232

RESULT 31
 US-09-144-776B-2
 ; Sequence 2, Application US/09144776B
 ; Patent No. 6399332
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert A. Olson
 ; Sina Bavari
 ; TITLE OF INVENTION: Bacterial Superantigen
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Charles H. Harris
 ; STREET: US Army MRC -504 Scott Street
 ; MCMR-JA (Charles H. Harris-Patent
 ; Acty)
 ; CITY: FORT DETRICK
 ; STATE: MARYLAND
 ; COUNTRY: USA
 ; ZIP: 21702-5012
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh 7.5
 ; SOFTWARE: Microsoft Word 6.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/144,776B
 ; FILING DATE: 01-Sep-1998
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/882,431
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Charles H. Harris
 ; REGISTRATION NUMBER: 34,616
 ; REFERENCE/DOCKET NUMBER: <Unknown>
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 619-2065
 ; TELEFAX: (301) 619-7714
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 257
 ; TYPE: Amino Acid
 ; STRANDEDNESS: Unknown
 ; TOPOLOGY: Unknown
 ; MOLECULE TYPE: Peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-144-776B-2

Query Match 81.9%; Score 1014; DB 4; Length 257;
 Best Local Similarity 82.0%; Pred. No. 9.7e-97;
 Matches 191; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
 QY 1 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDOFLNTLLFKGFTG 60
 DB 25 SEKSEINEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDOFL-HTILFKGFTD 84
 QY 61 HPWYNDLLVLDGSKDATNKYKGVVDLYGAYGYOCAGTGNKTKACMYGGVTLHDNNRLT 120

Db 85 HSWNDLLVRFDSKDIVDKYKGGKVDLYGAYAGYQACAGTGNKTACMYGGVTLHNNRLT 144
 QY 121 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 Db 145 EKKVPINLWIDGKQNTVPLETKNKNVTVOELDLQARRYLQEKYINLYNSDVPDGRKVQ 204
 QY 181 RGLIVFHSSSEGSTVSYDLFDAQGYPTDLLRIYRDNKTINSENHIALYLYTT 233
 Db 205 RGLIVFHTSTEPSVNYDLFCAQGYSNLTLRIYRDNKTINSENHIDIVLYTS 257

RESULT 32
 US-09-144-776B-4
 ; Sequence 4, Application US/09144776B
 ; Patent No. 6399332
 ; GENERAL INFORMATION:
 ; APPLICANT: Robert G. Ulrich,
 ; Mark A. Olson
 ; Sina Bavari
 ; TITLE OF INVENTION: Bacterial Superantigen
 ; Vaccines
 ; NUMBER OF SEQUENCES: 25
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Charles H. Harris
 ; STREET: US Army MRC - 504 Scott Street
 ; MCMR-JA (Charles H. Harris-Patent
 ; Atty)
 ; CITY: FORT DETRICK
 ; STATE: MARYLAND
 ; COUNTRY: USA
 ; ZIP: 21702-5012
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: Apple Macintosh
 ; OPERATING SYSTEM: Macintosh 7.5
 ; SOFTWARE: Microsoft Word 6.0
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/144,776B
 ; FILING DATE: 01-Sep-1998
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/882,431
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Charles H. Harris
 ; REGISTRATION NUMBER: 34,616
 ; REFERENCE/DOCKET NUMBER: <Unknown>
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 619-2065
 ; TELEFAX: (301) 619-7714
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 233
 ; TYPE: Amino Acid
 ; STRANDEDNESS: Unknown
 ; TOPOLOGY: Unknown
 ; MOLECULE TYPE: Peptide
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Query Match 81.6%; Score 1010; DB 4; Length 233;
 Best Local Similarity 81.9%; Pred. No. 2.2e-96;
 Matches 190; Conservative 16; Mismatches 26; Indels 0; Gaps 0;
 QY 2 EKSEINEKDKRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFETGH 61
 Db 2 EKSEINEKDKRKSELOGTALGNLKOIYYNEKAITENKESDDQFQHTLLFKGFETDH 61
 QY 62 PWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQACAGTGNKTACMYGGVTLHNNRLTE 121
 Db 62 SWYNDLLVRFDSKDIVDKYKGGKVDLYGAYAGYQACAGTGNKTACMYGGVTLHNNRLTE 121

QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 181
 Db 122 EKKVPINLWIDGKQNTVPLETKNKNVTVOELDLQARRYLQEKYINLYNSDVPDGRKVQ 181
 QY 182 GLIVFHSSSEGSTVSYDLFDAQGYPTDLLRIYRDNKTINSENHIALYLYTT 233
 Db 182 GLIVFHTSTEPSVNYDLFCAQGYSNLTLRIYRDNKTINSENHIDIVLYTS 233

RESULT 33
 US-08-896-933-25
 ; Sequence 25, Application US/08896933
 ; Patent No. 6221351
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 ; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
 ; FILE REFERENCE: 09629/005002
 ; CURRENT APPLICATION NUMBER: US/08/896,933
 ; CURRENT FILING DATE: 1997-07-18
 ; EARLIER APPLICATION NUMBER: 08/252,978
 ; EARLIER FILING DATE: 1994-06-02
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 25
 ; LENGTH: 228
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 ; US-08-896-933-25

Query Match 53.1%; Score 657; DB 3; Length 228;
 Best Local Similarity 56.0%; Pred. No. 6.5e-60;
 Matches 126; Conservative 31; Mismatches 68; Indels 0; Gaps 0;
 QY 7 INEKDLRKSELOGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFETGHVND 66
 Db 2 VKEKELHKSELSSTALNNMKSHYADKNPIIGENKSTGQDQFLENTLLYKFFTDLINFED 61
 QY 67 LLVDLGSKDATNKYKGGKVDLYGAYGYQACAGTGNKTACMYGGVTLHNNRLTEKKVP 126
 Db 62 LLINPNSKEMAQHPKSNVDVPIRYSINCYGGIDTACTYGGVTPHEGKNLKKERKIP 121
 QY 127 INLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQGLIVF 186
 Db 122 INLWINGVQKEVSLDKVQTDKNKNVTVOELDLQARRYLQKDLKLYNNDTLGGKIQRKIEF 181
 QY 187 HSSEGSTVSYDLFDAQGYPTDLLRIYRDNKTINSENHIALYLY 231
 Db 182 DSSDGSKVSVDLFDVKGDFPEKRLIYSDNKTLSLSTLHIDIVLY 226

RESULT 34
 US-09-314-235-25
 ; Sequence 25, Application US/09314235
 ; Patent No. 633845
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 ; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
 ; FILE REFERENCE: 09629/005004
 ; CURRENT APPLICATION NUMBER: US/09/314,235
 ; CURRENT FILING DATE: 1999-05-18
 ; EARLIER APPLICATION NUMBER: 08/896,933
 ; EARLIER FILING DATE: 1997-07-18
 ; EARLIER APPLICATION NUMBER: 08/252,978
 ; EARLIER FILING DATE: 1994-06-02
 ; EARLIER APPLICATION NUMBER: 07/891,718
 ; EARLIER FILING DATE: 1992-06-01
 ; EARLIER APPLICATION NUMBER: US91/00342
 ; EARLIER FILING DATE: 1991-01-17
 ; EARLIER APPLICATION NUMBER: 07/466,577
 ; EARLIER FILING DATE: 1990-01-17
 ; EARLIER APPLICATION NUMBER: 07/416,530

```

; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-314-235-25

Query Match          53.1%; Score 657; DB 4; Length 228;
Best Local Similarity 56.0%; Pred. No. 6.5e-60;
Matches 126; Conservative 31; Mismatches 68; Indels 0; Gaps 0

QY      7 INEKDLRKSELOCTALGNLAKIYYINEKAITENKESDDQFLENTLLFKGFTTGHFWYND 66
DB      2 VKEELHKKSEUSSTALNNKHGSADKNPIIGENKSTGDFLENTLLYKXFFTDLINFED 61

QY      67 LLVDLGSKDATNKYKGVKVDLYGAVYQVQAGGTPNKATACWGGVTLHNNRLITBEKVP 126
DB      62 LLINFNSKEMAHQHFKSXNDVVPYRYSINCYGGBIDATCTAGYGVTPHESGNLKRKKIP 121

QY      127 INLWDIGQTTVPIDKVTSKVETVQBELDLQARHYLHGKFGLYNSDSFGGKVQGLIVF 186
DB      122 INLWINGQKVEVSLDKVQTDKKNYTVQBELDAQARYLQKDLKYNNDTLGGKIQRKIEF 181

QY      187 HSESGTSYDLDFAQGVQVPTDLLRIYRDKNKTINSENHLIALYLY 231
DB      182 DSDSGSKSYDLFDVKGDFPKQLRIYSDNKTISTEHLHIDIVLY 226

RESULT 35
US-09-144-776B-19
; Sequence 19, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
;           Mark A. Olson
;           Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
;           Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MMC - 504 Scott Street
;           MCWR-JA (Charles H. Harris-Patent
;           Att'y)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid

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Db 1 SHDQFLQHTLFGFTTSHWYNDLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGGTN 60

QY 103 KTACMYGGVTLHDNNRLTEKK 124

Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 37

US-08-446-918A-2
; Sequence 2, Application US/08446918A
; Patent No. 5705151
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmslie, Robyn E.
; TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,918A
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 552
; ATTORNEY/AGENT INFORMATION:
; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-29
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-918A-2

Query Match 24.5%; Score 303.5; DB 1; Length 255;
Best Local Similarity 34.6%; Pred. No. 2.7e-23;
Matches 84; Conservative 44; Mismatches 96; Indels 19; Gaps 8;
QY 2 EKSEINEKDLRKXSELQGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
Db 17 ESQDPKPEDELHKSKFTG-LMENKVKLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 74
QY 62 PWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQC-----AGGTENKTACMYGGV 111
Db 75 GNYDNVRVEFNKDLADKYDKYDVFEGANYYYQCYFSKKTNDINSHQTDKRTKCMYGGV 134
QY 112 TLHDNNRLTEKKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYN 171
Db 135 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVNKKLYE 192
QY 172 SDSFGKVGQRLIVFHSSEGSTVSIDLFDAGQGYPD--TLRIYRDNKTINSENHLIALY 229
Db 193 FNN--SPYETGYIKFIENENS-FWYDMMPAGDKFDQSKYLMYNDNKNVDSKDVKIEVY 249
QY 230 LYT 232
Db 250 LTT 252

RESULT 39

US-08-896-933-28
; Sequence 28, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,

RESULT 38
US-08-580-806-2
; Sequence 2, Application US/08580806
; Patent No. 5935568
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmslie, Robyn E.
; APPLICANT: Potter, Terence A.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,806
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-29-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 255 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-580-806-2

Query Match 24.5%; Score 303.5; DB 2; Length 255;
Best Local Similarity 34.6%; Pred. No. 2.7e-23;
Matches 84; Conservative 44; Mismatches 96; Indels 19; Gaps 8;
QY 2 EKSEINEKDLRKXSELQGTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
Db 17 ESQDPKPEDELHKSKFTG-LMENKVKLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 74
QY 62 PWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQC-----AGGTENKTACMYGGV 111
Db 75 GNYDNVRVEFNKDLADKYDKYDVFEGANYYYQCYFSKKTNDINSHQTDKRTKCMYGGV 134
QY 112 TLHDNNRLTEKKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYN 171
Db 135 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHYLVNKKLYE 192
QY 172 SDSFGKVGQRLIVFHSSEGSTVSIDLFDAGQGYPD--TLRIYRDNKTINSENHLIALY 229
Db 193 FNN--SPYETGYIKFIENENS-FWYDMMPAGDKFDQSKYLMYNDNKNVDSKDVKIEVY 249
QY 230 LYT 232
Db 250 LTT 252

RESULT 39

US-08-896-933-28
; Sequence 28, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,

;; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS

;; FILE REFERENCE: 09629/005002
;; CURRENT APPLICATION NUMBER: US/08/896,933
;; CURRENT FILING DATE: 1997-07-18
;; EARLIER APPLICATION NUMBER: 08/252,978
;; EARLIER FILING DATE: 1994-06-02
;; NUMBER OF SEQ ID NOS: 34
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 28
;; LENGTH: 238
;; TYPE: PRT
;; ORGANISM: Staphylococcus aureus
US-08-896-933-28

Query Match 24.1%; Score 298.5; DB 3; Length 238;

Best Local Similarity 34.2%; Pred. No. 7.9e-23;

Matches 80; Conservative 45; Mismatches 90; Indels 19; Gaps 9;

QY 11 DLKKSSELTGALGNLKOIYYNEKAITENK-ESDDQFLENTLLFKGFTGHPWYNDLLV 69

Db 9 ELHKSSEFTGT-MGNMK--YLDDHYVSATKWSVDKFLAHLDIYNSDKLKNYDKVKT 65

QY 70 DLGSDATNKYKGVKVDLYGAYGYQC-----AGGTPNKTCACMYGGVTLHDNNRLTEE 122

Db 66 ELLNEDLAKKYKDEVDVYGSNYVNCYFSSKDNVGVKVTGKTCMYGGITKEGHNFDNG 125

QY 123 --KKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180

Db 126 NLQNVLIIRY-ENKRNITISFE-VQTDKKSVTQAELDKARNFLINKNLYEFNS--SPYE 181

QY 181 RGLIVFHSSEGSTSVSYDLFDAQGQYPD--TLRIYRNKNTINSENHLIALYLT 232

Db 182 TGYIKFIENNGNTFWYDLMPAPGDKFDQSKYLMYNDNKIVDSKVKIEVHLTT 235

QY 181 RGLIVFHSSEGSTSVSYDLFDAQGQYPD--TLRIYRNKNTINSENHLIALYLT 232

Db 182 TGYIKFIENNGNTFWYDLMPAPGDKFDQSKYLMYNDNKIVDSKVKIEVHLTT 235

QY 181 RGLIVFHSSEGSTSVSYDLFDAQGQYPD--TLRIYRNKNTINSENHLIALYLT 232

Db 182 TGYIKFIENNGNTFWYDLMPAPGDKFDQSKYLMYNDNKIVDSKVKIEVHLTT 235

RESULT 40

US-09-314-235-28

;; Sequence 28, Application US/09314235

;; Patent No. 6338845

;; GENERAL INFORMATION:

;; APPLICANT: Terman, David S.

;; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,

;; FILE REFERENCE: 09629/005004

;; CURRENT APPLICATION NUMBER: US/09/314,235

;; CURRENT FILING DATE: 1999-05-18

;; EARLIER APPLICATION NUMBER: 08/896,933

;; EARLIER FILING DATE: 1997-07-18

;; EARLIER APPLICATION NUMBER: 08/252,978

;; EARLIER FILING DATE: 1994-06-02

;; EARLIER APPLICATION NUMBER: 07/891,718

;; EARLIER FILING DATE: 1992-06-01

;; EARLIER APPLICATION NUMBER: US91/00342

;; EARLIER FILING DATE: 1991-01-17

;; EARLIER APPLICATION NUMBER: 07/466,577

;; EARLIER FILING DATE: 1990-01-17

;; EARLIER APPLICATION NUMBER: 07/416,530

;; EARLIER FILING DATE: 1989-10-03

;; NUMBER OF SEQ ID NOS: 34

;; SOFTWARE: FastSeq for Windows Version 3.0

;; SEQ ID NO 28

;; LENGTH: 238

;; TYPE: PRT

;; ORGANISM: Staphylococcus aureus

US-09-314-235-28

Query Match 24.1%; Score 298.5; DB 4; Length 238;

Best Local Similarity 34.2%; Pred. No. 7.9e-23;

Matches 80; Conservative 45; Mismatches 90; Indels 19; Gaps 9;

QY 11 DLKKSSELTGALGNLKOIYYNEKAITENK-ESDDQFLENTLLFKGFTGHPWYNDLLV 69

Db 9 ELHKSSEFTGT-MGNMK--YLDDHYVSATKWSVDKFLAHLDIYNSDKLKNYDKVKT 65

QY 11 DLKKSSELTGALGNLKOIYYNEKAITENK-ESDDQFLENTLLFKGFTGHPWYNDLLV 69

Db 9 ELHKSSEFTGT-MGNMK--YLDDHYVSATKWSVDKFLAHLDIYNSDKLKNYDKVKT 65

QY 11 DLKKSSELTGALGNLKOIYYNEKAITENK-ESDDQFLENTLLFKGFTGHPWYNDLLV 69

Db 9 ELHKSSEFTGT-MGNMK--YLDDHYVSATKWSVDKFLAHLDIYNSDKLKNYDKVKT 65

QY 11 DLKKSSELTGALGNLKOIYYNEKAITENK-ESDDQFLENTLLFKGFTGHPWYNDLLV 69

Db 9 ELHKSSEFTGT-MGNMK--YLDDHYVSATKWSVDKFLAHLDIYNSDKLKNYDKVKT 65

QY 70 DLGSDATNKYKGVKVDLYGAYGYQC-----AGGTPNKTCACMYGGVTLHDNNRLTEE 122

Db 66 ELLNEDLAKKYKDEVDVYGSNYVNCYFSSKDNVGVKVTGKTCMYGGITKEGHNFDNG 125

QY 123 --KKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180

Db 126 NLQNVLIIRY-ENKRNITISFE-VQTDKKSVTQAELDKARNFLINKNLYEFNS--SPYE 181

QY 181 RGLIVFHSSEGSTSVSYDLFDAQGQYPD--TLRIYRNKNTINSENHLIALYLT 232

Db 182 TGYIKFIENNGNTFWYDLMPAPGDKFDQSKYLMYNDNKIVDSKVKIEVHLTT 235

QY 181 RGLIVFHSSEGSTSVSYDLFDAQGQYPD--TLRIYRNKNTINSENHLIALYLT 232

Db 182 TGYIKFIENNGNTFWYDLMPAPGDKFDQSKYLMYNDNKIVDSKVKIEVHLTT 235

RESULT 41

US-08-896-933-26

;; Sequence 26, Application US/08896933

;; Patent No. 6221351

;; GENERAL INFORMATION:

;; APPLICANT: Terman, David S.

;; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,

;; FILE REFERENCE: 09629/005002

;; CURRENT APPLICATION NUMBER: US/08/896,933

;; CURRENT FILING DATE: 1997-07-18

;; EARLIER APPLICATION NUMBER: 08/252,978

;; EARLIER FILING DATE: 1994-06-02

;; NUMBER OF SEQ ID NOS: 34

;; SOFTWARE: FastSeq for Windows Version 3.0

;; SEQ ID NO 26

;; LENGTH: 239

;; TYPE: PRT

;; ORGANISM: Staphylococcus aureus

US-08-896-933-26

Query Match 23.9%; Score 296.5; DB 3; Length 239;

Best Local Similarity 34.9%; Pred. No. 1.3e-22;

Matches 84; Conservative 42; Mismatches 96; Indels 19; Gaps 8;

QY 2 EKSEINEKDLRKSELOQTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTTGH 61

Db 1 ESQDPKPDDELHKSSKFTG-LMENMKVLYDDNHVSAI-NVKSIDQFLYDLIYSIKDTKL 58

QY 62 PWYNDLLVGLSGDATNKYKGVKVDLYGAYGYQC-----AGGTPNKTCACMYGGV 111

Db 59 GYNDVRFVFNKDLADKYKDVDFGANYYYCYFVKSTNTDINSHQTDKRTCMYGGV 118

QY 112 TLHDNNRLTEEEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGFLYN 171

Db 119 TEHNGNQLDKYRSLTVRVPEDGK-NLLSPD-VQTNKKKVTQAELDYLTRHYLVKNKKLYE 176

QY 172 SDSFGGKVQGLIVFHSSEGSTSVSYDLFDAQGQYPD--TLRIYRNKNTINSENHLIALY 229

Db 177 FNN--SPYETGYIKFIENENS-FWYDLMPAPGDKFDQSKYLMYNDNKIVDSKVKIEV 233

QY 230 L 230

Db 234 L 234

QY 230 L 230

Db 234 L 234

QY 230 L 230

Db 234 L 234

QY 230 L 230

Db 234 L 234

QY 230 L 230

Db 234 L 234

QY 230 L 230

Db 234 L 234

QY 230 L 230

Db 234 L 234

QY 230 L 230

Db 234 L 234

QY 230 L 230

Db 234 L 234

QY 230 L 230

Db 234 L 234

QY 230 L 230

Db 234 L 234

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; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-314-235-26

Query Match      23.9%; Score 296.5; DB 4; Length 239;
Best Local Similarity 34.9%; Pred. No. 1.3e-22;
Matches 84; Conservative 42; Mismatches 96; Indels 19; Gaps 8;

QY 2 EKSEINEKDLRKSELOCTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTTG 61
DB 1 ESQDPKPDELHKSCKFTG-LMENMKVLYDDNHVSAI-NVKS:DDQFLYFDLIYSIKDTKL 58

QY 62 PWNDDLVLGSKDATNKYKGVLDLYGAYGYQC-----AGGTPNKTCMYGGV 111
DB 59 GNYDNVRVEFKNLDADKYKVDVFGANYYYQCYFSKKTNDINSHQTDKRTCMYGGV 118

QY 112 TLHNNRLTEEEKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYN 171
DB 119 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDLVTRHYLVKNKKLYE 176

QY 172 SDSFGGKVQRLIVFHSSEGSTSVSYDLFDAQGQYDP--TLRIYRDNKTINSNHLIAL 229
DB 177 FNN--SPYETGYIKFIENENS-FWYDMPAPGKDFQSKYLMYNDNKNWVDKVKIEV 233

QY 230 L 230
DB 234 L 234

RESULT 43
US-09-414-276-8
; Sequence 8, Application US/09414276
; Patent No. 6392121
; GENERAL INFORMATION:
; APPLICANT: Mason, Hugh
; APPLICANT: Palmer, Kenneth
; APPLICANT: Hefferon, Kathleen
; APPLICANT: Mor, Tsafir
; APPLICANT: Artzen, Charles
; TITLE OF INVENTION: Gemini Virus Vectors for Gene Expression in Plants
; FILE REFERENCE: 4868/84453
; CURRENT APPLICATION NUMBER: US/09/414,276
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 266
; TYPE: PRT
; ORGANISM: bean yellow dwarf virus
US-09-414-276-8

Query Match      23.9%; Score 296.5; DB 4; Length 266;
Best Local Similarity 34.0%; Pred. No. 1.5e-22;
Matches 83; Conservative 45; Mismatches 97; Indels 19; Gaps 8;

QY 1 SEKSEINEKDLRKSELOCTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTTG 60
DB 27 AESQDPKPDELHKSCKFTG-LMENMKVLYDDNHVSAI-NVKS:DDQFLYFDLIYSIKDTK 84

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QY 61 HPWYNDDLVLGSKDATNKYKGVLDLYGAYGYQC-----AGGTPNKTCMYGG 110
DB 85 LGNYDNVRVEFKNLDADKYKVDVFGANYYYQCYFSKKTNDINSHQTDKRTCMYGG 144

QY 111 TLHNNRLTEEEKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLY 170
DB 145 VTEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDLVTRHYLVKNKKLY 202

QY 171 NSDSFGGKVQRLIVFHSSEGSTSVSYDLFDAQGQYDP--TLRIYRDNKTINSNHLIAL 228
DB 203 EFNN--SPYETGYIKFIENENS-FWYDMPAPGKDFQSKYLMYNDNKNWVDKVKIEV 259

QY 229 YLYT 232
DB 260 YLYT 263

RESULT 44
US-09-144-776B-6
; Sequence 6, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army WMC -504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-144-776B-6

Query Match      23.9%; Score 296.5; DB 4; Length 266;
Best Local Similarity 33.6%; Pred. No. 1.5e-22;
Matches 82; Conservative 46; Mismatches 97; Indels 19; Gaps 8;

QY 1 SEKSEINEKDLRKSELOCTALGNLKOIYYNEKAITENKESDDQFLENTLLFKGFTTG 60
DB 27 AESQDPKPDELHKSCKFTG-LMEDMKVLYDDNHVSAI-NVKS:DDQFLYFDLIYSIKDTK 84

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[illegible]

QY 61 HPWYNDLLVDLGSKDATNKYKGKKVDLYGAYYGQCAG-----TPNKTACMYGG 110

Db 85 LGYNDVRVEFKNLADKYKDYVDFGANAYYQCAFSKTKINDINSHQTDKRTCTMYGG 144
Qy 111 VTHDNNRLTEKKVPIVNLWDGQKQTVTPIDKVKTSKKEVTVQELDLQARHYLHGKFGLY 170
Db 145 VTEHNGQLDKYSITVRFEEDGK-NLLSPD-VOYNKKKVTQAEGLDYLTRHLYVKNKKLY 202
Qy 171 NSDSFGGKVGORGLIVFHSSSGSVSYDLFDQAQOYPD--TLRIYRDNKTINSENLHIAL 228
Db 203 EFN--SPYETGYIKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNKNWDSKDVKIEV 259
Qy 229 YLYT 232
Db 260 YLYT 263

RESULT 47
US-08-896-933-29
; Sequence 29, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-896-933-29

Query Match 23.0%; Score 284.5; DB 3; Length 221;
Best Local Similarity 35.1%; Pred. No. 2e-21;
Matches 79; Conservative 41; Mismatches 86; Indels 19; Gaps 10;
Qy 16 SELOGTAL-GNLKQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLG 72
Db 7 SOLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHDLIYN---VSGPNYDKLKTLEK 63
Qy 73 SKDATNKYKGGKVDLYGAYGYQC-AGGTPNKTKACMYGGVTLHDNNRLTEKKVPIVNLWI 131
Db 64 NQEMATLFDKKNVDIYGYEYVHLCYLCEAERSACIYGGVTNHEGHNLEIPKIVKVS 123
Qy 132 DGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQORGLIVFHSSEG 191
Db 124 DGIO-SLSFD-IEINKMVTQAEGLDYKVRKYLTDNKNQLYNGP--SKYETGYIKFIPKN 179
Qy 192 STVSVDLPD---AQGOYPTDLLRIYRDNKTINSENLHIALYLYT 232
Db 180 ESFWFDLPPEFTQSKY----LMYKDNELDNTSQTIEVLYT 220

RESULT 48
US-09-314-235-29
; Sequence 29, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02

; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-314-235-29

Query Match 23.0%; Score 284.5; DB 4; Length 221;
Best Local Similarity 35.1%; Pred. No. 2e-21;
Matches 79; Conservative 41; Mismatches 86; Indels 19; Gaps 10;
Qy 16 SELOGTAL-GNLKQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLG 72
Db 7 SOLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHDLIYN---VSGPNYDKLKTLEK 63
Qy 73 SKDATNKYKGGKVDLYGAYGYQC-AGGTPNKTKACMYGGVTLHDNNRLTEKKVPIVNLWI 131
Db 64 NQEMATLFDKKNVDIYGYEYVHLCYLCEAERSACIYGGVTNHEGHNLEIPKIVKVS 123
Qy 132 DGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQORGLIVFHSSEG 191
Db 124 DGIO-SLSFD-IEINKMVTQAEGLDYKVRKYLTDNKNQLYNGP--SKYETGYIKFIPKN 179
Qy 192 STVSVDLPD---AQGOYPTDLLRIYRDNKTINSENLHIALYLYT 232
Db 180 ESFWFDLPPEFTQSKY----LMYKDNELDNTSQTIEVLYT 220

RESULT 49
US-08-973-391C-13
; Sequence 13, Application US/08973391C
; Patent No. 6632441
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoehr, Jennifer
; APPLICANT: Ohlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973,391C
; CURRENT FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 13
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-973-391C-13

Query Match 22.8%; Score 282.5; DB 4; Length 251;
Best Local Similarity 33.8%; Pred. No. 3.9e-21;
Matches 80; Conservative 44; Mismatches 94; Indels 19; Gaps 10;
Qy 4 SBEINEKDLRKSELOGTAL-GNLKQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
Db 25 SEVFQAQDPDPSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHDLIYN---VS 81
Qy 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-AGGTPNKTKACMYGGVTLHDNNRL 119
Db 82 GPNYDKLKTLEKNQEMATLFDKKNVDIYGYEYVHLCYLCEAERSACIYGGVTNHEGHN 141

QY 120 TEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKV 179
Db 142 EIPKIVKVSIDGIQ-SLSFD-IEINKKXVTAQELDYKVKYLTNDKNQLYTNGP--SKY 197
QY 180 ORGLIVPHSSEGSTVSYDLFD----AQGVPTDLLRIYRDKNKTINSENLHIALYLT 232
Db 198 ETGYIKFIPKNKESFWDFPEFTQSKY----LMIYKDNETLDSNTSQIEVYLTT 250

RESULT 50

US-08-973-391C-14
; Sequence 14, Application US/08973391C
; Patent No. 6632441
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stroehr, Jennifer
; APPLICANT: Ohlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973,391C
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-973-391C-14

Query Match 22.6%; Score 279.5; DB 4; Length 221;
Best Local Similarity 34.7%; Pred. No. 6.6e-21;
Matches 78; Conservative 41; Mismatches 87; Indels 19; Gaps 10;
QY 16 SELOQTAL-GNLKQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFTGHPWYNDLVLG 72
Db 7 SOLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHLIYN---VSGPNYDKLTKELK 63
QY 73 SKDATNKYKGVLDYGVAYGYQC-AGGTPNKATACMYGGVTLHDNRLTEKKVPINLWI 131
Db 64 NQEMATLFDKKNVDIYGVYHLCYLVCENASACIYGGVTNHEGNHLEIPKIVKVS 123
QY 132 DGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQORGLIVPHSSEG 191
Db 124 DGIIQ-SLSFD-IEINKKXVTAQELDYKVKYLTNDKNQLYTNGP--SKYETGYIKFIPKNK 179
QY 192 STVSYDLFD----AQGVPTDLLRIYRDKNKTINSENLHIALYLT 232
Db 180 ESFWDFPEFTQSKY----LMIYKDNETLDSNTSQIEVYLTT 220

RESULT 51

US-09-144-776B-16
; Sequence 16, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army WMC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK

; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-144-776B-16

Query Match 22.4%; Score 277.5; DB 4; Length 251;
Best Local Similarity 33.3%; Pred. No. 1.3e-20;
Matches 79; Conservative 44; Mismatches 95; Indels 19; Gaps 10;
QY 4 SEINEKDLRKKSELOQTAL-GNLKQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFTG 60
Db 25 SQEFAQQDPDPSOLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHLIYN---VS 81
QY 61 HPWYNDLVLGSKDATNKYKGVLDYGVAYGYQC-AGGTPNKATACMYGGVTLHDNRL 119
Db 82 GPNYDKLTKELKQEMATLFDKKNVDIYGVYHLCYLVCENASACIYGGVTNHEGNHL 141
QY 120 TEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKV 179
Db 142 EIPKIVKVSIDGIQ-SLSFD-IEINKKXVTAQELDYKVKYLTNDKNQLYTNGP--SKY 197
QY 180 ORGLIVPHSSEGSTVSYDLFD----AQGVPTDLLRIYRDKNKTINSENLHIALYLT 232
Db 198 ETGYIKFIPKNKESFWDFPEFTQSKY----LMIYKDNETLDSNTSQIEVYLTT 250

RESULT 52

US-08-896-933-27
; Sequence 27, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-27

Thu Aug 12 13:48:06 2004

Query Match 21.9%; Score 271.5; DB 3; Length 239;
 Best Local Similarity 31.8%; Pred. No. 4.9e-20;
 Matches 77; Conservative 47; Mismatches 101; Indels 17; Gaps 8;

QY 2 EKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
 DB 1 ESQPDPTDELHAKSKFTG-LMENMKVLDHVVYSATKVK-SVDKFLAHLDIYNSDKKL 58

QY 62 PWNDDLVDLGSKDATNKYKGGVDLYGAYGYQC-----AGGTENKTACMYGGVTLH 114
 DB 59 KNYDKVKTLELNEGAKKYKDEVDVGSNYVNCYFSSKDNVKGKVTGCKTOMYGGITKH 118

QY 115 DNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNS 172
 DB 119 EGNHFDNGNLQNLIRVY-ENKRNITISFE-VQTDKKSVAQELDIKARNFLINKNLYEF 176

QY 173 DSFGGKVGRLIVFHSSEGSTVSYDLFDAQOQYD--TLRIYRDNKTINSENHLIALYL 230
 DB 177 NS--SPYETGYIKFIENNGNTFTWDLMPAPGDKRFDQSKYLMYNDNKTVDKSKVLEVHL 234

QY 231 YT 232
 DB 235 TT 236

RESULT 54
 US-08-896-933-21
 ; Sequence 21, Application US/08896933
 ; Patent No. 6221351
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 ; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
 ; FILE REFERENCE: 09629/005002
 ; CURRENT APPLICATION NUMBER: US/08/896,933
 ; CURRENT FILING DATE: 1997-07-18
 ; EARLIER APPLICATION NUMBER: 08/252,978
 ; EARLIER FILING DATE: 1994-06-02
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 21
 ; LENGTH: 239
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 ; US-08-896-933-21

Query Match 21.4%; Score 264.5; DB 3; Length 239;
 Best Local Similarity 32.7%; Pred. No. 2.6e-19;
 Matches 80; Conservative 47; Mismatches 95; Indels 23; Gaps 11;

QY 2 EKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
 DB 1 ESQPDKPEDELHAKSKFTG-LMENVK-VLYNDHVSAINVKSINEFFDLIYLSIKDTKL 58

QY 62 PWNDDLVDLGSKDATNKYKGGVDLYGAYGYQC-----AGGTENKTACMYGG 110
 DB 59 GNYDNVRVFEKKNKLDADKYKDYVDVFGANY-YCYFSKTKTNIDSHENTKRTK-CMYGG 116

QY 111 VTLHNNRLTEE-EKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFG 169
 DB 117 VTEHGNQLDKYRSITVRVFDGK-NLLSPD-VQTNKKKVTAGOLDLTHYLKVKKL 174

QY 170 YNSDGFSGKVGRLIVFHSSEGSTVSYDLFDAQOQYD--TLRIYRDNKTINSENHLIA 227
 DB 175 YEFNN--SPYETGYIKFIENENS-FWYDMWPAKGNKFPQSKYLMYNNNDKWDKSKVKIE 231

QY 228 LYLTT 232
 DB 232 VYLTT 236

RESULT 55
 US-09-314-235-21
 ; Sequence 21, Application US/09314235
 ; Patent No. 6338845
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 ; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
 ; FILE REFERENCE: 09629/005004
 ; CURRENT APPLICATION NUMBER: US/09/314,235
 ; CURRENT FILING DATE: 1999-05-18
 ; EARLIER APPLICATION NUMBER: 08/896,933
 ; EARLIER FILING DATE: 1997-07-18
 ; EARLIER APPLICATION NUMBER: 08/252,978
 ; EARLIER FILING DATE: 1994-06-02
 ; EARLIER APPLICATION NUMBER: 07/891,718
 ; EARLIER FILING DATE: 1992-06-01
 ; EARLIER APPLICATION NUMBER: US91/00342

Query Match 21.9%; Score 271.5; DB 4; Length 239;
 Best Local Similarity 31.8%; Pred. No. 4.9e-20;
 Matches 77; Conservative 47; Mismatches 101; Indels 17; Gaps 8;

QY 2 EKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
 DB 1 ESQPDPTDELHAKSKFTG-LMENMKVLDHVVYSATKVK-SVDKFLAHLDIYNSDKKL 58

QY 62 PWNDDLVDLGSKDATNKYKGGVDLYGAYGYQC-----AGGTENKTACMYGGVTLH 114
 DB 59 KNYDKVKTLELNEGAKKYKDEVDVGSNYVNCYFSSKDNVKGKVTGCKTOMYGGITKH 118

QY 115 DNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNS 172
 DB 119 EGNHFDNGNLQNLIRVY-ENKRNITISFE-VQTDKKSVAQELDIKARNFLINKNLYEF 176

QY 173 DSFGGKVGRLIVFHSSEGSTVSYDLFDAQOQYD--TLRIYRDNKTINSENHLIALYL 230
 DB 177 NS--SPYETGYIKFIENNGNTFTWDLMPAPGDKRFDQSKYLMYNDNKTVDKSKVLEVHL 234

QY 231 YT 232
 DB 235 TT 236

RESULT 53
 US-09-314-235-27
 ; Sequence 27, Application US/09314235
 ; Patent No. 6338845
 ; GENERAL INFORMATION:
 ; APPLICANT: Terman, David S.
 ; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
 ; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
 ; FILE REFERENCE: 09629/005004
 ; CURRENT APPLICATION NUMBER: US/09/314,235
 ; CURRENT FILING DATE: 1999-05-18
 ; EARLIER APPLICATION NUMBER: 08/896,933
 ; EARLIER FILING DATE: 1997-07-18
 ; EARLIER APPLICATION NUMBER: 08/252,978
 ; EARLIER FILING DATE: 1994-06-02
 ; EARLIER APPLICATION NUMBER: 07/891,718
 ; EARLIER FILING DATE: 1992-06-01
 ; EARLIER APPLICATION NUMBER: US91/00342
 ; EARLIER FILING DATE: 1991-01-17
 ; EARLIER APPLICATION NUMBER: 07/466,577
 ; EARLIER FILING DATE: 1990-01-17
 ; EARLIER APPLICATION NUMBER: 07/416,530
 ; EARLIER FILING DATE: 1989-10-03
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 27
 ; LENGTH: 239
 ; TYPE: PRT
 ; ORGANISM: Staphylococcus aureus
 ; US-09-314-235-27

Query Match 21.9%; Score 271.5; DB 4; Length 239;
 Best Local Similarity 31.8%; Pred. No. 4.9e-20;
 Matches 77; Conservative 47; Mismatches 101; Indels 17; Gaps 8;

QY 2 EKSEINEKDLRKSELOGTALGNLQIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
 DB 1 ESQPDPTDELHAKSKFTG-LMENMKVLDHVVYSATKVK-SVDKFLAHLDIYNSDKKL 58

QY 62 PWNDDLVDLGSKDATNKYKGGVDLYGAYGYQC-----AGGTENKTACMYGGVTLH 114
 DB 59 KNYDKVKTLELNEGAKKYKDEVDVGSNYVNCYFSSKDNVKGKVTGCKTOMYGGITKH 118

QY 115 DNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNS 172
 DB 119 EGNHFDNGNLQNLIRVY-ENKRNITISFE-VQTDKKSVAQELDIKARNFLINKNLYEF 176

EARLIER FILING DATE: 1991-01-17
EARLIER APPLICATION NUMBER: 07/466,577
EARLIER FILING DATE: 1990-01-17
EARLIER APPLICATION NUMBER: 07/416,530
EARLIER FILING DATE: 1989-10-03
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 21
LENGTH: 239
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-314-235-21

Query Match 21.4%; Score 264.5; DB 4; Length 239;
Best Local Similarity 32.7%; Pred. No. 2.6e-19;
Matches 80; Conservative 47; Mismatches 95; Indels 23; Gaps 11;
QY 2 EKSEINEKDLKKSELOQTALCNLKQIYYNEKAITENKESDDOFLNTLLFKGFTTG 61
Db 1 ESQDPKPELHKSSKFTG-LMENMK-VLYNNDHVSAINVKSINEFFDLIYLSIKDTKL 58
QY 62 PWYNDLLVGLGSKDAATNKYKGVLDLYGAYGYQC-----AGGTPNKTCMYGG 110
Db 59 GYNDVVRVEFKNLDADKYKDVDFGANY-YQYFSSKKTNNIDSHENTKRT-CMYGG 116
QY 111 VTLHNNRLTE-EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFG 169
Db 117 VTEHGNQLDKYRSITVRVFDGK-NLLSPD-VQTNKKKVTAEQLDYLTRHYLVKNKKL 174
QY 170 YNSDSFGGKVGRLVFSHSEGSTVSYDLFDAQQGYPD--TLRLRYRNKNTINSENHLIA 227
Db 175 YEFNN--SPYETGYIKFIENENS-FWYDMMPAPGKFPQSKYLMYNNDRKVDKVKIE 231
QY 228 LYLTT 232
Db 232 VYLTT 236

RESULT 56
US-09-144-776B-14
Sequence 14, Application US/09144776B
Patent No. 6399332
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MRC -504 Scott Street
MCWR-JA (Charles H. Harris-Patent
Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616

REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 266
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-144-776B-14

Query Match 21.2%; Score 262.5; DB 4; Length 266;
Best Local Similarity 30.9%; Pred. No. 4.9e-19;
Matches 75; Conservative 49; Mismatches 102; Indels 17; Gaps 8;
QY 1 SEKSEINEKDLKKSELOQTALCNLKQIYYNEKAITENKESDDOFLNTLLFKGFTTG 60
Db 27 AESQDPDPPELHKASKFTG-LMENMKVLYDDHVTVSATKVK-SVDKFRADHLLYINISDKK 84
QY 61 HPWYNDLLVGLGSKDAATNKYKGVLDLYGAYGYQC-----AGGTPNKTCMYGGVTL 113
Db 85 LKAYDKVKTELLNEGLAKYKDEVDVYGSNYYVNCYFSSKDNVGVYTGKTCMYGGITK 144
QY 114 HDNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFG 171
Db 145 HEGNHFDNGNLQNLVIRVY-ENKENTISFE-VQTDKKSVTAEQLDIKARNFLNKKNL 202
QY 172 SDSFGGKVGRLVFSHSEGSTVSYDLFDAQQGYPD--TLRLRYRNKNTINSENHLIALY 229
Db 203 FNS--SPYETGYIKFIENNGNTFWYDMMPAPGKFPQSKYLMYNDKNTVDSKSVKIEVH 260
QY 230 LYT 232
Db 261 LTT 263

RESULT 57
US-08-896-933-20
Sequence 20, Application US/08896933
Patent No. 6221351
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/005002
CURRENT APPLICATION NUMBER: US/08/896,933
CURRENT FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 220
TYPE: PRT
ORGANISM: Streptococcus pyogenes
US-08-896-933-20

Query Match 18.9%; Score 234; DB 3; Length 220;
Best Local Similarity 30.3%; Pred. No. 3.3e-16;
Matches 69; Conservative 41; Mismatches 96; Indels 22; Gaps 9;
QY 14 KKSELOQTALCNLKQIYYNEKA--IT-ENKESDDOFLNTLLFKGFTTGHPWYNDLLVD 70
Db 5 KPSQLQESNLVKTFFKIYIFFMVTLVTHENVKSVQLLSHDLIYN---VSGNVDKLTKE 61
QY 71 LQSKDATNKYKGVLDLYGAYGYQC-AGGTPNKTCMYGGVTLHDNNRLTEKKVPINL 129
Db 62 LKNQEMATLFDKNVDIYGVYHLCYLCEAERSACLYGGVTNHEGNHLEIPKKIVKV 121
QY 130 WIDGKQT-TVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVGRLVIFHS 188

STREET: US Army MRMC -504 Scott Street
MCMR-JA (Charles H. Harris-Patent
Att'y)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144, 776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 82
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-144-776B-18

Query Match 17.4%; Score 215; DB 4; Le
Best Local Similarity 51.2%; Pred. No. 7.2e-15;
Matches 41; Conservative 11; Mismatches 28;
QY 45 DQFLENTLLKGFTHGHPWVNDLLVGLGSKDATNKYKGVK
DB 3 DQFLENTLLYKFFTDINFDLLINFSKEMAHQFASKV
QY 105 ACTYGGVTLHDNNRLTEKK 124
DB 63 ACTYGGVTPHEGNLKSREK 82

RESULT 60
US-08-220-378-1
Sequence 1, Application US/08220378
Patent No. 5545716
GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Ant
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:

DB 122 SIDGIQSLSPDIEQIKNG-----NCSRISTYVRKYLTDNKNQLYTNGP--SKYETGYIKFIP 175
QY 189 SEGSTVSVDLFD-----AQGVPTDLLRIYRDNKTINSENHLIALYLT 232
DB 176 KNKESFWDFPPEFTQSKY----LMIYKDNETLDSNTSQIEVYLTT 219

RESULT 58
US-09-314-235-20
Sequence 20, Application US/09314235
Patent No. 6338845
GENERAL INFORMATION:
APPLICANT: Terman, David S.
TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
FILE REFERENCE: 09629/005004
CURRENT APPLICATION NUMBER: US/09/314,235
CURRENT FILING DATE: 1999-05-18
EARLIER APPLICATION NUMBER: 08/896,933
EARLIER FILING DATE: 1997-07-18
EARLIER APPLICATION NUMBER: 08/252,978
EARLIER FILING DATE: 1994-06-02
EARLIER APPLICATION NUMBER: 07/891,718
EARLIER FILING DATE: 1992-06-01
EARLIER APPLICATION NUMBER: US91/00342
EARLIER FILING DATE: 1991-01-17
EARLIER APPLICATION NUMBER: 07/466,577
EARLIER FILING DATE: 1990-01-17
EARLIER APPLICATION NUMBER: 07/416,530
EARLIER FILING DATE: 1989-10-03
NUMBER OF SEQ IDS: 34
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 220
TYPE: PRT
ORGANISM: Streptococcus pyogenes
US-09-314-235-20

Query Match 18.9%; Score 234; DB 4; Length 220;
Best Local Similarity 30.3%; Pred. No. 3.3e-16;
Matches 69; Conservative 41; Mismatches 96; Indels 22; Gaps 9;
QY 14 KSELGDTALGNLKOIYYNEKA--IT-ENKESDDQFLENTLLFKGFFTGHPWYNDLLVD 70
DB 5 KPSQLQRSNLVTKFKIYIFMVRVTLTHENVKSVQQLSHDLIYN--VSGNYDKLKE 61
QY 71 LGSKDATNKYKGVKVDLYGAYYQOC--AGTGNKTKACTMGVTLHDNNRLTEKKVPINL 129
DB 62 LKQEMATLFDKXNDVIYGVYVHLCVLCENASACLYGGVTHHEGNHLEIPKKIWKV 121
QY 130 WIDGKQT-TVPIDKVTSKVEVTQVBLDQARHYLHGKGLYNSDSFGKVQGLIVFHS 188
DB 122 SIDGIQSLSPDIEQIKNG-----NCSRISTYVRKYLTDNKNQLYTNGP--SKYETGYIKFIP 175
QY 189 SEGSTVSVDLFD-----AQGVPTDLLRIYRDNKTINSENHLIALYLT 232
DB 176 KNKESFWDFPPEFTQSKY----LMIYKDNETLDSNTSQIEVYLTT 219

RESULT 59
US-09-144-776B-18
Sequence 18, Application US/09144776B
Patent No. 639332
GENERAL INFORMATION:
APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:

```
/ APPLICATION NUMBER: US/08/220,378
/ FILING DATE:
/ CLASSIFICATION: 530
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/941,497
/ FILING DATE: 08-SEP-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Saliwanchik, David R.
/ REGISTRATION NUMBER: 31,794
/ REFERENCE/DOCKET NUMBER: UFI26.C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 904-375-8100
/ TELEFAX: 904-372-5800
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 45 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-220-378-1

Query Match 17.2%; Score 213; DB 1; Length 45;
Best Local Similarity 95.6%; Pred. No. 4.9e-15;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKXSELQGTALGNLKOIYYNEKAITENKESDD 45
Db 1 SEKSEINEKDLRKXSELQGTALGNLKOIYYNEKAITENKESHD 45

RESULT 61
US-08-696-012-1
; Sequence 1, Application US/08696012
; Patent No. 5859207
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; APPLICANT: Griggs, Nathan D.
; TITLE OF INVENTION: Superantigen Agonist and Antagonist
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,012
; FILING DATE: 12-AUG-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/220,378
; FILING DATE: 29-MAR-1994
; APPLICATION NUMBER: US 07/941,497
; FILING DATE: 08-SEP-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UFI26.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
```

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/ LENGTH: 45 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-08-696-012-1

Query Match 17.2%; Score 213; DB 2; Length 45;
Best Local Similarity 95.8%; Pred. No. 4.9e-15;
Matches 43; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKXSELQGTALGNLKOIYYNEKAITENKESDD 45
Db 1 SEKSEINEKDLRKXSELQGTALGNLKOIYYNEKAITENKESHD 45

RESULT 62
US-08-896-933-30
; Sequence 30, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 30
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-896-933-30

Query Match 14.0%; Score 173.5; DB 3; Length 208;
Best Local Similarity 26.7%; Pred. No. 5.4e-10;
Matches 59; Conservative 41; Mismatches 76; Indels 45; Gaps 11;

QY 40 NKESDDQFLENTLLFKGFETGHPW-YNDLLVDLGSKDA-----TNKYKGK----- 83
Db 1 DSKKDISNVKSDLLYA--YTITPYDYKCRVNFSTHTLNTIDTQYRGDKYVVISSEMSYE 58
QY 84 -----KVDLYGAYGYQCAGGTPNKTACWYGVTLDNNRLTEKKVFPINLWIDGK 134
Db 59 ASQKFKRDDHVDVFGLFYILNSHTG-----EYIGGITPAQNNKYNH--KLLGNLFISGE 111
QY 135 QTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDS--FGKVQKGLIVFHSSEGS 192
Db 112 SQONLNKKIILEKDIVTFOEIDFKIRKYLMDNYKIYDATSPYVSGRIEIG-----TKDGK 166
QY 193 TVSYDLFDA--QGYPTDTLLRIYRDNKTINSENL-HIALYL 230
Db 167 HEQIDLDFSPNEGTRSDIFAK-YKDNRIINMKNFSEFDIYL 206

RESULT 63
US-09-314-235-30
; Sequence 30, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
```


EARLIER APPLICATION NUMBER: US91/00342
EARLIER FILING DATE: 1991-01-17
EARLIER APPLICATION NUMBER: 07/466, 577
EARLIER FILING DATE: 1990-01-17
EARLIER APPLICATION NUMBER: 07/416, 530
EARLIER FILING DATE: 1989-10-03
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 34
LENGTH: 27
TYPE: PRT
ORGANISM: Staphylococcal
US-09-314-235-34

Query Match 10.4%; Score 131; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 7e-07;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKXSELQGTALGNLK 27
Db 1 SEKSEINEKDLRKXSELQGTALGNLK 27

RESULT 67
US-08-220-378-2
Sequence 2, Application US/08220378
Patent No. 5545716
GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,378
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UFI26.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-220-378-2

Query Match 10.4%; Score 129; DB 1; Length 28;
Best Local Similarity 78.6%; Pred. No. 1.2e-06;
Matches 22; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 39 ENKESDDQLENTLLPKGFTHPWYND 66
Db 1 ENKESDDQFLQHTILPKGFTHDSWYND 28

RESULT 68
US-08-696-012-2
Sequence 2, Application US/08696012
Patent No. 5859207
GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,012
FILING DATE: 12-AUG-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/220,378
FILING DATE: 29-MAR-1994
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08-SEP-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UFI26.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-696-012-2

Query Match 10.4%; Score 129; DB 2; Length 28;
Best Local Similarity 78.6%; Pred. No. 1.2e-06;
Matches 22; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 39 ENKESDDQLENTLLPKGFTHPWYND 66
Db 1 ENKESDDQFLQHTILPKGFTHDSWYND 28

RESULT 69
US-08-838-413A-22
Sequence 2, Application US/08838413A
Patent No. 6075119
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: PEPTIDES USEFUL FOR
TITLE OF INVENTION: REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME
NUMBER OF SEQUENCES: 31

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,413A
FILING DATE: 07-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MORRIS, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2016-4010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)751-6849
TELEFAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 24
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE: PEPTIDE
US-08-838-413A-22

Query Match 10.3%; Score 127; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 1.5e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 147 KKEVTVOELDQARHYLHGKFGY 170
Db 1 KKEVTVOELDQARHYLHGKFGY 24

RESULT 70
US-08-220-378-5
Sequence 5, Application US/08220378
Patent No. 5545716
GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,378
FILING DATE: 12-AUG-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 29-MAR-1994
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08-SEP-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF126.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,413A
FILING DATE: 07-APR-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: MORRIS, MARY J.
REGISTRATION NUMBER: 34,398
REFERENCE/DOCKET NUMBER: 2016-4010
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)751-6849
TELEFAX: (212)751-6849
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 24
TYPE: AMINO ACID
STRANDEDNESS: UNKNOWN
TOPOLOGY: UNKNOWN
MOLECULE TYPE: PEPTIDE
US-08-838-413A-22

Query Match 10.2%; Score 126; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 102 NKTACMYGGVTLHDNNELTEKK 124
Db 1 NKTACMYGGVTLHDNNELTEKK 23

RESULT 71
US-08-696-012-5
Sequence 5, Application US/08696012
Patent No. 5859207
GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/696,012
FILING DATE: 12-AUG-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 29-MAR-1994
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08-SEP-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF126.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 23 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
```



```
; MOLECULE TYPE: peptide
US-08-696-012-5
Query Match      10.2%; Score 126; DB 2; Length 23;
Best Local Similarity 100.0%; Pred. No. 1.8e-06;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      102 NKTACMYGGVTLHDNNRLTEKK 124
Db      1 NKTACMYGGVTLHDNNRLTEKK 23

RESULT 72
US-08-220-378-6
; Sequence 6, Application US/08220378
; Patent No. 5545716
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; APPLICANT: Griggs, Nathan D.
; TITLE OF INVENTION: Superantigen Agonist and Antagonist
; NUMBER OF SEQUENCES: 10
; TITLE OF INVENTION: Peptides
; ADDRESS: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,012
; FILING DATE: 12-AUG-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/220,378
; FILING DATE: 29-MAR-1994
; APPLICATION NUMBER: US 07/941,497
; FILING DATE: 08-SEP-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF126.C1
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-696-012-6
Query Match      10.0%; Score 124; DB 2; Length 29;
Best Local Similarity 78.6%; Pred. No. 4.1e-06;
Matches 22; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy      121 EEKVPINLWDGKQTTVPIDKVKTSK 148
Db      1 EEKVPINLWDGKQNTVPLETVKTKK 28

RESULT 74
US-09-144-776B-24
; Sequence 24, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
```

MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/144,776B
FILING DATE: 01-Sep-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/882,431
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 79
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-144-776B-24

Query Match 9.8%; Score 121; DB 4; Length 79;
Best Local Similarity 34.6%; Pred. No. 3.6e-05;
Matches 27; Conservative 15; Mismatches 32; Indels 4; Gaps 2;
QY 43 SDQFLFNTLLFGFTGHPWYNDLVLSGSDATNKYKGVLDLYGAYGYQC-AGGTP 101
Db 1 SVQQLSHDIYN--VSGPNYDKLTELKNOEMATLFRKKNVDIYGVYHLCLVCNA 57
QY 102 NKTACMYGGVTLHDNNRL 119
Db 58 ERSACIYGGVTNHEGNHL 75

RESULT 75
US-08-220-378-4
Sequence 4, Application US/08220378
Patent No. 5545716
GENERAL INFORMATION:
APPLICANT: Johnson, Howard M.
APPLICANT: Pontzer, Carol H.
APPLICANT: Griggs, Nathan D.
TITLE OF INVENTION: Superantigen Agonist and Antagonist
TITLE OF INVENTION: Peptides
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/220,378
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/941,497
FILING DATE: 08-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.

REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF126.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 22 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-220-378-4
Query Match 9.7%; Score 120; DB 1; Length 22;
Best Local Similarity 95.5%; Pred. No. 7.1e-06;
Matches 21; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 83 KKVLDLYGAYGYQCAGGTPNKT 104
Db 1 KVKDYGAYGYQCAGGTPNKT 22
Search completed: August 12, 2004, 13:34:05
Job time : 11.2135 secs